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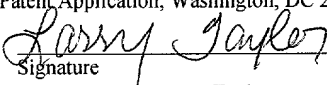
BGI-130CP

Page 1 of 2

Customer No. 000959  
Case Docket No. BGI-130CP

Assistant Commissioner for Patents  
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Sir:

Transmitted herewith for filing is the patent application of:

**Inventors:** Markus Pompejus *et al.*

**For:** "*Corynebacterium Glutamicum Genes Encoding Proteins Involved in DNA Replication, Protein Synthesis, and Pathogenesis*"

Enclosed are:

- ☒ 63 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 6 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 14 pages of Table 4;
- ☒ 93 pages of Appendix A;
- ☒ 30 pages of Appendix B;
- ☒ 631 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney; and
- ☒ A pre-paid acknowledgment postcard.

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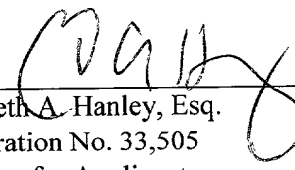
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**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS, AND  
PATHOGENESIS**

5    **Related Applications**

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/144448, filed July 16, 1999, and U.S. Provisional Patent Application Serial No. 60/149402, filed August 17, 1999. The entire contents of both of the above referenced applications is hereby incorporated by this reference.

10

**Background of the Invention**

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals',  
15 include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful  
20 organism for this purpose is *Corynebacterium glutamicum*, a gram positive bacterium lacking human pathogenicity. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

25

**Summary of the Invention**

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C.*  
30 *glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as DNA replication, ribosome and pathogenesis (RRP) proteins.

*C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in  
35 industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The RRP nucleic acid molecules of the invention, therefore, can be used to

identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the RRP nucleic acids of the invention, or modification of the sequence of the RRP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The RRP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The RRP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The RRP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function in *C. glutamicum* involved in the replication of DNA, in protein synthesis, or of contributing to the pathogenicity of the microorganism. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an RRP protein of the invention may affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For

example, by improving the rate at which DNA replication occurs (*e.g.*, by optimizing the activity of one or more DNA polymerase, or by improving the rate at which the topoisomerases or helicases of the invention unwind DNA) it may be possible to increase the rate of cell division, which in turn increases the number of viable fine-chemical-producing *C. glutamicum* cells present in large-scale culture settings.

5 Similarly, by improving the rate at which mRNA is translated to protein (*e.g.*, by optimizing the activity of one or more of the ribosomal proteins) it may be possible to increase the number of proteins in the cell which participate in the synthesis of one or more desired fine chemicals, or in an overall increase in the rate of cell division (due to

10 increased growth and metabolism), both of which should lead to increased production of one or more fine chemicals from large-scale fermentor cultures of these microorganisms. Alterations in the DNA replication proteins of the invention may also permit increased fidelity in the replicative process, thereby increasing the genetic stability and viability of the microorganism and lessening the chance that another

15 engineered mutation improving fine chemical production from the microorganism will not be inadvertently mutagenized by error-prone replication. The RRP proteins of the invention involved in pathogenesis are themselves fine chemicals; by increasing the number or by engineering the corresponding genes such that the expression of these proteins is removed from cellular repression pathways, or by mutagenizing the proteins

20 such that feedback regulatory regions are removed, it may be possible to increase the yield, production, and/or efficiency of production of these proteins from large-scale fermentor culture of organisms containing such mutations.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as RRP proteins, which are capable of, for example, performing a

25 function in *C. glutamicum* involved in the replication of DNA, in protein synthesis, or of contributing to the pathogenicity of the microorganism. Nucleic acid molecules encoding an RRP protein are referred to herein as RRP nucleic acid molecules. In a preferred embodiment, an RRP protein participates in *C. glutamicum* DNA replication, ribosome function, or in the pathogenesis of the organism, or possesses a *C. glutamicum*

30 enzymatic or proteolytic activity. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an RRP protein or biologically active portions thereof, as well as nucleic acid fragments

35 suitable as primers or hybridization probes for the detection or amplification of RRP-encoding nucleic acids (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in

Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred RRP proteins of the present invention also preferably possess at least one of the RRP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an RRP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the replication of DNA, in protein synthesis, or in the pathogenicity of the microorganism. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an RRP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or may contribute to the pathogenicity of the microorganism, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More

preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* RRP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which  
5 such vectors have been introduced. In one embodiment, such a host cell is used to produce an RRP protein by culturing the host cell in a suitable medium. The RRP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an RRP gene has been introduced or altered. In one  
10 embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated RRP sequence as a transgene. In another embodiment, an endogenous RRP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered RRP gene. In another embodiment, an endogenous or  
15 introduced RRP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional RRP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an RRP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the RRP gene is  
20 modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

25 In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

30 Still another aspect of the invention pertains to an isolated RRP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated RRP protein or portion thereof can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or may contribute to the pathogenicity of the microorganism. In another preferred embodiment, the isolated RRP  
35 protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in

the replication of *C. glutamicum* DNA, to participate in *C. glutamicum* protein synthesis, or may contribute to the pathogenicity of the microorganism.

The invention also provides an isolated preparation of an RRP protein. In preferred embodiments, the RRP protein comprises an amino acid sequence of

5 Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about

10 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated RRP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the replication of *C. glutamicum* DNA, to participate in *C. glutamicum* protein synthesis, or may contribute to the

15 pathogenicity of the microorganism, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated RRP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more

20 preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of RRP proteins also have one or more of the RRP bioactivities described herein.

The RRP polypeptide, or a biologically active portion thereof, can be operatively

25 linked to a non-RRP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the RRP protein alone. In other preferred embodiments, this fusion protein participates in the replication of *C. glutamicum* DNA, participates in *C. glutamicum* protein synthesis, or contributes to the pathogenicity of the microorganism. In particularly preferred embodiments, integration

30 of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an RRP protein, either by interacting with the protein itself or a substrate or binding partner of the RRP protein, or by modulating the transcription or

35 translation of an RRP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the

expression of an RRP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an RRP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates RRP protein activity or RRP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* processes involved in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of the microorganism. The agent which modulates RRP protein activity can be an agent which stimulates RRP protein activity or RRP nucleic acid expression. Examples of agents which stimulate RRP protein activity or RRP nucleic acid expression include small molecules, active RRP proteins, and nucleic acids encoding RRP proteins that have been introduced into the cell. Examples of agents which inhibit RRP activity or expression include small molecules and antisense RRP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant RRP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

#### **Detailed Description of the Invention**

The present invention provides RRP nucleic acid and protein molecules which are involved in *C. glutamicum* DNA replication, protein synthesis, or pathogenesis. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (e.g., where increased activity of a ribosome permits increased production of fine chemical

biosynthetic proteins, which may result in increased yields, production, or efficiency of production of one or more fine chemicals from the modified *C. glutamicum*), or may have an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of the activity or number of copies of a *C. glutamicum* DNA synthesis protein results in an increase in the rate of *C. glutamicum* cell division, resulting in greater numbers of viable cells in culture, which in turn permits increased production in a large-scale culture setting). Aspects of the invention are further explicated below.

## 10 I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), toxins, and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

### A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in



proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3<sup>rd</sup> edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids - technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E. (1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of  $\alpha$ -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and

resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain  $\beta$ -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase.

- 5 Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction  
10 catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine  
15 from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

- Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3<sup>rd</sup> ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted  
20 amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways,  
25 see Stryer, L. Biochemistry, 3<sup>rd</sup> ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

#### *B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses*

- 30 Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of  
35 metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications

of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins  
5 may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such  
10 molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999)  
15 Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

20 Thiamin (vitamin B<sub>1</sub>) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B<sub>2</sub>) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B<sub>6</sub>' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-  
25 5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- $\beta$ -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of  $\beta$ -alanine and pantoic acid. The  
30 enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to  $\beta$ -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of  
35 panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B<sub>5</sub>), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the  $\alpha$ -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B<sub>12</sub>) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B<sub>12</sub> is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B<sub>6</sub>, pantothenate, and biotin. Only Vitamin B<sub>12</sub> is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

### *C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses*

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA

synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

- 5        Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the
- 10    development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine,
- 15    folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide
- 20    metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

- The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides",
- 25    Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from
- 30    ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell.
- 35    Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction

reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

5 *D. Trehalose Metabolism and Uses*

Trehalose consists of two glucose molecules, bound in  $\alpha$ ,  $\alpha$ -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

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II. Activities of the Genes of the Invention

In order for a population of a particular type of bacterial cells to survive in an environment, at least three activities are necessary. First, the cells must be able to divide efficiently, such that the population is at least maintained, if not increased. Second, the cells must be able to efficiently express those genes encoding proteins necessary for normal cellular functioning. Finally, the cells must be able to influence their interaction with the surrounding environment, either by adaptation to the prevailing environmental conditions, by physical movement to preferred surroundings, or by directly altering the surrounding environment such that their own viability is improved. Critical processes involved in each of the aforementioned activities include replication of the bacterial genome, the action of the ribosome in protein synthesis, and anticellular or cell lytic activities (such as those involved in the pathogenesis of an organism).

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*A. DNA Replication*

In order for a cell (*e.g.*, a bacterial cell) to divide to form viable progeny cells, the cellular genome must be replicated. This is a multistep process, in which the tightly packaged DNA must first be locally freed from topological constraints, the two strands of the double helix must be unwound, a DNA polymerase must synthesize a new strand of DNA complementary to one of the original strands, and both the old and the new strands must be repackaged. Each of these steps is described in greater detail in the following section (see, *e.g.*, Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York, and references therein; and

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Griffiths, A.J.F. *et al.*, (1993) *An Introduction to Genetic Analysis*, 5<sup>th</sup> ed., Freeman: New York p. 304-332 and references therein).

The general structure of genomic DNA in bacterial cells has been characterized. Bacterial chromosomes are usually circular in nature, and bacterial cells may also  
5 contain one or more different types of plasmids (also circular pieces of DNA, although usually significantly smaller in size than the bacterial chromosome) which may be replicated and incorporated into the daughter cell simultaneously with the chromosome. Replication of either of these circular pieces of genetic information typically begins at a single designated origin of replication (*ori*). Replication of the DNA may then take place  
10 either in one direction around the circle (rolling circle replication) until the origin is again reached, or it may occur in both directions simultaneously ( $\theta$ -mechanism).

The *ori* site has a particular structure which permits the initiation of replication. First, the *ori* region typically contains multiple sequences which serve as binding sites for initiator proteins. The binding of the initiator proteins (*e.g.*, DnaA in *E. coli*) to these  
15 binding sites at the origin takes place in an ATP-dependent fashion. Upon ATP hydrolysis, the DNA bends around these DNA-associated molecules, and the two strands of DNA at the site separate, forming an open complex.

The molecule responsible for the actual synthesis of the new DNA molecule is a DNA polymerase. For replication purposes, the DNA polymerase utilized by the cell is  
20 the DNA polymerase III (Pol III) holoenzyme. This complex comprises 10 molecules, each of which has a different function in the complex. For example, the dimeric  $\gamma$  subunit acts to associate the  $\beta$  subunit with a primed DNA template in an ATP-dependent fashion. The  $\beta$  subunit is the 'processivity factor' – the portion of the holoenzyme which specifically associates with the DNA template and which permits the  
25 template to 'slide' along the DNA due to its ring-like structure. The  $\alpha$  subunit catalyzes the reaction which adds the new dNTP to the nascent nucleotide strand, and the  $\epsilon$  subunit contains the 3'-5' exonuclease activity.

A significant topological barrier to DNA synthesis exists due to the structure of a DNA molecule and to that of the bacterial chromosome. Not only must the double helix  
30 of the DNA molecule be split such that a single strand may be replicated, but this unwinding process results in increased positive supercoiling of the chromosome. Two types of enzymes permit these processes to occur despite the topological constraints: helicase unwinds the double helix in an ATP-dependent fashion, introducing positive supercoils into the bacterial chromosome. Gyrase introduces negative supercoils into  
35 the bacterial genome (in an ATP-dependent fashion), counteracting the positive supercoils introduced by the helicase. The result of their combined is a replication fork: a split between the two strands of DNA in which replication of each strand of the DNA

can occur. Single-stranded binding proteins (SSBs) bind to the unwound DNA molecules to prevent them from reassociating.

In order for Pol III to initiate DNA synthesis, it must have a sequence from which to prime synthesis. Primase (*E. coli* DnaG) synthesizes RNA primers as starting sequences for Pol III. The Pol III complex gamma subunit associates with the newly synthesized primers and subsequently associates with the dimeric beta Pol III subunits, initiating DNA synthesis. Replication of each strand takes place simultaneously, but because Pol III polymerizes dNTPs only in the 5'-3' direction, only one strand (the 3'-5' leading strand) can be continuously replicated. The other strand (the complementary lagging strand) is replicated in short fragments (Okazaki fragments), due to the lack of progressivity of the polymerase in this direction. These fragments are subsequently ligated by DNA ligase to form a single strand. Incorrectly added bases are excised by the 3'-5' exonuclease activity of Pol III and the nick sealed by DNA ligase.

Bacterial DNA replication is terminated at a site opposite to the origin at which terminator proteins bind. The association of these proteins with the DNA prevents the replication fork from progressing. The RNA primer used to initiate DNA synthesis is degraded by DNA polymerase I (Pol I) or ribonuclease H (RnaseH), and Pol I adds the appropriate dNTPs to the gap. Finally, DNA ligase seals the nicks. To achieve semiconservative replication, the two strands of the parental bacterial chromosome are separated by topoisomerases and are each paired with the complementary daughter strand.

### *B. Protein Synthesis*

Protein synthesis is a multistep process which converts mRNA to the corresponding polypeptide chain (see, *e.g.*, Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York, and references therein; and Griffiths, A.J.F. *et al.*, (1993) *An Introduction to Genetic Analysis*, 5<sup>th</sup> ed., Freeman: New York p. 391-398 and references therein). As the initiator codon (AUG, encoding methionine) first becomes accessible after being transcribed from the DNA by RNA polymerase, a translation initiation complex forms. This complex is comprised of the mRNA molecule itself, an initiation tRNA molecule (charged with methionine, corresponding to the first AUG codon of the mRNA molecule, and which has also been formylated to form the N-terminus of the nascent polypeptide), initiation factors, and the ribosome itself.

The bacterial ribosome (the 70S ribosome) contains two subunits. The first subunit is large (50S) while the second is small (30S). Each subunit contains a complex of RNA and protein molecules which assemble soon after or during their synthesis.



These complexes are globular in shape, and the large subunit contains a long channel through which it is believed that the nascent polypeptide chain leaves the ribosome. There are at least three known sites of activity in the bacterial ribosome: one to bind a charged tRNA (aminoacyl tRNA), one to bind a tRNA associated with the nascent polypeptide chain, and the third to expel the uncharged tRNA from the complex. Ribosomes may occur singly or in groups, termed 'polyribosomes' or 'polysomes'. These complexes are plentiful within the cell; one *E. coli* cell may contain as many as 15,000 ribosomes, constituting up to one quarter of the total biomass of the cell.

- Upon the binding of the initiator tRNA<sup>met</sup> in complex with the initiation factor IF-2 and GTP, the 30S ribosomal subunit binds such that the tRNA anticodon is associated with the peptidyl site in this molecule. The binding of the 50S subunit to this complex causes hydrolysis of the bound GTP, with concomitant release of the initiation factors. The amino-acid-charged tRNA corresponding to the second codon of the mRNA is positioned in the aminoacyl tRNA site in the ribosome (by the action of the elongation factor EF-Tu). The methionine attached to the tRNA in the peptidyl site and the amino acid bound to the tRNA in the aminoacyl site react to form a peptide bond, catalyzed by the peptidyltransferase activity of the 23S rRNA in the complex. Two simultaneous translocation steps subsequently occur in a GTP-dependent fashion: the nascent polypeptide-bound (peptidyl) tRNA remaining in the aminoacyl site is translocated to the peptidyl site of the ribosome (with concomitant displacement of the now uncharged tRNA in the peptidyl site to the ejection site), and the mRNA moves one codon site relative to the ribosome such that the next codon is exposed to the aminoacyl-tRNA site on the ribosome.

- This cycle of amino acid addition and elongation of the peptide chain continues until a stop codon (UAA, UGA, UAG) is reached. There do not exist tRNA molecules specific for these stop codons; thus, no amino acid can be added. Instead, one of two release factors (specific to the particular codon in question) binds to the mRNA at the stop codon in a complex with release factor 3 and GTP. The release of the nascent polypeptide chain is accomplished by the hydrolysis of this GTP, and the remaining bound ribosomal subunits are dissociated through the activity of the ribosomal recycling factor.

### C. Pathogenesis

- Bacteria possess numerous mechanisms by which they are able to survive and even to adapt to environments with suboptimal growth conditions. These include protective elements (*e.g.*, the cell wall, which prevents osmotic lysis), the ability to switch to the utilization of different nutrient sources (*e.g.*, inorganic compounds, or

carbon sources), and the ability to adjust to different stresses (*e.g.*, temperature stress, osmotic stress, pH stress, or oxygen stress) by the activation of a sigma factor regulatory cascade. Under growth conditions in a complex environment containing cells other than the bacterium, many bacteria are capable of another survival mechanism: pathogenesis.

- 5           In order to survive in a host (*e.g.*, a plant, animal, or human host), bacteria must be able to not only defend themselves against killing or removal by host immune systems, but also to proliferate. Many bacteria have developed multiple mechanisms by which each goal may be accomplished (see, *e.g.*, Stanier *et al.* (1986) *The Microbial World* 5<sup>th</sup> ed., Prentice Hall: Englewood Cliffs and references therein; and Hacker, J.
- 10   (1999) "Prokaryotes in Medicine" in "Biology of the Prokaryotes, Lengeler *et al.*, eds., Thieme Verlag: Stuttgart, p. 815-849, and references therein). Many bacteria produce peptide or protein toxins (*e.g.*, hemolysins, or diphtheria toxin from *Corynebacterium diphtheriae*) which act to specifically or nonspecifically destroy host cells. Frequently these toxins are directed to immune cells which would otherwise act to remove the
- 15   bacteria from the host. Such toxins may exert their lethal effect in a variety of ways, including by inhibition of protein synthesis in the target cell (*e.g.*, exotoxin A from *Pseudomonas aeruginosa* or diphtheria toxin), by interfering with cellular signal transduction in the target cell (*e.g.*, anthrax lethal toxin, cholera toxin), or by simply creating holes in the target cell membrane which lead to cell lysis (*e.g.*, hemolysins).
- 20   These toxic activities manifest as a disease, for example, diphtheria, tuberculosis (*Mycobacterium bovis* or *M. tuberculosis*), anthrax (*Bacillus anthracis*).

Proliferation (*i.e.*, colonization) of the bacterial cells depends on special factors termed adhesion factors or adhesins. These frequently proteinaceous molecules at the cell surface of the bacterium permit the bacterium to bind to one or more specific host

25   cells or surfaces. This not only permits the bacterium to not be removed by circulatory and excretory processes, but it also limits the exposure of the bacterium to the host immune system, since the bacteria remain stationary and sometimes even inaccessible once adhered to a surface.

- Corynebacterium glutamicum* is a soil bacterium not known to be pathogenic,
- 30   but its genome surprisingly includes several genes which are typically associated with bacterial pathogenesis, but the expression of which has never been observed. Similar situations have been observed in other bacteria: a bacterial species may have stains which are virulent (disease causing) and avirulent (nonpathogenic). A classic example of this is *E. coli*, from which both virulent (*e.g.*, enteropathogenic species) and avirulent
- 35   (*e.g.*, K-12 strains) are well known. Certain bacteria are typically not pathogenic, but may still contain within their genome genes encoding proteins involved in pathogenicity, such as adhesins or toxins. These may be a evolutionary remnant, or may

simply only be expressed under specific conditions which the bacterium rarely encounters.

### III. Elements and Methods of the Invention

5       The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as RRP nucleic acid and protein molecules, which participate in *C. glutamicum* DNA replication, protein synthesis, or pathogenesis. In one embodiment, the RRP molecules participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* ribosome activity, or in the pathogenicity of the microorganism. In a  
10   preferred embodiment, the activity of the RRP molecules of the present invention with regard to DNA replication, protein synthesis, or pathogenesis has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the RRP molecules of the invention are modulated in activity, such that the *C. glutamicum* cellular processes in which the RRP molecules participate (e.g., DNA  
15   replication, protein synthesis, or pathogenesis) are also altered in activity, resulting either directly or indirectly in a modulation of the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

      The language, "RRP protein" or "RRP polypeptide" includes proteins which participate in a number of cellular processes related to *C. glutamicum* DNA replication,  
20   protein synthesis, or pathogenesis. For example, an RRP protein may be involved in the replication of *C. glutamicum* DNA, in *C. glutamicum* ribosome activity, or in the pathogenicity of the microorganism. Examples of RRP proteins include those encoded by the RRP genes set forth in Table 1 and Appendix A. The terms "RRP gene" or "RRP nucleic acid sequence" include nucleic acid sequences encoding an RRP protein, which  
25   consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of RRP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term  
30   "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon  
35   source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or

a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The language "pathogenicity" or "pathogenesis" is art-recognized and includes the activity of an organism, such as a bacterial organism, to bring about a disease state in a host (*e.g.*, cholera, diphtheria, or anthrax). Such disease states are typically the result of cell lytic activity of the organism, which may occur through the expression and release of cytotoxins (*e.g.*, cholera toxin, diphtheria toxin, or anthrax toxin). Other bacterial proteins or peptides not pertaining specifically to cell lysis but contributing to the colonization of the host by the bacterium may also be considered pathogenesis proteins, such as, but not limited to, adhesins. The term "DNA replication" is art-recognized and includes all of the activities associated with the replication of DNA *in vivo* or *in vitro*, and for the purposes of the invention, particularly within bacterial cells. These activities include but are not limited to the assembly of DNA polymerases, the unwinding of DNA, the incorporation of new dNTPs into the nascent DNA strand, the excision and replacement of erroneous bases, and the termination of replication. The term "protein synthesis" is art-recognized and includes the process of converting mRNA codons into amino acids in a growing polypeptide chain, as catalyzed by the ribosome. The term "ribosome function" or "ribosome activity" is art-recognized and includes all of the functions of a ribosome, including, but not limited to, the binding of mRNA, the binding of an aminoacyl-tRNA and a peptidyl-tRNA, and the catalysis of the addition of the next amino acid to the growing polypeptide chain.

In another embodiment, the RRP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an RRP protein of the invention may affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by improving the rate at which DNA replication occurs (*e.g.*, by optimizing the activity of one or more DNA polymerase, or by

improving the rate at which the topoisomerases or helicases of the invention unwind DNA) it may be possible to increase the rate of cell division, which in turn increases the number of viable fine-chemical-producing *C. glutamicum* cells present in large-scale culture settings. Similarly, by improving the rate at which mRNA is translated to protein (e.g., by optimizing the activity of one or more of the ribosomal proteins) it may be possible to increase the number of proteins in the cell which participate in the synthesis of one or more desired fine chemicals, or in an overall increase in the rate of cell division (due to increased growth and metabolism), both of which should lead to increased production of one or more fine chemicals from large-scale fermentor cultures of these microorganisms. Alterations in the DNA replication proteins of the invention may also permit increased fidelity in the replicative process, thereby increasing the genetic stability and viability of the microorganism and lessening the chance that another engineered mutation improving fine chemical production will not be inadvertently mutagenized by error-prone replication. The RRP proteins of the invention involved in pathogenesis are themselves fine chemicals; by increasing the number or by engineering the corresponding genes such that the expression of these proteins is removed from cellular repression pathways, or by mutagenizing the proteins such that feedback regulatory regions are removed, it may be possible to increase the yield, production, and/or efficiency of production of these proteins from large-scale fermentor culture of organisms containing such mutations.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* RRP DNAs and the predicted amino acid sequences of the *C. glutamicum* RRP proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins that participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* ribosome activity, or in the pathogenicity of this microorganism.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at

least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The RRP protein or a biologically active portion or fragment thereof of the invention can participate in *C. glutamicum* DNA replication, in *C. glutamicum* protein  
5 synthesis, or in the pathogenicity of this microorganism, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections.

10 *A. Isolated Nucleic Acid Molecules*

One aspect of the invention pertains to isolated nucleic acid molecules that encode RRP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of RRP-encoding nucleic acid (*e.g.*, RRP DNA). As used herein, the term  
15 "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20  
20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank  
25 the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated RRP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the  
30 nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule  
35 having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* RRP DNA can be isolated from a *C. glutamicum* library

using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

- 5 Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of
- 10 Appendix A). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL).
- 15 Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an
- 20 appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an RRP nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of

25 Appendix A correspond to the *Corynebacterium glutamicum* RRP DNAs of the invention. This DNA comprises sequences encoding RRP proteins (i.e., the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix

30 A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA or RXN number having the designation "RXA", or "RXN" followed by 5 digits (i.e., RXA00823 or RXN00625). Each of these sequences comprises up to three parts: a 5' upstream region, a coding

35 region, and a downstream region. Each of these three regions is identified by the same RXA or RXN designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be

distinguished by their differing RXA or RXN designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA or RXN designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequences in Appendix B designated RXA00823 and RXN00625 are translations of the coding regions of the nucleotide sequence of nucleic acid molecules RXA00823 and RXN00625, respectively, in Appendix A. Each of the RXA and RXN nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1. For example, as set forth in Table 1, the nucleic acid sequence of RXA01064 is SEQ ID NO:13, and the amino acid sequence of RXA01064 is SEQ ID NO:14.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA or RXN designation. For example, SEQ ID NO:3, designated, as indicated on Table 1, as "F RXA00625", is an F-designated gene, as are SEQ ID NOs: 7, 17, and 25 (designated on Table 1 as "F RXA00538", "F RXA01594", and "F RXA00562", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown



in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an RRP protein. The nucleotide sequences determined from the cloning of the RRP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning RRP homologues in other cell types and organisms, as well as RRP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone RRP homologues. Probes based on the RRP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an RRP protein, such as by measuring a level of an RRP-encoding nucleic acid in a sample of cells, e.g., detecting RRP mRNA levels or determining whether a genomic RRP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or

equivalent (e.g., an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism. Proteins involved in *C. glutamicum* DNA replication, in ribosome function/activity, or in the pathogenesis of this microorganism, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an RRP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of RRP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the RRP nucleic acid molecules of the invention are preferably biologically active portions of one of the RRP proteins. As used herein, the term "biologically active portion of an RRP protein" is intended to include a portion, e.g., a domain/motif, of an RRP protein that can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, or has an activity as set forth in Table 1. To determine whether an RRP protein or a biologically active portion thereof can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, an assay of enzymatic/protein activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an RRP protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the RRP protein or peptide (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the RRP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same RRP protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic

acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (e.g., a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 38% identical to the nucleotide sequence designated RXA00823 (SEQ ID NO:9), a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA01064 (SEQ ID NO:13), and a nucleotide sequence which is greater than and/or at least 45% identical to the nucleotide sequence designated RXA02363 (SEQ ID NO:35). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* RRP nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of RRP proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the RRP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an RRP protein, preferably a *C. glutamicum* RRP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the RRP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in RRP that are the result of natural

variation and that do not alter the functional activity of RRP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* RRP DNA of the invention can be isolated based on their homology to the *C. glutamicum* RRP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* RRP protein.

In addition to naturally-occurring variants of the RRP sequence that may exist in the population, the one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded RRP protein, without altering the functional ability of the RRP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the RRP proteins (Appendix B) without altering the activity of said RRP protein, whereas an "essential" amino acid residue is required for RRP protein activity. Other amino acid residues, however, (e.g.,

those that are not conserved or only semi-conserved in the domain having RRP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering RRP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding RRP proteins that contain changes in amino acid residues that are not essential for RRP activity. Such RRP proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the RRP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of participating in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an RRP protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated

mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an RRP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an RRP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an RRP activity described herein to identify mutants that retain RRP activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding RRP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire RRP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an RRP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO:5 (RXN02943) comprises nucleotides 1 to 1668). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding RRP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding RRP disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of RRP mRNA, but

5 more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of RRP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of RRP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed

10 using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic

15 acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil,

20 dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-

25 isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into

30 which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA

35 and/or genomic DNA encoding an RRP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the

case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

10 In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a  
15 chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they  
20 have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave RRP mRNA transcripts to thereby inhibit translation of RRP mRNA. A ribozyme having specificity for an RRP-encoding nucleic acid can be designed based upon the nucleotide sequence of an RRP DNA molecule disclosed  
25 herein (*i.e.*, SEQ ID NO:9 (RXA00823 in Appendix A)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an RRP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, RRP mRNA can be used to select a catalytic RNA  
30 having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, RRP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an RRP nucleotide sequence (*e.g.*, an RRP promoter and/or enhancers) to form triple helical structures that prevent  
35 transcription of an RRP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.



*B. Recombinant Expression Vectors and Host Cells*

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an RRP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting  
5 another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial  
10 vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression  
15 vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-  
20 associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which are  
25 operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory  
30 sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and  
35 those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI<sup>q</sup>*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *amy*, *SPO2*,  $\lambda$ -*P<sub>R</sub>*-

or  $\lambda$  P<sub>L</sub>, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF $\alpha$ , AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., RRP proteins, mutant forms of RRP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of RRP proteins in prokaryotic or eukaryotic cells. For example, RRP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein

from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the RRP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant RRP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1,  $\lambda$ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident  $\lambda$  prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.*

20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the RRP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1  
5 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2  $\mu$ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J.  
10 (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the RRP proteins of the invention can be expressed in insect cells  
15 using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the RRP proteins of the invention may be expressed in  
20 unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for  
25 plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018). In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature*  
30 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of  
35 Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to RRP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) (1986).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be

identical to the parent cell, but are still included within the scope of the term as used herein.

5 A host cell can be any prokaryotic or eukaryotic cell. For example, an RRP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

10 Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., linear DNA or RNA (e.g., a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (e.g., a plasmid, phage, phasmid, phagemid, 15 transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*), and other laboratory manuals. 20

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is 25 generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an RRP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (e.g., cells that have incorporated 30 the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an RRP gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the RRP gene.

35 Preferably, this RRP gene is a *Corynebacterium glutamicum* RRP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous

recombination, the endogenous RRP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous RRP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous RRP protein). In the homologous recombination vector, the altered portion of the RRP gene is flanked at its 5' and 3' ends by additional nucleic acid of the RRP gene to allow for homologous recombination to occur between the exogenous RRP gene carried by the vector and an endogenous RRP gene in a microorganism. The additional flanking RRP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced RRP gene has homologously recombined with the endogenous RRP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an RRP gene on a vector placing it under control of the lac operon permits expression of the RRP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous RRP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced RRP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional RRP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an RRP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the RRP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described RRP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an RRP protein. Accordingly, the invention further provides methods for producing RRP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of

invention (into which a recombinant expression vector encoding an RRP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered RRP protein) in a suitable medium until RRP protein is produced. In another embodiment, the method further comprises isolating RRP proteins from the medium or  
5 the host cell.

### C. Isolated RRP Proteins

Another aspect of the invention pertains to isolated RRP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically  
10 active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of RRP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the  
15 language "substantially free of cellular material" includes preparations of RRP protein having less than about 30% (by dry weight) of non-RRP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-RRP protein, still more preferably less than about 10% of non-RRP protein, and most preferably less than about 5% non-RRP protein. When the RRP protein or biologically active portion  
20 thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of RRP protein in which the protein is separated from  
25 chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of RRP protein having less than about 30% (by dry weight) of chemical precursors or non-RRP chemicals, more preferably less than about 20% chemical precursors or non-RRP chemicals, still more preferably less than  
30 about 10% chemical precursors or non-RRP chemicals, and most preferably less than about 5% chemical precursors or non-RRP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the RRP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* RRP protein in a  
35 microorganism such as *C. glutamicum*.

An isolated RRP protein or a portion thereof of the invention can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the



pathogenicity of this microorganism, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an RRP protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the RRP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the RRP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred RRP proteins of the present invention also preferably possess at least one of the RRP activities described herein. For example, a preferred RRP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can participate in the replication of *C. glutamicum* DNA, in *C. glutamicum* protein synthesis, or in the pathogenicity of this microorganism, or which has one or more of the activities set forth in Table 1.

In other embodiments, the RRP protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the RRP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%,

or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the RRP activities described herein. Ranges and identity values intermediate to the  
5 above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence  
10 of Appendix B.

Biologically active portions of an RRP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an RRP protein, e.g., an amino acid sequence shown in Appendix B or the amino acid sequence of a protein  
15 homologous to an RRP protein, which include fewer amino acids than a full length RRP protein or the full length protein which is homologous to an RRP protein, and exhibit at least one activity of an RRP protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an RRP protein. Moreover, other biologically active portions, in which other regions of the  
20 protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an RRP protein include one or more selected domains/motifs or portions thereof having biological activity.

RRP proteins are preferably produced by recombinant DNA techniques. For  
25 example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the RRP protein is expressed in the host cell. The RRP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an RRP protein,  
30 polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native RRP protein can be isolated from cells (e.g., endothelial cells), for example using an anti-RRP antibody, which can be produced by standard techniques utilizing an RRP protein or fragment thereof of this invention.

The invention also provides RRP chimeric or fusion proteins. As used herein, an  
35 RRP "chimeric protein" or "fusion protein" comprises an RRP polypeptide operatively linked to a non-RRP polypeptide. An "RRP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an RRP protein, whereas a "non-RRP

polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the RRP protein, *e.g.*, a protein which is different from the RRP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to

5 indicate that the RRP polypeptide and the non-RRP polypeptide are fused in-frame to each other. The non-RRP polypeptide can be fused to the N-terminus or C-terminus of the RRP polypeptide. For example, in one embodiment the fusion protein is a GST-RRP fusion protein in which the RRP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant RRP

10 proteins. In another embodiment, the fusion protein is an RRP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an RRP protein can be increased through use of a heterologous signal sequence.

Preferably, an RRP chimeric or fusion protein of the invention is produced by

15 standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid

20 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric

25 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An RRP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the RRP protein.

30 Homologues of the RRP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the RRP protein. As used herein, the term "homologue" refers to a variant form of the RRP protein which acts as an agonist or antagonist of the activity of the RRP protein. An agonist of the RRP protein can retain substantially the same, or a subset, of the biological activities of the RRP protein. An antagonist of the

35 RRP protein can inhibit one or more of the activities of the naturally occurring form of the RRP protein, by, for example, competitively binding to a downstream or upstream member of a biochemical cascade which includes the RRP protein, by binding to a target

molecule with which the RRP protein interacts, such that no functional interaction is possible, or by binding directly to the RRP protein and inhibiting its normal activity.

In an alternative embodiment, homologues of the RRP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the RRP protein for RRP protein agonist or antagonist activity. In one embodiment, a variegated library of RRP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of RRP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential RRP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of RRP sequences therein. There are a variety of methods which can be used to produce libraries of potential RRP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential RRP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the RRP protein coding can be used to generate a variegated population of RRP fragments for screening and subsequent selection of homologues of an RRP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an RRP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the RRP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of RRP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into

replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the  
5 frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify RRP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated RRP library, using methods well known in the art.

10

#### *D. Uses and Methods of the Invention*

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of  
15 genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of RRP protein regions required for function; modulation of an RRP protein activity; modulation of DNA synthesis; modulation of protein synthesis; modulation of *C. glutamicum* pathogenesis; and modulation of cellular production of a desired compound, such as a  
20 fine chemical.

The RRP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides  
25 the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is not pathogenic in humans, it is  
30 related to species which are human pathogens, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to  
35 distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the

disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

- 5           In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and  
10 *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

- The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of  
15 the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable  
20 labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that  
25 these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

- The RRP nucleic acid molecules encoding proteins involved in the pathogenicity of *C. glutamicum* are also useful for purposes of genetic engineering of this microorganism. Frequently, the insertion of genetic information into the genome of an  
30 organism is a disruptive process, which may inadvertently impair the regulation or coding regions of multiple different genes. The RRP pathogenicity genes of the invention are not necessary for the continued survival of the organism in an artificial culture setting, and are not likely to add any benefit to the productivity of the organism for one or more fine chemicals. These genes, then, may serve as useful insertion points  
35 for the addition of genetic material to the genome of *C. glutamicum*, since their disruption should not affect the viability or the productivity of this microorganism.

The RRP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The processes involved in DNA replication, protein synthesis and pathogenesis in which the molecules of the invention participate are utilized by a wide variety of species; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the RRP nucleic acid molecules of the invention may result in the production of RRP proteins having functional differences from the wild-type RRP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an RRP protein, either by interacting with the protein itself or a substrate or binding partner of the RRP protein, or by modulating the transcription or translation of an RRP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more RRP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the RRP protein is assessed.

The alteration of activity or number of one or more of the RRP proteins of the invention involved in DNA replication may affect fine chemical production from a *C. glutamicum* (or related bacterial) cell containing such mutations. For example, by improving the rate at which a DNA polymerase of the invention synthesizes DNA, it may be possible to improve the overall replication rate of the genomic DNA. Similarly, by optimizing the activity of the topoisomerases or gyrases of the invention, it may be possible to more quickly unwind the DNA, thereby permitting increased progressivity of the polymerase complex along the bacterial chromosome. Further, it may be possible to engineer one or more of the proteins involved in DNA replication such that they are improved for function under conditions of high temperature and nonoptimal pH, such as those found in large-scale fermentor culture (e.g., amino acid replacements may be made such that the resulting structure of one of these proteins retains activity but is improved for stability at high temperature or acidic/basic pH). Improving the rate of DNA synthesis in *C. glutamicum* or related bacteria may permit more rapid rates of cell division, leading to increased numbers of cells present in large-scale cultures of the

bacterium. Relatively increased numbers of cells, each of which is producing one or more desired fine chemicals, should result in relatively increased yield, production, or efficiency of production of one or more fine chemicals from the culture.

Also, by manipulating one or more of the RRP genes of the invention, it may be possible to increase the overall fidelity of replication in *C. glutamicum* or related bacterial cells. For example, the 3'-5' exonuclease activities of Pol III or Pol I (which are responsible for excising inappropriately incorporated bases from the growing DNA strand) may be optimized such that more incorrect bases are detected and removed. Similarly, the polymerization activity of the DNA polymerases of the invention may be improved such that the error rate in base incorporation is decreased. Both such modifications should result in improved fidelity in the replicated DNA, which in turn should decrease the rate of introduced mutations. Fewer introduced mutations not only helps to ensure that any other engineered genes will not be undesirably altered by random mutation, but also may permit increased viability of the cells in culture, since random mutations may impair the activity of genes necessary for cell survival. As before, increased numbers of viable cells in culture should result in increased yield, production, and/or efficiency of production of one or more fine chemicals produced by those cells.

Mutations in genes and proteins involved in protein synthesis (*e.g.*, ribosomal genes and proteins) may also have a significant effect on the production of one or more fine chemicals from *C. glutamicum* or related bacterial cultures. For example, by improving the rate of protein synthesis (*e.g.*, by improving the rate of assembly of the ribosome, by improving the progressivity of the ribosome, or by increasing the rate at which the ribosome is able to productively bind to mRNA, all of which may be accomplished by altering the binding sites for the various ribosomal components such that binding and association of ribosomal proteins to each other or to tRNAs or to mRNAs are improved) it may be possible to increase the rate at which proteins involved in the synthesis of desired fine chemicals are produced, thereby potentially improving the production of one or more of these fine chemicals. This increased protein production may also permit increased growth and cell division of the cell, since increased cellular metabolism (which may occur due to the presence of increased numbers of metabolic proteins) may also result in more rapid cell division, thereby increasing the number of cells in a culture of the bacterium containing such mutation(s). Increased numbers of viable cells in large-scale fermentor culture, each of which is producing one or more desired fine chemicals, should result in an increase in yield, production, and/or efficiency of production of these fine chemicals.



Alteration of the number of the RRP proteins of the invention involved in the pathogenicity of *C. glutamicum* (e.g., hemolysin and invasins) may also increase the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum* cells containing such mutations. These pathogenesis proteins may be of utility for the survival of *C. glutamicum* cells in their natural environments. However, in the artificial environment of fermentor culture, nutrients are typically supplied in excess, and there should be no other organisms with which these bacteria need to compete. Thus, the synthesis of these pathogenesis proteins represents the utilization of energy and biomaterials which could instead be shifted to the production of one or more desired fine chemicals. Thus, by decreasing the number of such pathogenesis genes in *C. glutamicum*, it may be possible to increase the available intermediate compounds (e.g., nucleotides, amino acids, or energy molecules such as ATP) such that metabolism in general, and fine chemical production in particular is increased.

These RRP proteins involved in pathogenesis may themselves also be considered desirable fine chemicals. These proteins may have significant pharmaceutical applications, as, for example, antimicrobial or antifungal agents. Further, although *C. glutamicum* is not a human pathogen, its pathogenesis proteins (e.g., hemolysins or adhesins) may be similar in structure and activity to those from bacterial species which are significant human pathogens (e.g., *E. coli* or *Pseudomonas* spp.) These *C. glutamicum* pathogenesis proteins may thus serve as useful targets for the development of vaccines or therapeutics against various human pathogens. By mutagenizing the genes encoding these proteins such that their synthesis and/or translation is no longer repressed by cellular regulatory mechanisms, or such that their production is no longer subject to feedback inhibition (e.g., by mutagenizing regulatory regions upstream or downstream of the gene, or by mutagenizing regulatory regions on the protein itself) greater numbers of these proteins may be able to be expressed and harvested from culture.

The aforementioned mutagenesis strategies for RRP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated RRP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally

occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

### Exemplification

10

#### **Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032**

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 10 ml/l  $\text{KH}_2\text{PO}_4$  solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l  $(\text{NH}_4)_2\text{SO}_4$ , 1 g/l NaCl, 2 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 0.2 g/l  $\text{CaCl}_2$ , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l  $\text{FeSO}_4 \times \text{H}_2\text{O}$ , 10 mg/l  $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$ , 3 mg/l  $\text{MnCl}_2 \times 4\text{H}_2\text{O}$ , 30 mg/l  $\text{H}_3\text{BO}_3$ , 20 mg/l  $\text{CoCl}_2 \times 6\text{H}_2\text{O}$ , 1 mg/l  $\text{NiCl}_2 \times 6\text{H}_2\text{O}$ , 3 mg/l  $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$ , 500 mg/l complexing agent (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-pantothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20

µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge  
5 Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

10 **Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.**

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley &  
15 Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or  
20 Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

**Example 3: DNA Sequencing and Computational Functional Analysis**

25 Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., Science, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-  
30 GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

**Example 4: *In vivo* Mutagenesis**

*In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or  
35 yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D.

(1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to one of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) Strategies 7: 32-34.

5 **Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum***

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the

gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

5        Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through  
10    the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional  
15    terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

#### 20    **Example 6: Assessment of the Expression of the Mutant Protein**

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene  
25    product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the  
30    binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

35        To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process,

total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

#### **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) Appl. Microbiol. Biotechnol., 32:205-210; von der Osten *et al.* (1998) Biotechnology Letters, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as  $\text{NH}_4\text{Cl}$  or  $(\text{NH}_4)_2\text{SO}_4$ ,  $\text{NH}_4\text{OH}$ , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on

the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like

5 standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

10 Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers

15 such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH<sub>4</sub>OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-

20 organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

25 For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance

30 of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD<sub>600</sub> of 0.5 – 1.5 using cells grown on agar plates, such as CM plates

35 (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the

media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

#### **Example 8 – *In vitro* Analysis of the Function of Mutant Proteins**

- 5           The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3<sup>rd</sup> ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2<sup>nd</sup> ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3<sup>rd</sup> ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

- 20           The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

- 25           The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

#### **Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product**

- 35           The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing



the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example, 5 Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 10 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 15 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 20 determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these 25 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

#### **Example 10: Purification of the Desired Product from *C. glutamicum* Culture**

30 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 35 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

### **Example 11: Analysis of the Gene Sequences of the Invention**

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to RRP nucleic acid molecules of the invention. BLAST protein searches can be performed with the

XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to RRP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped

5 BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-  
10 17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described  
15 in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap  
20 weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present  
25 in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the  
30 sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP  
35 program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this

analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP  
5 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For  
10 example, a value of "40,345" in this column represents "40.345%".

#### **Example 12: Construction and Operation of DNA Microarrays**

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are  
15 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose,  
20 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized  
25 molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers  
30 which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270:  
35 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-

1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the  
5 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be  
10 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),  
15 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray  
20 technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons  
25 of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

### **Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)**

30 The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*,  
35 during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*,  $^{35}\text{S}$ -methionine,  $^{35}\text{S}$ -cysteine,  $^{14}\text{C}$ -labelled amino acids,  $^{15}\text{N}$ -amino acids,  $^{15}\text{NO}_3$  or  $^{15}\text{NH}_4^+$  or  $^{13}\text{C}$ -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

10 **Equivalents**

Those skilled of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an RRP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an RRP protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.



8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1  
5 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of claim 1.
11. The vector of claim 10, which is an expression vector.  
10
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium*  
15 or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule  
results in the modulation in production of a fine chemical from said cell.  
20
16. The host cell of claim 15, wherein said fine chemical is selected from the group  
consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine  
and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated  
fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors,  
25 polyketides, and enzymes.
17. A method of producing a polypeptide comprising culturing the host cell of claim 12  
in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated RRP polypeptide from *Corynebacterium glutamicum*, or a portion  
30 thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production  
of a fine chemical production.  
35

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 5 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 15 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 20 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 30 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 35 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

5 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

10 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS  
INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS, AND  
PATHOGENESIS**

5

**Abstract of the Disclosure**

Isolated nucleic acid molecules, designated RRP nucleic acid molecules, which  
encode novel RRP proteins from *Corynebacterium glutamicum* are described. The  
invention also provides antisense nucleic acid molecules, recombinant expression  
10 vectors containing RRP nucleic acid molecules, and host cells into which the expression  
vectors have been introduced. The invention still further provides isolated RRP  
proteins, mutated RRP proteins, fusion proteins, antigenic peptides and methods for the  
improvement of production of a desired compound from *C. glutamicum* based on  
genetic engineering of RRP genes in this organism.

15

TABLE 1: Genes in the Application

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXN00625	VV0135	5	946	(D90902) extracellular nuclease [Synecocystis sp.]
3	4	F RXA00625	GR00163	9320	8982	(D90902) extracellular nuclease [Synecocystis sp.]
5	6	RXN02943	VV0103	1671	4	(D90902) extracellular nuclease [Synecocystis sp.]
7	8	F RXA00538	GR00139	1272	4	(D90902) extracellular nuclease [Synecocystis sp.]
9	10	RXA00823	GR00221	3566	4345	ENDONUCLEASE III (EC 4.2.99.18)
11	12	RXA02145	GR00639	12248	13864	ENDONUCLEASE III (EC 4.2.99.18)
13	14	RXA01064	GR00297	937	1572	THERMONUCLEASE PRECURSOR (EC 3.1.31.1)
15	16	RXN01594	VV0229	12195	11377	HEMOLYSIN
17	18	F RXA01594	GR00447	2580	3323	HEMOLYSIN
19	20	RXA01718	GR00488	540	55	HEMOLYSIN
21	22	RXN03148	VV0146	626	991	HEMOLYSIN
23	24	RXN00562	VV0103	5761	6483	HEMOLYSIN III
25	26	F RXA00562	GR00150	405	1034	HEMOLYSIN III
27	28	RXN00890	VV0099	18771	20069	HEMOLYSIN
29	30	F RXA00890	GR00242	15953	17227	HEMOLYSIN
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
31	32	RXN01772	VV0050	28644	33681	/K/J Superfamily II DNA and RNA helicases
33	34	F RXA01772	GR00502	4731	2368	/K/J Superfamily II DNA and RNA helicases
35	36	RXA02363	GR00685	10755	15554	/K/J Superfamily II DNA and RNA helicases
37	38	RXN01606	VV0137	5576	2901	Hypothetical ATP-Dependent RNA Helicase
39	40	F RXA01797	GR00508	1249	542	/L Superfamily II DNA and RNA(?) helicases (SNF2 family)
41	42	RXN01030	VV0015	32429	33604	Hypothetical ATP-dependent RNA helicase
43	44	F RXA01030	GR00295	2007	3182	/L Superfamily II DNA and RNA(?) helicases (SNF2 family)
45	46	RXA01739	GR00493	4702	5298	Superfamily I DNA and RNA helicases
47	48	RXA02359	GR00685	1666	3534	Superfamily I DNA and RNA helicases
49	50	RXN02764	VV0317	2787	4	DNA HELICASE II (EC 3.6.1.-)
51	52	F RXA02764	GR00769	2787	4	Superfamily I DNA and RNA helicases
53	54	RXA01736	GR00493	3	2870	(AL021646) putative ATP-dependent DNA helicase [Mycobacterium tuberculosis]
55	56	RXA00095	GR00014	4677	2389	DNA HELICASE II (EC 3.6.1.-)
57	58	RXN02819	VV0088	6162	5116	ATP-DEPENDENT DNA HELICASE
59	60	F RXA02819	GR00800	615	4	ATP-DEPENDENT DNA HELICASE
61	62	RXA01157	GR00328	1610	6	ATP-DEPENDENT DNA HELICASE
63	64	RXN01876	VV0145	188	2038	ATP-DEPENDENT DNA HELICASE REP (EC 3.6.1.-)
65	66	F RXA01876	GR00536	2796	1324	ATP-DEPENDENT DNA HELICASE REP (EC 3.6.1.-)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
67	68	RXA00544	GR00140	1639	3168	REPLICATIVE DNA HELICASE (EC 3.6.1.-)
69	70	RXA01866	GR00533	326	6	ATP-DEPENDENT HELICASE HRP A
71	72	RXA01867	GR00533	853	362	ATP-DEPENDENT HELICASE HRP A
73	74	RXN03166	VV03322	2933	699	ATP-DEPENDENT HELICASE HRP A
75	76	F RXA00361	GR00072	1853	6	ATP-DEPENDENT HELICASE HRP A
77	78	RXN02293	VV0127	19979	22366	ATP-DEPENDENT HELICASE HRP B
79	80	F RXA02293	GR00662	2819	5206	ATP-dependent helicase
81	82	RXA02755	GR00766	951	2945	PROBABLE ATP-DEPENDENT HELICASE DING
83	84	RXN01374	VV0091	7624	8865	Hypothetical ATP-Dependent RNA Helicase
85	86	F RXA01374	GR00400	885	4	PROBABLE ATP-DEPENDENT HELICASE HEPA
87	88	RXN00817	VV0054	35789	33396	PROBABLE ATP-DEPENDENT HELICASE HEPA
89	90	F RXA00809	GR00218	514	5	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
91	92	F RXA00817	GR00219	6388	4679	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
93	94	RXN00103	VV0129	11188	15747	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
95	96	F RXA00103	GR00014	15860	11301	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
97	98	RXN02357	VV0051	23376	17077	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
99	100	F RXA01363	GR00395	1408	2106	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
101	102	F RXA02357	GR00685	3	1205	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
103	104	F RXA02785	GR00776	5314	3856	PROBABLE ATP-DEPENDENT HELICASE LHR (EC 3.6.1.-)
105	106	RXA01740	GR00493	5275	6735	PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-)
107	108	RXN01683	VV0179	1	7842	DNA GYRASE SUBUNIT A (EC 5.99.1.3)
109	110	F RXA01682	GR00468	1	234	DNA GYRASE SUBUNIT A (EC 5.99.1.3)
111	112	F RXA01683	GR00468	146	895	DNA GYRASE SUBUNIT A (EC 5.99.1.3)
113	114	F RXA01684	GR00469	3	875	DNA GYRASE SUBUNIT A (EC 5.99.1.3)
115	116	RXN01688	VV0179	1	930	DNA GYRASE SUBUNIT B (EC 5.99.1.3)
117	118	F RXA01688	GR00471	1	564	DNA GYRASE SUBUNIT B (EC 5.99.1.3)
119	120	RXN01689	VV0221	1920	3035	DNA GYRASE SUBUNIT B (EC 5.99.1.3)
121	122	F RXA01689	GR00472	3	728	DNA GYRASE SUBUNIT B (EC 5.99.1.3)
123	124	F RXA01735	GR00492	1213	1494	DNA GYRASE SUBUNIT B (EC 5.99.1.3)
125	126	RXN03093	VV0054	36970	38808	DNA TOPOISOMERASE I (EC 5.99.1.2)
127	128	F RXA00798	GR00213	2525	171	DNA TOPOISOMERASE I (EC 5.99.1.2)
129	130	RXN00990	VV0210	4962	4498	ATP-DEPENDENT RNA HELICASE DEAD
131	132	F RXA00990	GR00281	2	454	ATP-DEPENDENT RNA HELICASE DEAD
133	134	RXN00994	VV0106	356	6	ATP-DEPENDENT RNA HELICASE DEAD
135	136	F RXA00994	GR00282	797	1138	ATP-DEPENDENT RNA HELICASE DEAD
137	138	RXN02468	VV0211	760	1983	ATP-DEPENDENT RNA HELICASE DEAD
139	140	F RXA02463	GR00713	141	254	ATP-DEPENDENT RNA HELICASE DEAD
141	142	F RXA02468	GR00714	760	1290	ATP-DEPENDENT RNA HELICASE DEAD
143	144	RXA00050	GR00008	5451	3256	ATP-DEPENDENT RNA HELICASE DEAD
145	146	RXA02682	GR00754	6902	6576	ATP-DEPENDENT RNA HELICASE DEAD
147	148	RXN00542	VV0079	36158	36832	DNA-BINDING PROTEIN
149	150	F RXA00542	GR00140	1	519	SINGLE-STRAND BINDING PROTEIN
151	152	RXN02833	VV0050	823	41	CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA
153	154	F RXA02833	GR00822	627	49	CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA
155	156	RXA01480	GR00422	14550	12658	DNA PRIMASE (EC 2.7.7.-)
157	158	RXN03163	VV0204	4514	6010	PRIMOSOMAL PROTEIN N'
159	160	F RXA02241	GR00654	8446	10473	PRIMOSOMAL PROTEIN N', replication factor Y

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
161	162	RXN00061	VV0044	4256	1590	DNA POLYMERASE I (EC 2.7.7.7)
163	164	F RXA00060	GR00009	9187	11643	DNA POLYMERASE I (EC 2.7.7.7)
165	166	F RXA00061	GR00009	11643	11852	DNA POLYMERASE I (EC 2.7.7.7)
167	168	RXA02657	GR00752	11033	14614	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
169	170	RXA01238	GR00358	2965	4365	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
171	172	RXN00407	VV0086	55677	58340	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
173	174	F RXA00407	GR00091	3	578	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
175	176	F RXA00415	GR00092	4519	6480	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
177	178	RXN00414	VV0086	55331	55684	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
179	180	F RXA00414	GR00092	4172	4591	DNA POLYMERASE III, DELTA' SUBUNIT (EC 2.7.7.7)
181	182	RXN00807	VV0009	63097	61856	DNA POLYMERASE III, DELTA' SUBUNIT (EC 2.7.7.7)
183	184	F RXA00807	GR00216	423	1541	DNA POLYMERASE III, EPSILON CHAIN (EC 2.7.7.7)
185	186	RXA00214	GR00032	13046	13756	DNA POLYMERASE III, EPSILON CHAIN (EC 2.7.7.7)
187	188	RXA01255	GR00365	4919	3840	DNA POLYMERASE III, EPSILON CHAIN (EC 2.7.7.7)
189	190	RXN00066	VV0012	816	4	DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7)
191	192	F RXA00066	GR00010	4494	5306	DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7)
193	194	RXN01637	VV0156	666	4	DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7)
195	196	F RXA01637	GR00455	312	10848	DNA LIGASE (EC 6.5.1.2)
197	198	RXA00212	GR00032	12407	12316	DNA LIGASE (EC 6.5.1.2)
199	200	RXA00213	GR00032	12888	12316	EXODEOXYRIBONUCLEASE SMALL SUBUNIT (EC 3.1.11.6)
201	202	RXA00789	GR00209	1266	1024	EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6)
203	204	RXN00790	VV0321	1983	3044	EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6)
205	206	F RXA00790	GR00209	2315	1290	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
207	208	RXA00898	GR00245	567	1355	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
209	210	RXN03175	VV0331	1248	466	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
211	212	F RXA02883	GR10020	779	1690	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
213	214	RXA00341	GR00059	3584	4990	EXORIBONUCLEASE II (EC 3.1.13.1)
215	216	RXA02077	GR00628	7779	8174	RIBONUCLEASE III (EC 3.1.26.3)
217	218	RXN01563	VV0191	4413	3205	RIBONUCLEASE D (EC 3.1.26.3)
219	220	F RXA01563	GR00436	1916	1107	RIBONUCLEASE D (EC 3.1.26.3)
221	222	F RXA01713	GR00485	357	4	RIBONUCLEASE D (EC 3.1.26.3)
223	224	RXA02369	VV0102	3191	5479	RIBONUCLEASE E (EC 3.1.4.-)
225	226	RXN02370	GR00687	1338	547	RIBONUCLEASE E (EC 3.1.4.-)
227	228	F RXA02370	GR00393	5463	6254	RIBONUCLEASE E (EC 3.1.4.-)
229	230	RXA01356	VV0084	3731	4357	RIBONUCLEASE HII (EC 3.1.26.4)
231	232	RXN01786	VV0084	11253	10570	RIBONUCLEASE PH (EC 2.7.7.56)
233	234	F RXA01786	GR00505	1878	2318	RIBONUCLEASE PH (EC 2.7.7.56)
235	236	RXN00163	VV0084	10540	9923	RIBONUCLEASE PH (EC 2.7.7.56)
237	238	F RXA00163	GR00024	6432	5872	RIBONUCLEASE PH (EC 2.7.7.56)
239	240	RXA01424	GR00417	988	1296	RIBONUCLEASE P PROTEIN COMPONENT (EC 3.1.26.5)
241	242	RXA01481	GR00422	14596	15087	GUANYL-SPECIFIC RIBONUCLEASE SA3 (EC 3.1.27.3)
243	244	RXN00724	VV0052	1217	3193	ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1.-)
245	246	RXN01979	VV0105	18093	16513	ATP-DEPENDENT DNA HELICASE RECO (EC 3.6.1.-)
247	248	RXN01770	VV0015	50449	54213	DNA HELICASE II (EC 3.6.1.-)
249	250	RXN01378	VV0091	8756	10510	Hypothetical ATP-Dependent RNA Helicase
251	252	RXN02131	VV0100	23600	25170	DNA REPAIR HELICASE RAD25
254	254	RXN01066	VV0099	21112	21837	DNA REPAIR PROTEIN RECO



Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
255	256	RXN01389	VV0276	1350	667	DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2.7.7.6)
257	258	RXN02070	VV0222	8319	7198	MRP PROTEIN HOMOLOG
259	260	RXN02082	VV0318	21225	24134	CHROMOSOME SEGREGATION PROTEIN SMC2

## Ribosomal genes

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
261	262	RXA01495	GR00423	8970	8524	RIBOSOME-BINDING FACTOR A
263	264	RXA01893	GR00542	871	1425	RIBOSOME Recycling Factor (RRF)
265	266	RXA01568	GR00437	2764	2330	RIBOSOMAL-PROTEIN-ALANINE ACETYLTTRANSFERASE (EC 2.3.1.128)
267	268	RXA01661	GR00462	1132	1797	RNA METHYLTRANSFERASE (EC 2.1.1.-)
269	270	RXA01581	GR00440	777	1589	RNA METHYLTRANSFERASE (EC 2.1.1.-)
271	272	RXA00313	GR00053	3992	3054	RNA METHYLTRANSFERASE (EC 2.1.1.-)
273	274	RXN00460	VV0086	64848	64378	RNA METHYLTRANSFERASE (EC 2.1.1.-)
275	276	F RXA00460	GR00116	382	5	RNA METHYLTRANSFERASE (EC 2.1.1.-)
277	278	RXA02179	GR00641	15353	14526	23S RNA METHYLTRANSFERASE (EC 2.1.1.-)
279	280	RXA02522	GR00725	311	853	16S RNA PROCESSING PROTEIN RIMM
281	282	RXA00717	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
283	284	RXA02615	GR00744	973	338	RIBOSOMAL-PROTEIN-ALANINE ACETYLTTRANSFERASE (EC 2.3.1.128)
285	286	RXN01343	VV0025	33595	34302	LSU ribosomal protein L1P
287	288	F RXA01343	GR00389	13513	12863	LSU ribosomal protein L1P
289	290	RXN01951	GR00561	1218	1778	LSU ribosomal protein L2P
291	292	F RXA01950	GR00561	938	1321	LSU ribosomal protein L2P
293	294	RXA01286	GR00372	730	77	LSU ribosomal protein L3P
295	296	RXA01948	GR00561	3	605	LSU ribosomal protein L1E (= L4P)
297	298	RXN00706	VV0005	2208	2780	LSU ribosomal protein L5P
299	300	F RXA00711	GR00186	660	815	LSU ribosomal protein L5P
301	302	F RXA00706	GR00185	1	267	LSU ribosomal protein L5P
303	304	RXA00695	GR00181	5118	5651	LSU ribosomal protein L6P
305	306	RXA00543	GR00140	579	1004	LSU ribosomal protein L6P
307	308	RXA01335	GR00389	2736	2224	LSU ribosomal protein L9P
309	310	RXN02826	VV0025	33031	33465	LSU ribosomal protein L11P
311	312	F RXA02826	GR00807	67	465	LSU ribosomal protein L11P
313	314	RXA01334	GR00389	2143	1760	LSU ribosomal protein L12P (L7/L12)
315	316	RXA02037	GR00620	1	330	LSU ribosomal protein L13P
317	318	RXA00699	GR00181	6934	7377	LSU ribosomal protein L15P
319	320	RXA02042	GR00622	720	1133	LSU ribosomal protein L16P
321	322	RXA00670	GR00176	2420	1932	LSU ribosomal protein L17P
323	324	RXA00696	GR00181	5658	6059	LSU ribosomal protein L18P
325	326	RXA01353	GR00393	972	1310	LSU ribosomal protein L19P
327	328	RXA02420	GR00705	5954	6334	LSU ribosomal protein L20P
329	330	RXN02371	VV0102	318	4	LSU ribosomal protein L21P
331	332	F RXA02371	GR00687	6483	6752	LSU ribosomal protein L21P
333	334	RXA01949	GR00561	608	910	LSU ribosomal protein L23P

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
335	336	RXND00709	VV0005	1523	1888	LSU ribosomal protein L24P
337	338	F RXA00709	GR00186	2	340	LSU ribosomal protein L24P
339	340	RXA00710	GR00186	346	657	LSU ribosomal protein L24P
341	342	RXA02635	GR00748	7846	8079	LSU ribosomal protein L28P
343	344	RXA02043	GR00622	1136	1276	LSU ribosomal protein L29P
345	346	RXA00698	GR00181	6742	6924	LSU ribosomal protein L30P
347	348	RXA02633	GR00748	5506	5243	LSU ribosomal protein L31P
349	350	RXA02636	GR00748	8085	8246	LSU ribosomal protein L33P
351	352	RXA01423	GR00417	715	855	LSU ribosomal protein L34P
353	354	RXA02419	GR00705	5699	5890	LSU ribosomal protein L35P
355	356	RXA02190	GR00642	1277	2734	SSU ribosomal protein S1P
357	358	RXND1912	VV0150	876	1613	SSU ribosomal protein S2P
359	360	F RXA01912	GR00547	876	1646	SSU ribosomal protein S2P
361	362	RXA02041	GR00622	1	714	SSU ribosomal protein S3P
363	364	RXA00672	GR00176	4215	3613	SSU ribosomal protein S4P
365	366	RXA00697	GR00181	6103	6735	SSU ribosomal protein S5P
367	368	RXND0545	VV0079	35852	36118	SSU ribosomal protein S6P
369	370	F RXA00545	GR00141	562	816	SSU ribosomal protein S6P
371	372	RXA01279	GR00369	3240	2776	SSU ribosomal protein S7P
373	374	RXA00694	GR00181	4700	5095	SSU ribosomal protein S8P
375	376	RXND2038	VV0118	333	701	SSU ribosomal protein S9P
377	378	F RXA02038	GR00620	333	641	SSU ribosomal protein S9P
379	380	RXA01287	GR00372	1068	766	SSU ribosomal protein S10P
381	382	RXA00673	GR00176	4331	4242	SSU ribosomal protein S11P
383	384	RXA01280	GR00369	3615	3250	SSU ribosomal protein S12P
385	386	RXA02637	GR00748	8253	8555	SSU ribosomal protein S14P
387	388	RXA01487	GR00423	1172	906	SSU ribosomal protein S15P
389	390	RXA02752	GR00764	6709	7203	SSU ribosomal protein S16P
391	392	RXA02389	GR00695	504	764	SSU ribosomal protein S20P
393	394	RXA00671	GR00176	3492	2479	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN (EC 2.7.7.6)
395	396	RXND2981	VV0005	35599	35964	SSU ribosomal protein S13P
397	398	RXND3139	VV0129	35552	35304	SSU ribosomal protein S18P
399	400	RXND0673	VV0005	35970	36371	SSU ribosomal protein S11P
401	402	RXND0714	VV0232	10755	11315	RIBOSOMAL-PROTEIN-ALANINE ACETYLTRANSFERASE (EC 2.3.1.128)
403	404	RXND0897	VV0140	3721	4725	RIBOSOMAL-PROTEIN-ALANINE ACETYLTRANSFERASE (EC 2.3.1.128)
405	406	RXND1380	VV0224	15361	17559	TEX PROTEIN

## Genes Involved in Pathogenesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
407	408	RXA00157	GR00023	11848	10586	INVASIN 1
409	410	RXA00208	GR00032	7947	7099	VULNIBACTIN UTILIZATION PROTEIN VIUB
411	412	RXA00967	GR00967	1351	989	VIRULENCE-ASSOCIATED PROTEIN I
413	414	RXA01149	GR00323	2501	2758	VIRULENCE-ASSOCIATED PROTEIN I

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
415	416	RXA01305	GR00376	4435	2570	SEROTYPE-SPECIFIC ANTIGEN 1 (EC 3.4.21.-)
417	418	RXA01453	GR00419	2655	2951	VIRULENCE-ASSOCIATED PROTEIN A'
419	420	RXA01824	GR00516	1367	2188	VULNIBACTIN UTILIZATION PROTEIN VIUB
421	422	RXA01832	GR00516	11787	10894	ANNEXIN VII
423	424	RXA02533	GR00726	3775	3209	(D90768) Immunity repressor protein [Escherichia coli]
425	426	RXN02727	VV0017	6287	5376	ANTIGEN 84

## Nucleases

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
427	428	RXN01575	VV00009	50041	49022	RIBONUCLEASE HI (EC 3.1.26.4)
429	430	RXN01966	VV0155	5673	5017	OLIGORIBONUCLEASE (EC 3.1.-.-)

**TABLE 2: GENES IDENTIFIED FROM GENBANK**

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disR1; disR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argI; argB; argD; argF; argR; argG; argH	N-acetylglutamyphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	arob	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	pand	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> pand gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4)1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
DI7429		Transposable element IS31831	Veres, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) <i>odhA</i> gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdtH; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Deshiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipicolinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95



GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Asparatase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydropyridine reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydropyridine reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydropyridine acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydropyridine acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetylhydroxy acid synthase large subunit; Acetylhydroxy acid synthase small subunit; Acetylhydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in <i>Corynebacterium glutamicum</i> : molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	ptsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the <i>Corynebacterium glutamicum</i> mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diptheriae</i> dxr from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
L35906	dxr	Diphtheria toxin repressor	Follette, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M13774		Prephenate dehydratase	Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16175	5S rRNA		Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M25819		Phosphoenolpyruvate carboxylase	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85106		23S rRNA gene insertion sequence	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	acdD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The Corynebacterium glutamicum acdD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminocycloleucine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5"-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepintec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of C. glutamicum fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	copI	PSI protein	Jolliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PSI, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PSI is similar to the <i>Mycobacterium</i> antigen 85 complex." <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase." <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydropicolinate reductase	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69103	csp2	Surface layer protein PS2	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X69104		IS3 related insertion element	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X70959	leuA	Isopropylmalate synthase	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X71489	icd	Isocitrate dehydrogenase (NADP+)	
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mttA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Railey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascal, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl- $\gamma$ -glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAV2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein, Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahn, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panB and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> ( <i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	Moreau, S. et al. "Analysis of the integration functions of $\phi$ phi:304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Y18059		Attachment site Corynebacterium 304L	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z29563	thrC	Threonine synthase	
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmrdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49824	orf1; sigB	?, SigB sigma factor	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
Z66534		Transposase	

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniaenes	21054							
Brevibacterium	ammoniaenes	19350							
Brevibacterium	ammoniaenes	19351							
Brevibacterium	ammoniaenes	19352							
Brevibacterium	ammoniaenes	19353							
Brevibacterium	ammoniaenes	19354							
Brevibacterium	ammoniaenes	19355							
Brevibacterium	ammoniaenes	19356							
Brevibacterium	ammoniaenes	21055							
Brevibacterium	ammoniaenes	21077							
Brevibacterium	ammoniaenes	21553							
Brevibacterium	ammoniaenes	21580							
Brevibacterium	ammoniaenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

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Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoadidophilum	21476							
Corynebacterium	acetoadidophilum	13870							
Corynebacterium	aceto glutamicum				B11473				
Corynebacterium	aceto glutamicum				B11475				
Corynebacterium	aceto glutamicum	15806							
Corynebacterium	aceto glutamicum	21491							
Corynebacterium	aceto glutamicum	31270							
Corynebacterium	acetophillum				B3671				
Corynebacterium	ammonia genes	6872						2399	
Corynebacterium	ammonia genes	15511							
Corynebacterium	fujio kense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514																	
Corynebacterium	glutamicum	21516																	
Corynebacterium	glutamicum	21299																	
Corynebacterium	glutamicum	21300																	
Corynebacterium	glutamicum	39684																	
Corynebacterium	glutamicum	21488																	
Corynebacterium	glutamicum	21649																	
Corynebacterium	glutamicum	21650																	
Corynebacterium	glutamicum	19223																	
Corynebacterium	glutamicum	13869																	
Corynebacterium	glutamicum	21157																	
Corynebacterium	glutamicum	21158																	
Corynebacterium	glutamicum	21159																	
Corynebacterium	glutamicum	21355																	
Corynebacterium	glutamicum	31808																	
Corynebacterium	glutamicum	21674																	
Corynebacterium	glutamicum	21562																	
Corynebacterium	glutamicum	21563																	
Corynebacterium	glutamicum	21564																	
Corynebacterium	glutamicum	21565																	
Corynebacterium	glutamicum	21566																	
Corynebacterium	glutamicum	21567																	
Corynebacterium	glutamicum	21568																	
Corynebacterium	glutamicum	21569																	
Corynebacterium	glutamicum	21570																	
Corynebacterium	glutamicum	21571																	
Corynebacterium	glutamicum	21572																	
Corynebacterium	glutamicum	21573																	
Corynebacterium	glutamicum	21579																	
Corynebacterium	glutamicum	19049																	
Corynebacterium	glutamicum	19050																	

Corynebacterium	glutanicum	19051																	
Corynebacterium	glutanicum	19052																	
Corynebacterium	glutanicum	19053																	
Corynebacterium	glutanicum	19054																	
Corynebacterium	glutanicum	19055																	
Corynebacterium	glutanicum	19056																	
Corynebacterium	glutanicum	19057																	
Corynebacterium	glutanicum	19058																	
Corynebacterium	glutanicum	19059																	
Corynebacterium	glutanicum	19060																	
Corynebacterium	glutanicum	19185																	
Corynebacterium	glutanicum	13286																	
Corynebacterium	glutanicum	21515																	
Corynebacterium	glutanicum	21527																	
Corynebacterium	glutanicum	21544																	
Corynebacterium	glutanicum	21492																	
Corynebacterium	glutanicum				B8183														
Corynebacterium	glutanicum				B8182														
Corynebacterium	glutanicum				B12416														
Corynebacterium	glutanicum				B12417														
Corynebacterium	glutanicum				B12418														
Corynebacterium	glutanicum				B11476														
Corynebacterium	glutanicum	21608																	
Corynebacterium	glutanicum				P973														
Corynebacterium	nitrolophilus	21419																	
Corynebacterium	spec.				P4445														
Corynebacterium	spec.				P4446														
Corynebacterium	spec.	31088																	
Corynebacterium	spec.	31089																	
Corynebacterium	spec.	31090																	
Corynebacterium	spec.	31090																	



FERM: Fermentation Research Institute, Chiba, Japan

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

CBS: Centraalbureau voor Schimmelmcultures, Baarn, NL

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

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TABLE 4: ALIGNMENT RESULTS

rx00545	390	GB_HTG3:AC009314	204881	AC009314	Homo sapiens clone NH0465K04, *** SEQUENCING IN PROGRESS ***; 12	Homo sapiens	35,128	24-Aug-99
		GB_HTG3:AC009314	204881	AC009314	unordered pieces.			
		GB_EST36:A1920042	696	A1920042	Homo sapiens clone NH0465K04, *** SEQUENCING IN PROGRESS ***; 12	Homo sapiens	35,128	24-Aug-99
		GB_EST36:A1920042	696	A1920042	unordered pieces.			
rx00562	846	GB_PR3:HS470K1	103613	AL031780	1572 Pine Lambda Zap Xylem library Pinus taeda cDNA clone b12_PL3CSUH, mRNA sequence.	Pinus taeda	33,947	29-Jul-99
		GB_PR3:HS470K1	103613	AL031780	Human DNA sequence from clone 470K1 on chromosome 6p22.1-23. Contains ESTs, STSs, GSSs, genomic markers D6S263 and D6S277, and two ca repeat polymorphisms, complete sequence.	Homo sapiens	34,251	23-Nov-99
		GB_HTG1:HSJ976O13	102370	AL117354	Homo sapiens chromosome 1 clone RP5-976O13 map p21.2-22.2, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,928	25-Nov-99
		GB_HTG1:HSJ976O13	102370	AL117354	Homo sapiens chromosome 1 clone RP5-976O13 map p21.2-22.2, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,928	25-Nov-99
rx00625	965	GB_PR4:AC005049	106928	AC005049	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	37,446	21-Aug-99
		GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	35,759	30-Nov-99
		GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	35,759	30-Nov-99
rx00670	612	GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	41,206	17-Jun-98
		GB_BA1:SC6G4	41055	AL031317	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Streptomyces coelicolor	55,410	20-Aug-98
		GB_HTG3:AC009422	140233	AC009422	Homo sapiens clone 44_N_8, *** SEQUENCING IN PROGRESS ***; 17 unordered pieces.	Homo sapiens	36,394	22-Aug-99
rx00671	1137	GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	38,172	17-Jun-98
		GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	67,810	20-Aug-98
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	40,541	27-Aug-99
rx00672	726	GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	38,167	17-Jun-98
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	37,027	27-Aug-99
		GB_BA1:MBU15140	2136	U15140	Mycobacterium bovis ribosomal proteins IF-1 (infA), L36 (rpmJ), S13 (rpsM) and S11 (rpsK) genes, complete cds. and S4 (rpsD) gene, partial cds.	Mycobacterium bovis	71,933	28-OCT-1996
rx00673	525	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	63,238	20-Aug-98
		GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	33,461	17-Jun-98
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	37,965	27-Aug-99
rx00694	519	GB_BA1:MLSPCOPER	6858	X17524	M.luteus DNA for spectinomycin (spc) operon.	Micrococcus luteus	68,093	07-DEC-1992
		GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	74,611	02-MAR-1998
		GB_BA1:MLCB2492	37144	Z98756	Mycobacterium leprae cosmid B2492.	Mycobacterium leprae	66,408	28-Aug-97
rx00695	657	GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	69,863	17-Jun-98
		GB_BA1:MSGY42	36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	38,880	03-DEC-1996
		GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	67,580	02-MAR-1998
rx00696	525	GB_BA1:MLSPCOPER	6858	X17524	M.luteus DNA for spectinomycin (spc) operon.	Streptomyces coelicolor	65,873	02-MAR-1998
		GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Micrococcus luteus	65,145	07-DEC-1992
		GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	65,779	17-Jun-98
rx00697	756	GB_BA1:MSGY42	36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	67,353	17-Jun-98
		GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Mycobacterium tuberculosis	39,516	03-DEC-1996
rx00698	306	GB_BA1:BSUB0019	212610	Z99122	Bacillus subtilis complete genome (section 19 of 21); from 3597091 to 3809700.	Streptomyces coelicolor	67,764	02-MAR-1998
		GB_BA1:BSUB0019	212610	Z99122	Bacillus subtilis complete genome (section 19 of 21); from 3597091 to 3809700.	Bacillus subtilis	39,465	24-Jun-99

TABLE 4: ALIGNMENT RESULTS

	GB_IN2:AC008370	132171	AC008370	Drosophila melanogaster, chromosome 2R, region 44B-44C, BAC clones BACR09N11 and BACR40A15, complete sequence.	Drosophila melanogaster	32,558	3-Aug-99
	GB_HTG2:AC006878	159941	AC006878	Caenorhabditis elegans clone Y54H5, *** SEQUENCING IN PROGRESS *** 8 unordered pieces.	Caenorhabditis elegans	36,066	26-Feb-99
rx000699	567	GB_BA1:SCSECYDNA 6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	65,009	02-MAR-1998
		GB_BA1:MLSPCOPER 6658	X17524	M.luteus DNA for spectinomycin (spo) operon.	Micrococcus luteus	61,538	07-DEC-1992
		GB_BA1:MTCY210 36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	61,989	17-Jun-98
rx000706	696	GB_BA1:MTCY210 36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	67,960	17-Jun-98
		GB_BA1:MSGY42 36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	39,757	03-DEC-1996
		GB_BA1:MLSPCOPER 6658	X17524	M.luteus DNA for spectinomycin (spo) operon.	Micrococcus luteus	67,686	07-DEC-1992
rx000709	489	GB_BA1:MTCY210 36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	69,897	17-Jun-98
		GB_BA1:MSGY42 36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	41,401	03-DEC-1996
		GB_BA1:MLCB2492 37144	Z98756	Mycobacterium leprae cosmid B2492.	Mycobacterium leprae	68,660	28-Aug-97
rx000710	435	GB_BA1:MTCY210 36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	69,746	17-Jun-98
		GB_BA1:MSGY42 36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	37,709	03-DEC-1996
		GB_BA1:MLCB2492 37144	Z98756	Mycobacterium leprae cosmid B2492.	Mycobacterium leprae	68,129	28-Aug-97
rx000717	1083	GB_PAT:178753 1187	178753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
		GB_PAT:192042 1187	192042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1:MTCH125 37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
rx000789	366	GB_PRR:AC007463 166892	AC007463	Homo sapiens BAC clone NH0244L12 from 2, complete sequence.	Homo sapiens	41,047	22-OCT-1999
		GB_IN2:AC004420 79987	AC004420	Drosophila melanogaster DNA sequence (P1 DS02649 (D132)), complete sequence.	Drosophila melanogaster	34,670	20-Jun-98
rx000790	1185	GB_BA1:MTV012 70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	40,331	23-Jun-99
		GB_EST23:AI085588 492	AI085588	oy68d10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:1670995 3, mRNA sequence.	Homo sapiens	34,167	24-Sep-98
		GB_HTG4:AC010097 198863	AC010097	Homo sapiens chromosome unknown clone NH037816, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	33,907	29-OCT-1999
		GB_HTG4:AC010097 198863	AC010097	Homo sapiens chromosome unknown clone NH037816, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	33,907	29-OCT-1999
rx000798	1278	GB_BA1:SCHE 40544	AL035636	Streptomyces coelicolor cosmid H5.	Streptomyces coelicolor	39,294	25-MAR-1999
		GB_BA1:MTY15C10 33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	37,619	17-Jun-98
		GB_PAT:AR053877 3107	AR053877	Sequence 3 from patent US 5834279.	Unknown.	62,090	29-Sep-99
rx000807	1365	GB_IN1:CELK07E12 58949	U00054	Caenorhabditis elegans cosmid K07E12.	Caenorhabditis elegans	38,743	11-MAY-1994
		GB_PL1:GYCPRK 1179	D83718	Glycyrrhiza echinata mRNA for polyketide reductase, complete cds.	Glycyrrhiza echinata	41,725	20-Feb-99
		GB_EST31:AU062517 350	AU062517	AU062517 Rice callus Oryza sativa cDNA clone C11644_1A, mRNA sequence.	Oryza sativa	43,366	20-MAY-1999
rx000817	2517	GB_BA1:MTY15C10 33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	56,778	17-Jun-98
		GB_GSS11:ACQ289275 682	ACQ289275	nbxb0034B24r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0034B24r, genomic survey sequence.	Oryza sativa	38,301	03-DEC-1998
rx000823	903	GB_IN1:CELO12469 11025	AU012469	Caenorhabditis elegans mRNA for DYS-1 protein, partial.	Caenorhabditis elegans	37,981	16-Nov-98
		GB_BA1:MTV025 121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	37,753	24-Jun-99
		GB_PL2:ATFCA0 200576	Z97335	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 0.	Arabidopsis thaliana	37,178	28-Jun-99
rx000890	1422	GB_PL2:ATFCA0 200576	Z97335	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 0.	Arabidopsis thaliana	37,016	28-Jun-99
		GB_BA1:MTCY27 27548	Z95208	Mycobacterium tuberculosis H37Rv complete genome; segment 104/162.	Mycobacterium tuberculosis	39,813	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

	GB_BA2.U32716	11618	U32716	Haemophilus influenzae Rd section 31 of 163 of the complete genome.	Haemophilus influenzae Rd	39,588	29-MAY-1998
	GB_HTG2.AC006842	299015	AC006842	Caenorhabditis elegans clone Y104H12X. *** SEQUENCING IN PROGRESS *** , 13 unordered pieces.	Caenorhabditis elegans	36,003	24-Feb-99
rx00898 912	GB_BA1:MSGY423	42741	AD000014	Mycobacterium tuberculosis sequence from clone Y423.	Mycobacterium tuberculosis	54,945	10-DEC-1996
	GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	39,532	17-Jun-98
	GB_IN1:CEC12C8	23674	Z81467	Caenorhabditis elegans cosmid C12C8, complete sequence.	Caenorhabditis elegans	36,170	23-Nov-98
rx00967 411	GB_HTG2.AC006244	92079	AC006244	Drosophila melanogaster chromosome 2 clone DS00212 (D463) map 60F-1-60F2 strain y, cn bw sp. *** SEQUENCING IN PROGRESS *** , 3 unordered pieces.	Drosophila melanogaster	38,765	30-Jul-99
	GB_GSS1:CNS00BE0	1101	AL056856	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR23K12 of RPC1-98 library from Drosophila melanogaster (fruit fly).	Drosophila melanogaster	34,772	4-Jun-99
	GB_HTG2.AC006244	92079	AC006244	genomic survey sequence.	Drosophila melanogaster	38,765	30-Jul-99
	GB_HTG2.AC006244	92079	AC006244	Drosophila melanogaster chromosome 2 clone DS00212 (D463) map 60F-1-60F2 strain y, cn bw sp. *** SEQUENCING IN PROGRESS *** , 3 unordered pieces.	Drosophila melanogaster	38,765	30-Jul-99
rx00990 488	GB_GSS8.AQ078675	565	AQ078675	CIT-HSP-2368L22, TF CIT-HSP Homo sapiens genomic clone 2368L22.	Homo sapiens	39,200	20-Aug-98
	GB_GSS8.AQ040280	323	AQ040280	genomic survey sequence.	Homo sapiens	38,434	11-Jul-98
	GB_PL1:ATF16J13	107600	AL049638	CIT-HSP-2328E18, TR CIT-HSP Homo sapiens genomic clone 2328E18, genomic survey sequence.	Homo sapiens	43,220	14-Apr-99
rx00994 451	GB_EST17:C74578	301	C74578	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project).	Arabidopsis thaliana	51,174	29-Sep-97
	GB_EST36:AF155027	827	AF155027	C74578 Rice panicle shorter than 3cm Oryza sativa cDNA clone E31890_1A, mRNA sequence.	Oryza sativa	35,268	22-Jul-99
	GB_EST8:AA023112	457	AA023112	AF155027 Zebrafish Kidney cDNA random primed, RZPD library no: 576. Danio rerio cDNA clone CHB0576D06232C3 T7 primer, mRNA sequence.	Danio rerio	41,869	21-Jan-97
rx01030 1299	GB_HTG3.AC011344	127964	AC011344	mh66c12, r1 Soares mouse placenta 4NBMP13.5 14.5 Mus musculus cDNA clone IMAGE:455926 5 similar to PIR.S10960 S10960 hypothetical protein - bovine ; mRNA sequence.	Mus musculus	37,718	06-OCT-1999
	GB_HTG3.AC011344	127964	AC011344	Homo sapiens chromosome 5 clone CIT-HSPC_287O14, *** SEQUENCING IN PROGRESS *** , 36 unordered pieces.	Homo sapiens	37,718	06-OCT-1999
	GB_BA1:RPXX04	237523	AJ235273	Homo sapiens chromosome 5 clone CIT-HSPC_287O14, *** SEQUENCING IN PROGRESS *** , 36 unordered pieces.	Homo sapiens	34,752	11-Nov-98
rx01064 759	GB_EST16:AA584614	489	AA584614	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4.	Rickettsia prowazekii	39,059	8-Sep-97
	GB_HTG2.AC007720	150070	AC007720	no08g11 s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100132 3, mRNA sequence.	Homo sapiens	38,859	3-Jun-99
	GB_HTG2.AC007720	150070	AC007720	Homo sapiens clone 31_B_4, *** SEQUENCING IN PROGRESS *** , 7 unordered pieces.	Homo sapiens	38,859	3-Jun-99
rx01149 381	GB_PR4:AC006971	115861	AC006971	unordered pieces.	Homo sapiens	37,401	08-MAY-1999
	GB_HTG4:AC007347	167025	AC007347	Homo sapiens clone 31_B_4, *** SEQUENCING IN PROGRESS *** , 7 unordered pieces.	Homo sapiens	36,364	31-OCT-1999
	GB_HTG4:AC007347	167025	AC007347	Homo sapiens PAC clone DJ0791C19 from 7p11.2-q11.21, complete sequence.	Homo sapiens	36,364	31-OCT-1999
rx01157 1705	GB_BA1:MTCY49	39430	ZZ3966	PROGRESS *** , 2 ordered pieces.	Homo sapiens	39,879	24-Jun-99
				PROGRESS *** , 2 ordered pieces.	Homo sapiens	39,879	24-Jun-99
				Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	39,879	24-Jun-99

**TABLE 4: ALIGNMENT RESULTS**

rx001238	1524	GB_BA2:SAUJ7894 GB_BA1:SAUJ3310 GB_PR4:AC007367 GB_PR4:AC007367 GB_HTG2:AC008157	2437 2437 197278 197278 171758	U77894 AJ223310 AC007367 AC007367 AC008157	Streptomyces avermitilis helicase-like protein gene, complete cds. Streptomyces avermitilis sab3 gene, complete CDS. Homo sapiens BAC clone NH0518G12 from 2, complete sequence. Homo sapiens BAC clone NH0518G12 from 2, complete sequence. Homo sapiens clone 45_P_22, *** SEQUENCING IN PROGRESS *** , 9 unordered pieces.	57,648 57,648 35,130 38,153 35,762	5-Jan-99 8-Apr-98 22-OCT-1999 22-OCT-1999 28-Jul-99
rx001255	1203	GB_EST37:A1944834 GB_EST1:T16608	388 235	A1944834 T16608	Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone b506a03 5', mRNA sequence. Homo sapiens	40,310 41,277	17-Aug-99 25-Jul-96
rx001279	588	GB_EST10:AA141530 GB_BA1:MLB1790G	515 37617	AA141530 Z14314	Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone CK01913 5prime, mRNA sequence. M.leprae genes rplL, rpoB, rpoC, end, rpsL, rpsG, efg, tuf, rpsJ, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and nkl gene. Mycobacterium smegmatis ribosomal protein S12 (rpsL) gene, complete cds. Mycobacterium smegmatis ribosomal protein S7 (rpsG) gene, complete cds. M.luteus str operon encoding ribosomal protein S12 (str or rpsL) ribosomal protein S7 (rpsG) EF-G (fus) and EF-Tu (tuf). M.leprae genes rplL, rpoB, rpoC, end, rpsL, rpsG, efg, tuf, rpsJ, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and nkl gene. Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes. Mycobacterium tuberculosis H37Rv complete genome, segment 33/162. P.rosea fus, tuf, rpsJ and rplC genes. Mycobacterium leprae cosmid B2492. Mycobacterium tuberculosis H37Rv complete genome, segment 34/162. Mycobacterium tuberculosis H37Rv complete genome, segment 34/162. Mycobacterium tuberculosis sequence from clone Y42. M.leprae genes rplL, rpoB, rpoC, end, rpsL, rpsG, efg, tuf, rpsJ, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and nkl gene. HS_2041_A2_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=20 Row=1, genomic survey sequence. Human Flt3 ligand gene and Flt3 ligand alternatively spliced isoform gene, complete cds. Human Flt3 ligand gene and Flt3 ligand alternatively spliced isoform gene, complete cds. Mycobacterium tuberculosis H37Rv complete genome, segment 31/162.	38,477 71,088	29-Nov-98 11-Feb-93
rx001280	489	GB_BA1:MLUSTROA GB_BA1:MLB1790G	5291 37617	M17788 Z14314	Mycobacterium leprae Mycobacterium leprae	76,408 65,644	23-Feb-95 11-Feb-93
rx001286	777	GB_BA2:ECOUW67_2 GB_BA1:MTV040 GB_BA1:PRFUSTUF GB_BA1:MLCB2492 GB_BA1:MTCY210 GB_BA1:MTCY210 GB_BA1:MSGY42 GB_BA1:MLB1790G	110000 15100 2742 37144 36804 36804 36526 37617	U18997 AL021943 X98830 Z98756 Z84395 Z84395 AD000005 Z14314	Escherichia coli Mycobacterium tuberculosis Planobispora rosea Mycobacterium leprae Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae	37,037 65,849 67,525 67,111 67,021 70,423 35,749 69,104	23-Jan-98 17-Jun-98 19-Nov-96 28-Aug-97 17-Jun-98 17-Jun-98 03-DEC-1996 11-Feb-93
rx001287	426	GB_BA1:MSGY42 GB_BA1:MLB1790G	36526 37617	AD000005 Z14314	Mycobacterium tuberculosis Mycobacterium leprae	35,749 69,104	03-DEC-1996 11-Feb-93
rx001305	1989	GB_GSS10:AQ242866	511	AQ242866	Homo sapiens	38,735	03-OCT-1998
rx001334	507	GB_PR2:HSU29874 GB_PR2:HSU29874 GB_PR2:HSU29874 GB_BA1:MTY20H10	6155 6155 6155 35980	U29874 U29874 U29874 Z92772	Homo sapiens Homo sapiens Homo sapiens Mycobacterium tuberculosis	38,791 36,655 66,075	29-Feb-96 29-Feb-96 17-Jun-98

**TABLE 4: ALIGNMENT RESULTS**

	GB_BA1:MLB1790G	37617	Z14314	Mleprae genes rplL, rpoB, rpoC, end, rpsL, rpsG, efg, tuf, rpsJ, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and mkl gene.	Mycobacterium leprae	64,969	11-Feb-93
	GB_BA1:MSGPRL	631	D16310	M. bovis rplL gene for ribosomal protein L7/L12.	Mycobacterium bovis	66,598	4-Feb-99
rx01335 636	GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	40,362	24-MAY-1999
	GB_BA1:SC6A5	43632	AL049485	Streptomyces coelicolor cosmid 6A5.	Streptomyces coelicolor	40,362	24-MAR-1999
	GB_EST30:AV002771	289	AV002771	AV002771 Mus musculus C57BL/6J kidney Mus musculus cDNA clone 0610020F04, mRNA sequence.	Mus musculus	41,667	24-Aug-99
rx01343 831	GB_BA1:MTY20H10	35980	Z92772	Mycobacterium tuberculosis H37Rv complete genome; segment 31/162.	Mycobacterium tuberculosis	66,908	17-Jun-98
	GB_BA1:SGNUSG	7235	X72787	S. griseus nusG, rplKAL gene cluster.	Streptomyces griseus	63,177	06-MAY-1998
	GB_BA1:STMVBR1	7409	D50624	Streptomyces virginiae VirA gene for NusG like protein, SecE like protein and ribosomal protein, aspartate aminotransferase and adenosine deaminase, complete cds.	Streptomyces virginiae	63,329	10-Feb-99
rx01353 462	GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	65,368	4-Jun-98
	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, tmdD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	65,368	27-OCT-1999
rx01356 750	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,013	19-Jun-98
	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21); from 1598421 to 1807200.	Bacillus subtilis	44,851	26-Nov-97
	GB_PL2:CRE132478	16445	AJ132478	Chlamydomonas reinhardtii STF1 gene, partial.	Chlamydomonas reinhardtii	37,200	29-Sep-99
	GB_GSS4:AC701168	552	AQ701168	HS_2129_A2_B06_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2129 Col=12 Row=C, genomic survey sequence.	Homo sapiens	40,541	6-Jul-99
rx01374 1365	GB_OV:FR24G11	34807	Z93780	Fugu rubripes genes encoding carboxymyl phosphate synthetase III, myosin light chain, MAP2.	Fugu rubripes	37,936	22-Nov-99
	GB_EST36:AI881479	601	AI881479	606069F03.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.	Zea mays	38,963	21-Jul-99
rx01423 264	GB_BA2:AE000733	15569	AE000733	Aquifex aeolicus section 55 of 109 of the complete genome.	Aquifex aeolicus	35,421	25-MAR-1998
	GB_BA1:SCH24	41625	AL049826	Streptomyces coelicolor cosmid H24.	Streptomyces coelicolor	57,854	11-MAY-1999
	GB_BA1:MSGDNAB	40571	L39923	Mycobacterium leprae cosmid L222 DNA sequence, 27 CDS features.	Mycobacterium leprae	41,634	29-Apr-97
	GB_BA1:MSORIREP	10430	X92503	M. smegmatis origin of replication and genes rpmH, dnaA, dnaN, gnd, recF, gyrB, gyrA.	Mycobacterium smegmatis	39,535	26-Aug-97
rx01424 432	GB_OV:CCU31864	2517	U31864	Cyprinus carpio stearyl-CoA desaturase mRNA, complete cds.	Cyprinus carpio	36,946	13-Sep-99
	GB_IN1:DMED10641	3733	AJ010641	Drosophila melanogaster mRNA for Dot protein, transcript II.	Drosophila melanogaster	36,768	9-Feb-99
	GB_IN1:DMED10642	4044	AJ010642	Drosophila melanogaster mRNA for Dot protein, transcript I, partial.	Drosophila melanogaster	36,768	6-Sep-99
rx01453 420	GB_BA1:PDENQOURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO8), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds; biotin [acyetyl-CoA carboxyl] ligase (bifA) gene, complete cds.	Paracoccus denitrificans	41,304	20-MAY-1993



TABLE 4: ALIGNMENT RESULTS

GB_BA2.AF108766	14548	AF108766	Rhodobacter sphaeroides AsmA (asma) gene, partial cds; YbaU (ybaU), anthranilate synthase component I (trpE), YibQ (yibQ), anthranilate synthase component II (trpG), anthranilate phosphoribosyltransferase (trpD), indole-3-glycerol phosphate synthase (trpC), molybdenum cofactor biosynthesis protein C (moaC), molybdenum cofactor biosynthesis protein A (moaA), LexA repressor (lexA), and glutamyl t-RNA synthetase (gluS) genes, complete cds; and citrate synthase (cisY) gene, partial cds.	Rhodobacter sphaeroides	41,388	9-Nov-99
GB_BA1.SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glyco-gen metabolism cluster1.	Streptomyces coelicolor	40,554	29-MAR-1999
GB_BA2.AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; tRNA-Asn gene, complete sequence.	Mycobacterium smegmatis	58,650	16-Jan-98
GB_BA1.MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	36,959	17-Jun-98
GB_PL1.AB009053	78145	AB009053	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2.	Arabidopsis thaliana	37,232	13-Feb-99
GB_HTG1.LMFL5628	32914	AL049187	Leishmania major chromosome 4 clone L5628 strain Freidlin, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Leishmania major	38,399	29-Apr-99
GB_HTG1.LMFL5628	32914	AL049187	Leishmania major chromosome 4 clone L5628 strain Freidlin, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Leishmania major	38,399	29-Apr-99
GB_PR3.HSJ182D15	79576	AL049612	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone dJ182D15, complete sequence.	Homo sapiens	37,438	23-Nov-99
GB_BA1.MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	38,182	17-Jun-98
GB_BA1.SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	56,923	10-Aug-98
GB_BA1.MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,021	22-Aug-97
GB_PL1.SCSETRPA	5020	X73297	S. cerevisiae spacer element.	Saccharomyces cerevisiae	34,921	30-DEC-1993
GB_PL2.YSCD9476	31184	U28372	Saccharomyces cerevisiae chromosome IV cosmid 9476.	Saccharomyces cerevisiae	34,921	1-Aug-97
GB_PL1.SCNJF1G	3522	Z11582	S. cerevisiae nuf1 gene.	Saccharomyces cerevisiae	34,921	27-MAR-1992
GB_BA1.AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	39,017	6-Feb-99
GB_PR4.HUAC004381	213541	AC004381	Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.	Homo sapiens	36,530	23-Nov-99
GB_BA1.AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	40,463	6-Feb-99
GB_BA1.MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	41,424	23-Jun-99
GB_EST1.D23343	381	D23343	RICC2654A Rice callus Oryza sativa cDNA clone C2654_1A, mRNA sequence.	Oryza sativa	37,831	8-Jul-99
GB_EST17.C73734	455	C73734	C73734 Rice panicle (longer than 10cm) Oryza sativa cDNA clone E20291_2A, mRNA sequence.	Oryza sativa	39,341	23-Sep-97
GB_BA1.MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,237	24-Jun-97
GB_BA1.U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	38,553	29-Sep-94
GB_PL1.AB025606	74282	AB025606	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F6N7, complete sequence.	Arabidopsis thaliana	35,699	20-Nov-99
GB_PR3.AF064861	133965	AF064861	Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.	Homo sapiens	37,600	2-Jun-98
GB_HTG2.AC003656_4110000	133965	AC003656	Homo sapiens clone P1 C124G1, *** SEQUENCING IN PROGRESS ***; 50 unordered pieces.	Homo sapiens	41,137	2-Dec-97
GB_HTG2.AC003656_4110000	133965	AC003656	Homo sapiens clone P1 C124G1, *** SEQUENCING IN PROGRESS ***; 50 unordered pieces.	Homo sapiens	41,137	2-Dec-97
GB_BA1.MTV036	24055	AL021931	Mycobacterium tuberculosis H37Rv complete genome; segment 19/162.	Mycobacterium tuberculosis	40,962	17-Jun-98
GB_BA1.MSGB1970CS39399	24055	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	61,370	15-Jun-96

**TABLE 4: ALIGNMENT RESULTS**

rx01683	2691	GB_BA1:MSGYRBA	6000	X94224	Drosophila melanogaster chromosome 3 clone BACR48E09 (D489) RPCI-98	32,737	2-Aug-99
		GB_BA1:MTCY10H4	39160	Z80233	48 E 9 map 61A1-61A4 strain Y; cn bw sp, *** SEQUENCING IN PROGRESS***, 9 unordered pieces.	67,476	12-Feb-97
		GB_BA1:MSGYRAB	5119	X84077	M.smegmatis gyrB and gyrA genes.	66,828	17-Jun-98
rx01688	953	GB_BA1:MTCY10H4	39160	Z80233	M.smegmatis gyrB and gyrA genes.	67,090	13-MAR-1996
		GB_BA1:MSORIREP	10430	X92503	Mycobacterium tuberculosis H37Rv complete genome; segment 2/162.	74,397	17-Jun-98
		GB_BA1:MSGYRAB	5119	X84077	Mycobacterium tuberculosis H37Rv complete genome; segment 2/162.	74,711	26-Aug-97
		GB_BA1:MSGYRAB	5119	X84077	M.smegmatis gyrB and gyrA genes.	74,711	13-MAR-1996
rx01689	1239	GB_BA1:MSORIREP	10430	X92503	M.smegmatis origin of replication and genes rpmH, dnaA, dnaN, gnd, recF, gyrB, gyrA.	63,470	26-Aug-97
		GB_BA1:MSGYRAB	6000	X94224	M.smegmatis gyrB and gyrA genes.	62,969	12-Feb-97
		GB_BA1:MSGYRAB	5119	X84077	M.smegmatis gyrB and gyrA genes.	62,886	13-MAR-1996
rx01718	609	GB_GSS13:ACQ473371	688	ACQ473371	CITBI-E1-2585J18, TR CITBI-E1 Homo sapiens genomic clone 2585J18, genomic survey sequence.	36,976	23-Apr-99
		GB_EST33:AV068888	264	AV068888	AV068888 Mus musculus small intestine C57BL/6J adult Mus musculus cDNA Mus musculus clone 2010307A09, mRNA sequence.	40,000	24-Jun-99
		GB_HTG3:AC008277	204008	AC008277	Homo sapiens clone NH0311B14, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	39,130	04-OCT-1999
rx01736	2891	GB_BA1:MTV014	58280	AL021646	Mycobacterium tuberculosis H37Rv complete genome; segment 137/162.	38,918	18-Jun-98
		GB_PL2:AF156928	2290	AF156928	Candida albicans foplypolylglutamate synthetase (fpgs) gene, complete cds.	34,894	22-Jun-99
		GB_GSS12:ACQ421204	483	ACQ421204	RPCI-11-167B4.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-167B4, genomic survey sequence.	39,085	23-MAR-1999
rx01739	720	GB_PRR3:HS503F6	51476	AL021153	Homo sapiens DNA sequence from BAC 503F6 on chromosome 22q11.2-12.1. Contains EST and STS.	35,484	23-Nov-99
		GB_OM:CFU73207	1845	U73207	Canis familiaris beta1 adrenergic receptor (dobeta1) gene, complete cds.	39,818	31-DEC-1997
		GB_PRR3:HS503F6	51476	AL021153	Homo sapiens DNA sequence from BAC 503F6 on chromosome 22q11.2-12.1. Contains EST and STS.	36,376	23-Nov-99
rx01740	1545	GB_BA1:U00016	42931	U00016	Mycobacterium leprae cosmid B1937.	57,820	01-MAR-1994
		GB_BA2:PAU73505	1332	U73505	Pseudomonas aeruginosa dihydroorotase (pyrC) gene, complete cds.	39,322	13-Nov-98
		GB_JN1:CEC52G5	42842	Z67881	Caenorhabditis elegans cosmid C52G5, complete sequence.	35,267	2-Sep-99
rx01772	5061	GB_BA2:AE001493	10792	AE001493	Helicobacter pylori, strain J99 section 54 of 132 of the complete genome.	46,571	20-Jan-99
		GB_EST5:N28852	555	N28852	yx59f11.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2660615, mRNA sequence.	38,561	4-Jan-96
		GB_EST5:N28844	628	N28844	yx59d11.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2660375, mRNA sequence.	38,118	4-Jan-96
rx01786	807	GB_PL1:AB006707	82315	AB006707	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYC6, complete sequence.	37,641	20-Nov-99
		GB_PRR4:AC006324	157310	AC006324	Homo sapiens clone DJ1164F05, complete sequence.	36,802	11-Nov-99
		GB_PL2:ATU29168	2692	U29168	Arabidopsis thaliana DNA repair protein homolog (XPBara) mRNA, complete cds.	38,808	6-Apr-98
rx01824	945	GB_EST19:AA760333	371	AA760333	vv75b10.r1 Striatogene mouse skin (#937313) Mus musculus cDNA clone IMAGE:12282195, mRNA sequence.	44,211	23-Jan-98
		GB_PRR2:CNS00YVE	34105	AL096807	Homo sapiens genomic region containing hypervariable minisatellites chromosome 8[8q24.3] of Homo sapiens.	36,374	11-OCT-1999

**TABLE 4: ALIGNMENT RESULTS**

rx01832	1017	GB_HTG3:AC008129_0110000	AC008129	Homo sapiens clone RPC111-473H3, *** SEQUENCING IN PROGRESS 136 unordered pieces.	Homo sapiens	38,877	24-Jul-99	
rx01832	1017	GB_GSS1:CNS006LB	929	AL065711	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR13L01 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	35,589	3-Jun-99
rx01866	421	GB_RO:MU SIGVCA	153	MG0955	Mouse Ig germline H-chain D region, 5' flank.	Mus musculus	43,421	27-Apr-93
rx01866	421	GB_BA2:AE001014	10636	AE001014	Archaeoglobus fulgidus section 93 of 172 of the complete genome.	Archaeoglobus fulgidus	38,377	15-DEC-1997
rx01866	421	GB_IN2:AC008370	132171	AC008370	Drosophila melanogaster, chromosome 2R, region 44B-44C, BAC clones BACR09N11 and BACR40A15, complete sequence.	Drosophila melanogaster	34,845	3-Aug-99
rx01867	531	GB_IN2:AC008370	132171	AC008370	Drosophila melanogaster, chromosome 2R, region 44B-44C, BAC clones BACR09N11 and BACR40A15, complete sequence.	Drosophila melanogaster	37,897	3-Aug-99
rx01867	531	GB_HTG1:HSJA9613	45302	AJ009613	BACR09N11 and BACR40A15, complete sequence.	Homo sapiens	38,717	11-Nov-98
rx01867	531	GB_EST15:AA520493	439	AA520493	Homo sapiens chromosome 17 clone cosmid 5L5 map p11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,413	16-Jul-97
rx01867	531	GB_GSS10:AQ225693	448	AQ225693	TGEST2261f08.r1 TgME49 invivo Bradyzoite cDNA size selected Toxoplasma gondii cDNA clone lgz261f08.r1 5', mRNA sequence.	Toxoplasma gondii	37,374	26-Sep-98
rx01876	1974	GB_PR3:AC005262	44235	AC005262	HS_2009_B2_B08_17 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=16 Row=D, genomic survey sequence.	Homo sapiens	37,374	6-Jul-98
rx01876	1974	GB_OV:CHKNTC	1185	M10013	Homo sapiens chromosome 19, cosmid F23990, complete sequence.	Homo sapiens	34,345	28-Apr-93
rx01876	1974	GB_OV:CHKNT	927	K02263	Chicken cardiac tropoin T form I mRNA, complete cds.	Gallus gallus	41,674	28-Apr-93
rx01876	1974	GB_OV:CHKNTC	1185	M10013	Chicken tropoin T mRNA.	Gallus gallus	40,065	28-Apr-93
rx01893	678	GB_OV:CHKNTC	1185	M10013	Chicken cardiac tropoin T form I mRNA, complete cds.	Gallus gallus	42,097	28-Apr-93
rx01893	678	GB_BA1:AB016498	596	AB016498	Thermus thermophilus frt gene for ribosome recycling factor gene (RRF), complete cds.	Thermus thermophilus	53,691	9-Apr-99
rx01912	861	GB_PR4:AC002531	197900	AC002531	Homo sapiens chromosome Y, clone 486_O_8, complete sequence.	Homo sapiens	33,628	13-OCT-1999
rx01912	861	GB_HTG5:AC008019	190459	AC008019	Mus musculus, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces.	Mus musculus	35,022	16-Nov-99
rx01912	861	GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid ZE1.	Streptomyces coelicolor	66,047	4-Jun-98
rx01912	861	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	38,225	19-Jun-98
rx01912	861	GB_BA2:AF034101	2162	AF034101	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. Streptomyces coelicolor ribosomal protein S2 (rpsB) and elongation factor Ts (tsf) genes, complete cds.	Mycobacterium tuberculosis	65,814	15-OCT-1999
rx01948	626	GB_BA1:MSRPLD	648	Y13226	Mycobacterium smegmatis rplD gene.	Streptomyces coelicolor	65,814	15-OCT-1999
rx01948	626	GB_BA1:MSGY42	36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium smegmatis	68,833	04-DEC-1997
rx01948	626	GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	35,313	03-DEC-1996
rx01948	626	GB_BA1:MBS100PER	5962	Y13228	Mycobacterium bovis BCG DNA for ribosomal S10 operon.	Mycobacterium tuberculosis	68,530	17-Jun-98
rx01948	626	GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium bovis BCG	66,197	04-DEC-1997
rx01948	626	GB_BA1:MSGY42	36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	65,962	17-Jun-98
rx01951	684	GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	38,765	03-DEC-1996
rx01951	684	GB_BA1:MSGY42	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	71,157	17-Jun-98
rx01951	684	GB_BA1:MSGY42	36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	38,179	03-DEC-1996
rx01951	684	GB_BA1:MLCB2492	37144	Z98756	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	38,179	03-DEC-1996
rx02037	353	GB_BA1:MLCB2492	37144	Z98756	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	70,425	28-Aug-97
rx02037	353	GB_PR4:AC004921	150332	AC004921	Mycobacterium leprae cosmid B2492.	Mycobacterium leprae	37,822	14-Jan-99
rx02037	353	GB_HTG6:AC008076	200000	AC008076	Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.	Homo sapiens	37,822	14-Jan-99
rx02037	353	GB_PR4:AC004921	150332	AC004921	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***. 18 unordered pieces.	Homo sapiens	41,860	02-DEC-1999
rx02037	353	GB_PR4:AC004921	150332	AC004921	Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.	Homo sapiens	37,685	14-Jan-99

**TABLE 4: ALIGNMENT RESULTS**

rx02038	492	GB_BA2:SCU43429	1740	U43429	Streptomyces coelicolor ribosomal protein L13 (rplM) and S9 (rpsI) genes, complete cds.	Streptomyces coelicolor	55,876	13-Jan-98
		GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	55,876	20-Aug-98
		GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,382	18-Jun-98
rx02041	737	GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.	Mycobacterium tuberculosis	70,041	17-Jun-98
		GB_BA1:MBS100PER	5662	Y13228	Mycobacterium bovis BCG DNA for ribosomal S10 operon.	Mycobacterium bovis BCG	70,041	04-DEC-1997
		GB_BA1:MSGY42	36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	39,945	03-DEC-1996
rx02042	537	GB_BA1:MSGY42	36526	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	42,015	03-DEC-1996
		GB_BA1:MTCY210	36804	Z84395	Mycobacterium tuberculosis complete genome; segment 34/162.	Mycobacterium tuberculosis	66,541	17-Jun-98
		GB_BA1:MLCB2492	37144	Z98756	Mycobacterium leprae cosmid B2492.	Mycobacterium leprae	66,504	28-Aug-97
rx02043	241	GB_BA1:AB017508	32050	AB017508	Bacillus halodurans C-129 genomic DNA, 32 kb fragment, complete cds.	Bacillus halodurans	48,305	14-Apr-99
		GB_EST1:D41045	356	D41045	RICCS3004A Rice shoot Oryza sativa cDNA, mRNA sequence.	Oryza sativa	43,697	11-Nov-94
rx02077	519	GB_BA1:CZA382	42369	AL078635	Amycolatopsis orientalis cosmid PCZA382.	Amycolatopsis orientalis	42,152	17-Aug-99
		GB_RO:RNPLECT	15231	X59601	Rat mRNA for plectin.	Rattus norvegicus	41,468	19-DEC-1996
		GB_BA2:AF148219	1989	AF148219	Nostoc PCC8009 fibrillin and photosystem I protein E (psaE) genes, complete cds; and formamidyrimidine-DNA glycosylase MutM (mutM) gene, partial cds.	Nostoc PCC8009	36,346	9-Jun-99
		GB_RO:RNPLECT	15231	X59601	Rat mRNA for plectin.	Rattus norvegicus	36,505	19-DEC-1996
rx02145	1740	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	64,033	17-Jun-98
		GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	37,609	15-Jun-96
		GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	37,609	15-Jun-96
rx02179	951	GB_EST5:X93280	344	X93280	SSVAET19 S. scrofa ovary Sus scrofa cDNA clone V1ae19 5', mRNA sequence.	Sus scrofa	39,649	14-MAY-1997
		GB_GSS11:ACQ324492	859	ACQ324492	mgxb0018H12r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0018H12r, genomic survey sequence.	Magnaporthe grisea	36,151	8-Jan-99
		GB_HTG3:AC011395	95036	AC011395	Homo sapiens chromosome 5 clone C17978SKB_18712, *** SEQUENCING IN PROGRESS ***	Homo sapiens	35,263	06-OCT-1999
rx02190	1581	GB_BA1:MTCY01B2	35938	Z95554	PROGRESS ***	Mycobacterium tuberculosis	76,141	17-Jun-98
		GB_BA1:MLACEA	37049	Z46257	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	72,172	22-MAY-1996
		GB_BA1:SC7H2	42655	AL109732	M. leprae aceA gene for isocitrate lyase.	Streptomyces coelicolor A3(2)	40,627	2-Aug-99
rx02241	584	GB_HTG3:AC010579	157658	AC010579	Streptomyces coelicolor cosmid 7H2.	Drosophila melanogaster	40,402	24-Sep-99
		GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCL-98 09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	40,402	24-Sep-99
		GB_HTG2:AC007946	97610	AC007946	Drosophila melanogaster chromosome 3 clone BACR03003 (D769) RPCL-98 03.O.3 map 96E-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	40,248	2-Aug-99
rx02293	2511	GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	40,557	2-Aug-99
		GB_BA2:U49051	2859	U49051	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	48,002	7-Aug-97
rx02357	6423	GB_BA2:U32787	12361	U32787	Simorhizobium meliloti putative DEAH family helicase HelO gene, complete cds.	Simorhizobium meliloti	36,309	29-MAY-1998
		GB_EST1:T47370	307	T47370	Haemophilus influenzae Rd section 102 of 163 of the complete genome.	Haemophilus influenzae Rd	40,850	1-Feb-95
		GB_PR1:HSVMYCLC2	11997	Z15030	yb13b07.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:71029 5' similar to contains L1 repetitive element, mRNA sequence.	Homo sapiens	40,012	9-Feb-99
					H.sapiens gene for ventricular myosin light chain 2.	Homo sapiens		

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**TABLE 4: ALIGNMENT RESULTS**

rx02522	666	GB_PL2:AC004135	73805	AC004135	Homo sapiens chromosome 19 clone C17B-E1_302311, *** SEQUENCING IN PROGRESS *** 73 unordered pieces.	Homo sapiens	35,634	31-OCT-1999
rx02522	666	GB_PL2:AC004135	73805	AC004135	Genomic sequence for Arabidopsis thaliana BAC T17H7 from Chromosome 1, Arabidopsis thaliana complete sequence.	Arabidopsis thaliana	38,052	29-MAY-1999
rx02522	666	GB_PL2:AC004135	73805	AC004135	Genomic sequence for Arabidopsis thaliana BAC T17H7 from Chromosome 1, Arabidopsis thaliana complete sequence.	Arabidopsis thaliana	36,157	29-MAY-1999
rx02533		GB_RO:MUSTRAA	6149	M36386	Mouse tumor rejection antigen P815A gene, complete cds.	Mus musculus	35,769	27-Apr-93
rx02615	759	GB_BA1:MSKATG	2307	X98718	M.smegmatis katG gene.	Mycobacterium smegmatis	37,349	16-Jan-97
rx02615	759	GB_BA2:MSUA6844	16951	U46844	Mycobacterium smegmatis catalase-peroxidase (katG), putative arabinosyl transferase (embC, embA, embB), genes complete cds and putative propionyl-coA carboxylase beta chain (pccB) genes, partial cds.	Mycobacterium smegmatis	39,783	12-MAY-1997
rx02633	387	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepC) gene, partial cds.	Corynebacterium glutamicum	39,893	04-MAY-1999
rx02633	387	GB_RO:RNY09164	6556	Y09164	R.norvegicus mRNA for sodium channel.	Rattus norvegicus	34,204	8-Jan-97
rx02633	387	GB_RO:RNY09164	6556	Y09164	R.norvegicus mRNA for sodium channel.	Rattus norvegicus	38,298	8-Jan-97
rx02635	357	GB_BA1:MTV018	53450	AL021899	Mycobacterium tuberculosis H37Rv complete genome; segment 90/162.	Mycobacterium tuberculosis	37,464	18-Jun-98
rx02635	357	GB_GSS1:MTAF0013813045		AF001381	Mycobacterium tuberculosis strain KIT10218 cosmid 10R, partial sequence.	Mycobacterium tuberculosis	36,667	9-Aug-97
rx02636	285	GB_BA1:SC6C5	18160	AL034492	Streptomyces coelicolor cosmid 6C5.	Streptomyces coelicolor	42,938	14-DEC-1998
rx02636	285	GB_BA1:MTV018	53450	AL021899	Mycobacterium tuberculosis H37Rv complete genome; segment 90/162.	Mycobacterium tuberculosis	41,036	18-Jun-98
rx02636	285	GB_GSS1:MTAF0013813045		AF001381	Mycobacterium tuberculosis strain KIT10218 cosmid 10R, partial sequence.	Mycobacterium tuberculosis	40,206	9-Aug-97
rx02637	426	GB_GSS1:MTAF0013813045		AF001381	genomic survey sequence.	Mycobacterium tuberculosis	45,091	9-Aug-97
rx02637	426	GB_PR4:AC006602	93610	AC006602	genomic survey sequence.	Mycobacterium tuberculosis	37,441	23-Feb-99
rx02657	3705	GB_PR4:AC007275	169904	AC007275	Homo sapiens Chromosome 15q11-q13 PAC clone pJD47619 from the Prader-Homo sapiens Williams/Angelman Syndrome region, complete sequence.	Homo sapiens	36,170	29-Jul-99
rx02657	3705	GB_PR4:AC007275	169904	AC007275	Homo sapiens clone NH0109F19, complete sequence.	Homo sapiens	34,783	29-Jul-99
rx02657	3705	GB_BA1:MTCY48	35377	Z74020	Homo sapiens clone NH0109F19, complete sequence.	Homo sapiens	63,678	17-Jun-98
rx02657	3705	GB_BA1:MLC1458	43839	AL049478	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	63,716	27-Aug-99
rx02682	450	GB_BA1:MSGB13GS	42923	L78823	Mycobacterium leprae cosmid L458.	Mycobacterium leprae	37,939	15-Jun-96
rx02682	450	GB_PR2:AC002379	118595	AC002379	Mycobacterium leprae cosmid B13 DNA sequence.	Mycobacterium leprae	36,552	23-Jul-97
rx02682	450	GB_EST18:T44994	452	T44994	Human BAC clone GS165104 from Tq21, complete sequence.	Homo sapiens	34,247	7-Jan-98
rx02755	2118	GB_EST14:AA395030	444	AA395030	8257 Lambda-PRL2 Arabidopsis thaliana cDNA clone 127P23T7, mRNA sequence.	Arabidopsis thaliana	31,806	30-OCT-1997
rx02755	2118	GB_BA1:MTCY274	39991	Z74024	26827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 111K20XP 3', mRNA sequence.	Arabidopsis thaliana	38,715	19-Jun-98
rx02755	2118	GB_BA1:SC2E1	38962	AL023797	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	53,300	4-Jun-98
rx02755	2118	GB_BA2:SKZ86111	7860	Z86111	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	52,970	27-OCT-1999
rx02755	2118	GB_BA1:MSGY151	37036	AD000018	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, muIT genes and 4 open reading frames.	Streptomyces lividans	56,905	10-DEC-1996
rx02755	2118	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis		

**TABLE 4: ALIGNMENT RESULTS**

rx02764	GB_BA1:MTCY130 GB_BA1:SC4H2	32514 38400	Z73902 AL022268	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162. Streptomyces coelicolor cosmid 4H2.	Mycobacterium tuberculosis Streptomyces coelicolor	39,419 56,729	17-Jun-98 6-Apr-98
rx02819 1070	GB_GSS14:AQ549674	479	AQ549674	RPC1-11-413C1, TV RPC1-11 Homo sapiens genomic clone RPC1-11-413C1, genomic survey sequence. RPC1-11-413C1, TV RPC1-11 Homo sapiens genomic clone RPC1-11-413C1, genomic survey sequence.	Homo sapiens Homo sapiens	40,705 38,696	28-MAY-1999 28-MAY-1999
rx02826 558	GB_BA1:MTY20H10 GB_BA1:SGNUSG GB_BA1:STMVBR41	35980 7235 7409	Z92772 X72787 D50624	Mycobacterium tuberculosis H37Rv complete genome; segment 31/162. S. griseus nusG, rplKAL1 gene cluster. Streptomyces virginiae VbrA gene for NusG like protein, SecE like protein and Streptomyces virginiae ribosomal protein, aspartate aminotransferase and adenosine deaminase, complete cds.	Mycobacterium tuberculosis Streptomyces griseus Streptomyces virginiae	67,387 65,946 65,766	17-Jun-98 06-MAY-1998 10-Feb-99
rx02833 906	EM_PAT:E11161	3521	E11161	Genomic DNA including an autonomous replication sequences (ars)	Corynebacterium glutanicum	98,343	08-OCT-1997 (Rel. 52, Created) 08-DEC-1998
	GB_BA2:MAU19185 GB_BA1:MLUDNAA	3952 4171	U19185 M34006	Mycobacterium avium RpmH (rpmH) and DnaA (dnaA) genes, complete cds; and DnaN (dhan) gene, partial cds. M. luteus ribonuclease P (mpa), 50S ribosomal subunit protein L34 (rpmH), DNA biosynthesis initiation protein (dnaA), and DNA polymerase III beta subunit (dhan) genes, complete cds.	Mycobacterium avium Micrococcus luteus	46,333 46,540	16-Feb-94

Customer Number: 000959

Attorney's  
Docket No. BGI-130CP

**DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED  
IN DNA REPLICATION, PROTEIN SYNTHESIS, AND PATHOGENESIS**

the specification of which:

  X   is attached hereto.

           was filed on                                  as Application Serial No.                                 

and was amended on                                 .  
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.



## CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

☒ no such applications have been filed.

☐ such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS  
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
			<input type="checkbox"/> Yes <input type="checkbox"/> No
			<input type="checkbox"/> Yes <input type="checkbox"/> No
			<input type="checkbox"/> Yes <input type="checkbox"/> No
			<input type="checkbox"/> Yes <input type="checkbox"/> No
			<input type="checkbox"/> Yes <input type="checkbox"/> No

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS  
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION


## CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/144,448  
(Application Serial No.)

July 16, 1999  
(Filing Date)

60/149,402  
(Application Serial No.)

August 17, 1999  
(Filing Date)

## CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

_____ (Application Serial No.)	_____ (Filing Date)	_____ (Status) (patented,pending,aband.)
_____ (Application Serial No.)	_____ (Filing Date)	_____ (Status) (patented,pending,aband.)

**POWER OF ATTORNEY:** As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Jeremiah Lynch	Reg. No. 17,425	Maria Laccotripe Zacharakis	Limited Recognition
Kevin J. Canning	Reg. No. 35,470		Under 37 C.F.R. § 10.9(b)
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Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS,  
 AND PATHOGENESIS

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 Thr Val Lys Pro Val Gly Glu Ser Arg Ile Phe Asp Asp Ala Ala Phe  
 20 25 30

acc ggc acc gca cgc cag cca ctc gca cag gaa ttc cag cca ctc aac 144  
 Thr Gly Thr Ala Arg Gln Pro Leu Ala Gln Glu Phe Gln Pro Leu Asn  
 35 40 45

gac agc gag aaa tcc ttc gtc ggc gta gtc aac cac ttc aag tcc aag 192  
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 50 55 60

ggc tct gtc act cgt gga gac gcc gac acc ggc gac ggc caa ggc aac 240  
 Gly Ser Val Thr Arg Gly Asp Ala Asp Thr Gly Asp Gly Gln Gly Asn  
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aac gcc aac gtt cgc gtc gca cag gca cag gca ctc atc gac cac ctg 288  
 Asn Ala Asn Val Arg Val Ala Gln Ala Gln Ala Leu Ile Asp His Leu  
 85 90 95

gaa aac cag gac gac tgg gca tcc aag cca atc ttc atc ctc ggc gac 336  
 Glu Asn Gln Asp Asp Trp Ala Ser Lys Pro Ile Phe Ile Leu Gly Asp  
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acc aac tcc tac gcc aag gaa acc gcg atg acc acc ctt tac ggc gct 384  
 Thr Asn Ser Tyr Ala Lys Glu Thr Ala Met Thr Thr Leu Tyr Gly Ala  
 115 120 125

ggc tac acc aac atc gcc acc gaa ttc gac gct ggc tac agc tac cag 432  
 Gly Tyr Thr Asn Ile Ala Thr Glu Phe Asp Ala Gly Tyr Ser Tyr Gln  
 130 135 140

ttc tcc ggc cgc att ggc agc ctc gac cac gca ctc ggc aac gaa gca 480  
 Phe Ser Gly Arg Ile Gly Ser Leu Asp His Ala Leu Gly Asn Glu Ala  
 145 150 155 160  
  
 gcc atg aag cac gtc atc gac gcc gag gtc tgg gac atc aac gct gac 528  
 Ala Met Lys His Val Ile Asp Ala Glu Val Trp Asp Ile Asn Ala Asp  
 165 170 175  
  
 gaa gca atc gca ttc gaa tac tcc cgt cga ctc aac aac acc tcc gac 576  
 Glu Ala Ile Ala Phe Glu Tyr Ser Arg Arg Leu Asn Asn Thr Ser Asp  
 180 185 190  
  
 gta ttc gag aac aac gtc ttc cgc tcc tcc gac cac gac ccg atc aag 624  
 Val Phe Glu Asn Asn Val Phe Arg Ser Ser Asp His Asp Pro Ile Lys  
 195 200 205  
  
 gtc gga ttc aac ctc agc gag acc act gag ccc acc att ccg gta gag 672  
 Val Gly Phe Asn Leu Ser Glu Thr Thr Glu Pro Thr Ile Pro Val Glu  
 210 215 220  
  
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 Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Thr Thr Pro Val Lys Pro  
 225 230 235 240  
  
 act gat ccg gta gag acc acg gat cca tct gag cca acc gac cct gca 768  
 Thr Asp Pro Val Glu Thr Thr Asp Pro Ser Glu Pro Thr Asp Pro Ala  
 245 250 255  
  
 gaa cct act gat cca gct gaa cca act gac cct gag gaa acg aag aag 816  
 Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Glu Glu Thr Lys Lys  
 260 265 270  
  
 cca gag gag ccg aag aac cct ggt tcc tcc aac gga agc tcc caa tac 864  
 Pro Glu Glu Pro Lys Asn Pro Gly Ser Ser Asn Gly Ser Ser Gln Tyr  
 275 280 285  
  
 gcc acc att gca gca atc atc gca gca atc cta ggt gcc att gct ttg 912  
 Ala Thr Ile Ala Ala Ile Ile Ala Ala Ile Leu Gly Ala Ile Ala Leu  
 290 295 300  
  
 gcc ttc cag ttc ttc cat tca agt tct aat taactcttag ggagtaatcc 962  
 Ala Phe Gln Phe Phe His Ser Ser Ser Asn  
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 cct 965

&lt;210&gt; 2

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 2

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Thr Gly Thr Ala Arg Gln Pro Leu Ala Gln Glu Phe Gln Pro Leu Asn

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Asn Ala Asn Val Arg Val Ala Gln Ala Gln Ala Leu Ile Asp His Leu		
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Glu Asn Gln Asp Asp Trp Ala Ser Lys Pro Ile Phe Ile Leu Gly Asp		
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Thr Asn Ser Tyr Ala Lys Glu Thr Ala Met Thr Thr Leu Tyr Gly Ala		
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Gly Tyr Thr Asn Ile Ala Thr Glu Phe Asp Ala Gly Tyr Ser Tyr Gln		
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Phe Ser Gly Arg Ile Gly Ser Leu Asp His Ala Leu Gly Asn Glu Ala		
145	150	155 160
Ala Met Lys His Val Ile Asp Ala Glu Val Trp Asp Ile Asn Ala Asp		
165	170	175
Glu Ala Ile Ala Phe Glu Tyr Ser Arg Arg Leu Asn Asn Thr Ser Asp		
180	185	190
Val Phe Glu Asn Asn Val Phe Arg Ser Ser Asp His Asp Pro Ile Lys		
195	200	205
Val Gly Phe Asn Leu Ser Glu Thr Thr Glu Pro Thr Ile Pro Val Glu		
210	215	220
Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Thr Thr Pro Val Lys Pro		
225	230	235 240
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Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Glu Glu Thr Lys Lys		
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Pro Glu Glu Pro Lys Asn Pro Gly Ser Ser Asn Gly Ser Ser Gln Tyr		
275	280	285
Ala Thr Ile Ala Ala Ile Ile Ala Ala Ile Leu Gly Ala Ile Ala Leu		
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Ala Phe Gln Phe Phe His Ser Ser Ser Asn		
305	310	

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&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS



&lt;222&gt; (1)..(339)

&lt;223&gt; FRXA00625

&lt;400&gt; 3

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 Glu Pro Thr Ile Pro Val Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp  
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cca act acc cca gtt aag cca act gat ccg gta gag acc acg gat cca 144  
 Pro Thr Thr Pro Val Lys Pro Thr Asp Pro Val Glu Thr Thr Asp Pro  
 35 40 45

tct gag cca acc gac cct gca gaa cct act gat cca gct gaa cca act 192  
 Ser Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Ala Glu Pro Thr  
 50 55 60

gac cct gag gaa acg aag aag cca gag gag ccg aag aac cct ggt tcc 240  
 Asp Pro Glu Glu Thr Lys Lys Pro Glu Glu Pro Lys Asn Pro Gly Ser  
 65 70 75 80

tcc aac gga agc tcc caa tac gcc acc att gca gca atc atc gca gca 288  
 Ser Asn Gly Ser Ser Gln Tyr Ala Thr Ile Ala Ala Ile Ile Ala Ala  
 85 90 95

atc cta ggt gcc att gct ttg gcc ttc cag ttc ttc cat tca agt tct 336  
 Ile Leu Gly Ala Ile Ala Leu Ala Phe Gln Phe Phe His Ser Ser Ser  
 100 105 110

aat taactcttag ggagtaatcc cct 362  
 Asn

&lt;210&gt; 4

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 4

Ser Asp His Asp Pro Ile Lys Val Gly Phe Asn Leu Ser Glu Thr Thr  
 1 5 10 15

Glu Pro Thr Ile Pro Val Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp  
 20 25 30

Pro Thr Thr Pro Val Lys Pro Thr Asp Pro Val Glu Thr Thr Asp Pro  
 35 40 45

Ser Glu Pro Thr Asp Pro Ala Glu Pro Thr Asp Pro Ala Glu Pro Thr  
 50 55 60

Asp Pro Glu Glu Thr Lys Lys Pro Glu Glu Pro Lys Asn Pro Gly Ser  
 65 70 75 80

Ser Asn Gly Ser Ser Gln Tyr Ala Thr Ile Ala Ala Ile Ile Ala Ala  
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Ile Leu Gly Ala Ile Ala Leu Ala Phe Gln Phe Phe His Ser Ser Ser  
 100 105 110

Asn

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 Met Ser Arg Ile Ser  
 1 5  
 ggc cgc act ctg gca atc gca ctt gcc ggt gca acc ggc gcc agc ctg 163  
 Ala Arg Thr Leu Ala Ile Ala Leu Ala Gly Ala Thr Ala Ala Ser Leu  
 10 15 20  
 gca gtt gtt cca gca gca aca gct aat cct gcc gga acc gct cct gtc 211  
 Ala Val Val Pro Ala Ala Thr Ala Asn Pro Ala Gly Thr Ala Pro Val  
 25 30 35  
 atc aac gaa atc tac gaa ggc ggt gga aac agc gga tgc ttg ttc tcc 259  
 Ile Asn Glu Ile Tyr Glu Gly Gly Gly Asn Ser Gly Ser Leu Phe Ser  
 40 45 50  
 aac gac ttc att gag ctc tac aac cca acc tca ggg gac att tcc ctc 307  
 Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser Gly Asp Ile Ser Leu  
 55 60 65  
 gac ggt tgg agc gtt acc tac tac gca gcc aac ggt aac tcc ggc gga 355  
 Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn Gly Asn Ser Gly Gly  
 70 75 80 85  
 acc aca aac ctg acc gga aac atc cct gcc aac ggt tac tac ctc atc 403  
 Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn Gly Tyr Tyr Leu Ile  
 90 95 100  
 cag caa cgc gca ggc agc aac aac acc ggc gct ctg cct acc cca gac 451  
 Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala Leu Pro Thr Pro Asp  
 105 110 115  
 gcc acc ggt aac ttg gca atg ggt gcc tcc caa gga tca gtt gca ctg 499  
 Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln Gly Ser Val Ala Leu  
 120 125 130  
 acc gac aac tct ggc cta acc gct gac ctt gtc gga ttc ggt ggc acg 547  
 Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val Gly Phe Gly Gly Thr  
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Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu Thr Ser Asn Lys Leu	
150 155 160 165	
tct gtt caa cgc aaa gaa gtt ggc gct gac tct gat aac aac tcc gta	643
Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser Asp Asn Asn Ser Val	
170 175 180	
gac ttc gag act gga gct cca act cca acg tcc tcg gga gga tcc gct	691
Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser Ser Gly Gly Ser Ala	
185 190 195	
cct gtt gac cca ggc gag cca gaa act cca gta aac cct ggg gaa aca	739
Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val Asn Pro Gly Glu Thr	
200 205 210	
gtc tcc atc gca caa atc caa gga acc ggt ctc gct acc cca ctc gag	787
Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu Ala Thr Pro Leu Glu	
215 220 225	
ggg cag acc gtc acc acc gaa ggt att gtc act gcc gtt tac gca gaa	835
Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr Ala Val Tyr Ala Glu	
230 235 240 245	
ggg ggc ttc aac ggt tac tac atc cag aca cct gga tct ggt act gca	883
Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro Gly Ser Gly Thr Ala	
250 255 260	
cca aag gtt gct ggc gac gca tcc gac ggc atc ttc gtc tac gtg gga	931
Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile Phe Val Tyr Val Gly	
265 270 275	
agc aat ggt tcc tac cca gag ctc ggc gca tct gtc acc gtc act ggc	979
Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser Val Thr Val Thr Gly	
280 285 290	
aag gcc acc gaa cac tac gag atg act cag cta ggc aac tcc tcc ttc	1027
Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu Gly Asn Ser Ser Phe	
295 300 305	
acc gtt tcg gac acc gca ttc gag cca gta acc cca ctc gaa ctg gac	1075
Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr Pro Leu Glu Leu Asp	
310 315 320 325	
acc gtt cct act ggc gat gac att cgc gaa gca tac gaa ggc atg ctg	1123
Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala Tyr Glu Gly Met Leu	
330 335 340	
ctg aag cca acc ggc gct cac acc gtg acc aac aac tac gca acc aac	1171
Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn Asn Tyr Ala Thr Asn	
345 350 355	
acc ttc ggt gaa att gcc ctc gcc cca ggt aac gag cct ttg tac cag	1219
Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn Glu Pro Leu Tyr Gln	
360 365 370	
gcc act caa atg gtg gca ccg gga gcc gaa gcg att gcg tac gag gcg	1267
Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala Ile Ala Tyr Glu Ala	
375 380 385	
gaa aac gtc gca aag caa att acg ctg gat gac gga cgc tcc ggc aac	1315
Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp Gly Arg Ser Gly Asn	

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tac act cgc ggc gac tcc agc acg cct atg gca tgg ctt gtg cag gac				1363
Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala Trp Leu Val Gln Asp				
410		415	420	
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Gly Gly Glu Thr Ile Lys Ser Ile Arg Thr Gly Asp Gln Val Glu Phe				
425		430	435	
cag gca cca gta atc ttc gat tac cgc tac gac ctg tgg aaa ttc cag				1459
Gln Ala Pro Val Ile Phe Asp Tyr Arg Tyr Asp Leu Trp Lys Phe Gln				
440		445	450	
cca acc acc cct gtc acc ggc aac acc gca agc tcc gac ctt cct atc				1507
Pro Thr Thr Pro Val Thr Gly Asn Thr Ala Ser Ser Asp Leu Pro Ile				
455		460	465	
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Thr Trp Asp Asp Thr Arg Ala Ala Glu Leu Ala Ser Ile Asn Asp Val				
470		475	480	485
gct ggc gaa ttc cac atc gca agc ttc aac gtg ctc aac tac ttc acc				1603
Ala Gly Glu Phe His Ile Ala Ser Phe Asn Val Leu Asn Tyr Phe Thr				
490		495	500	
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Ser Leu Gly Glu Asp Glu Pro Gly Cys Ser Ala Tyr Arg Asp Ile Asn				
505		510	515	
aac acc cca gtc acc gcc aac aac tgt aac gtc cgt ggc gct tac acc				1699
Asn Thr Pro Val Thr Ala Asn Asn Cys Asn Val Arg Gly Ala Tyr Thr				
520		525	530	
gaa gaa gca ctc gaa gat cag cag agc aag atc gtc gaa gca atc aac				1747
Glu Glu Ala Leu Glu Asp Gln Gln Ser Lys Ile Val Glu Ala Ile Asn				
535		540	545	
cgc ctt gac gtc gat gtt ctt				1768
Arg Leu Asp Val Asp Val Leu				
550		555		

&lt;210&gt; 6

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 6

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Gly	Thr	Ala	Pro	Val	Ile	Asn	Glu	Ile	Tyr	Glu	Gly	Gly	Gly	Asn	Ser
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Gly	Ser	Leu	Phe	Ser	Asn	Asp	Phe	Ile	Glu	Leu	Tyr	Asn	Pro	Thr	Ser
		50				55					60				

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 65 70 75 80  
 Gly Asn Ser Gly Gly Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn  
 85 90 95  
 Gly Tyr Tyr Leu Ile Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala  
 100 105 110  
 Leu Pro Thr Pro Asp Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln  
 115 120 125  
 Gly Ser Val Ala Leu Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val  
 130 135 140  
 Gly Phe Gly Gly Thr Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu  
 145 150 155 160  
 Thr Ser Asn Lys Leu Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser  
 165 170 175  
 Asp Asn Asn Ser Val Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser  
 180 185 190  
 Ser Gly Gly Ser Ala Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val  
 195 200 205  
 Asn Pro Gly Glu Thr Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu  
 210 215 220  
 Ala Thr Pro Leu Glu Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr  
 225 230 235 240  
 Ala Val Tyr Ala Glu Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro  
 245 250 255  
 Gly Ser Gly Thr Ala Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile  
 260 265 270  
 Phe Val Tyr Val Gly Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser  
 275 280 285  
 Val Thr Val Thr Gly Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu  
 290 295 300  
 Gly Asn Ser Ser Phe Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr  
 305 310 315 320  
 Pro Leu Glu Leu Asp Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala  
 325 330 335  
 Tyr Glu Gly Met Leu Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn  
 340 345 350  
 Asn Tyr Ala Thr Asn Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn  
 355 360 365  
 Glu Pro Leu Tyr Gln Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala  
 370 375 380  
 Ile Ala Tyr Glu Ala Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp

Time	Temperature	Pressure	Flow rate	Concentration	Sample	Analysis
0.00	25.00	1.00	1.00	1.00	1.00	1.00
0.05	25.00	1.00	1.00	1.00	1.00	1.00
0.10	25.00	1.00	1.00	1.00	1.00	1.00
0.15	25.00	1.00	1.00	1.00	1.00	1.00
0.20	25.00	1.00	1.00	1.00	1.00	1.00
0.25	25.00	1.00	1.00	1.00	1.00	1.00
0.30	25.00	1.00	1.00	1.00	1.00	1.00
0.35	25.00	1.00	1.00	1.00	1.00	1.00
0.40	25.00	1.00	1.00	1.00	1.00	1.00
0.45	25.00	1.00	1.00	1.00	1.00	1.00
0.50	25.00	1.00	1.00	1.00	1.00	1.00
0.55	25.00	1.00	1.00	1.00	1.00	1.00
0.60	25.00	1.00	1.00	1.00	1.00	1.00
0.65	25.00	1.00	1.00	1.00	1.00	1.00
0.70	25.00	1.00	1.00	1.00	1.00	1.00
0.75	25.00	1.00	1.00	1.00	1.00	1.00
0.80	25.00	1.00	1.00	1.00	1.00	1.00
0.85	25.00	1.00	1.00	1.00	1.00	1.00
0.90	25.00	1.00	1.00	1.00	1.00	1.00
0.95	25.00	1.00	1.00	1.00	1.00	1.00
1.00	25.00	1.00	1.00	1.00	1.00	1.00

1000

140

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 Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser Gly Asp Ile Ser Leu  
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gac ggt tgg agc gtt acc tac tac gca gcc aac ggt aac tcc ggc gga 355  
 Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn Gly Asn Ser Gly Gly  
 70 75 80 85

acc aca aac ctg acc gga aac atc cct gcc aac ggt tac tac ctc atc 403  
 Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn Gly Tyr Tyr Leu Ile  
 90 95 100

cag caa cgc gca ggc agc aac aac acc ggc gct ctg cct acc cca gac 451  
 Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala Leu Pro Thr Pro Asp  
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gcc acc ggt aac ttg gca atg ggt gcc tcc caa gga tca gtt gca ctg 499  
 Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln Gly Ser Val Ala Leu  
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acc gac aac tct ggc cta acc gct gac ctt gtc gga ttc ggt ggc acg 547  
 Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val Gly Phe Gly Gly Thr  
 135 140 145

tcc atg ttt gaa gga aca gct gct gca cct gag acc agc aac aaa ttg 595  
 Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu Thr Ser Asn Lys Leu  
 150 155 160 165

tct gtt caa cgc aaa gaa gtt ggc gct gac tct gat aac aac tcc gta 643  
 Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser Asp Asn Asn Ser Val  
 170 175 180

gac ttc gag act gga gct cca act cca acg tcc tcg gga gga tcc gct 691  
 Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser Ser Gly Gly Ser Ala  
 185 190 195

cct gtt gac cca ggc gag cca gaa act cca gta aac cct ggg gaa aca 739  
 Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val Asn Pro Gly Glu Thr  
 200 205 210

gtc tcc atc gca caa atc caa gga acc ggt ctc gct acc cca ctc gag 787  
 Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu Ala Thr Pro Leu Glu  
 215 220 225

ggt cag acc gtc acc acc gaa ggt att gtc act gcc gtt tac gca gaa 835  
 Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr Ala Val Tyr Ala Glu  
 230 235 240 245

ggt ggc ttc aac ggt tac tac atc cag aca cct gga tct ggt act gca 883  
 Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro Gly Ser Gly Thr Ala  
 250 255 260

cca aag gtt gct ggc gac gca tcc gac ggc atc ttc gtc tac gtg gga 931  
 Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile Phe Val Tyr Val Gly  
 265 270 275

agc aat ggt tcc tac cca gag ctc ggc gca tct gtc acc gtc act ggc 979  
 Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser Val Thr Val Thr Gly  
 280 285 290

aag gcc acc gaa cac tac gag atg act cag cta ggc aac tcc tcc ttc 1027  
 Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu Gly Asn Ser Ser Phe  
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 Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr Pro Leu Glu Leu Asp  
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 Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala Tyr Glu Gly Met Leu  
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 ctg aag cca acc ggc gct cac acc gtg acc aac aac tac gca acc aac 1171  
 Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn Asn Tyr Ala Thr Asn  
 345 350 355  
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 Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn Glu Pro Leu Tyr Gln  
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 Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala Ile Ala Tyr Glu Ala  
 375 380 385  
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 Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp Gly Arg Ser Gly Asn  
 390 395 400 405  
 tac act cgc ggc gac tcc agc acg cct atg gca tgg ctt gtg cag gac 1363  
 Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala Trp Leu Val Gln Asp  
 410 415 420  
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 Gly Gly

&lt;210&gt; 8

&lt;211&gt; 423

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 8

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Thr Ala Ala Ser Leu Ala Val Val Pro Ala Ala Thr Ala Asn Pro Ala  
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Gly Thr Ala Pro Val Ile Asn Glu Ile Tyr Glu Gly Gly Gly Asn Ser  
 35 40 45

Gly Ser Leu Phe Ser Asn Asp Phe Ile Glu Leu Tyr Asn Pro Thr Ser  
 50 55 60

Gly Asp Ile Ser Leu Asp Gly Trp Ser Val Thr Tyr Tyr Ala Ala Asn  
 65 70 75 80

Gly Asn Ser Gly Gly Thr Thr Asn Leu Thr Gly Asn Ile Pro Ala Asn  
 85 90 95



Gly Tyr Tyr Leu Ile Gln Gln Arg Ala Gly Ser Asn Asn Thr Gly Ala  
 100 105 110  
 Leu Pro Thr Pro Asp Ala Thr Gly Asn Leu Ala Met Gly Ala Ser Gln  
 115 120 125  
 Gly Ser Val Ala Leu Thr Asp Asn Ser Gly Leu Thr Ala Asp Leu Val  
 130 135 140  
 Gly Phe Gly Gly Thr Ser Met Phe Glu Gly Thr Ala Ala Ala Pro Glu  
 145 150 155 160  
 Thr Ser Asn Lys Leu Ser Val Gln Arg Lys Glu Val Gly Ala Asp Ser  
 165 170 175  
 Asp Asn Asn Ser Val Asp Phe Glu Thr Gly Ala Pro Thr Pro Thr Ser  
 180 185 190  
 Ser Gly Gly Ser Ala Pro Val Asp Pro Gly Glu Pro Glu Thr Pro Val  
 195 200 205  
 Asn Pro Gly Glu Thr Val Ser Ile Ala Gln Ile Gln Gly Thr Gly Leu  
 210 215 220  
 Ala Thr Pro Leu Glu Gly Gln Thr Val Thr Thr Glu Gly Ile Val Thr  
 225 230 235 240  
 Ala Val Tyr Ala Glu Gly Gly Phe Asn Gly Tyr Tyr Ile Gln Thr Pro  
 245 250 255  
 Gly Ser Gly Thr Ala Pro Lys Val Ala Gly Asp Ala Ser Asp Gly Ile  
 260 265 270  
 Phe Val Tyr Val Gly Ser Asn Gly Ser Tyr Pro Glu Leu Gly Ala Ser  
 275 280 285  
 Val Thr Val Thr Gly Lys Ala Thr Glu His Tyr Glu Met Thr Gln Leu  
 290 295 300  
 Gly Asn Ser Ser Phe Thr Val Ser Asp Thr Ala Phe Glu Pro Val Thr  
 305 310 315 320  
 Pro Leu Glu Leu Asp Thr Val Pro Thr Gly Asp Asp Ile Arg Glu Ala  
 325 330 335  
 Tyr Glu Gly Met Leu Leu Lys Pro Thr Gly Ala His Thr Val Thr Asn  
 340 345 350  
 Asn Tyr Ala Thr Asn Thr Phe Gly Glu Ile Ala Leu Ala Pro Gly Asn  
 355 360 365  
 Glu Pro Leu Tyr Gln Ala Thr Gln Met Val Ala Pro Gly Ala Glu Ala  
 370 375 380  
 Ile Ala Tyr Glu Ala Glu Asn Val Ala Lys Gln Ile Thr Leu Asp Asp  
 385 390 395 400  
 Gly Arg Ser Gly Asn Tyr Thr Arg Gly Asp Ser Ser Thr Pro Met Ala  
 405 410 415  
 Trp Leu Val Gln Asp Gly Gly

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<211> 903
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA00823
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Met Gly Ser Ile Thr																	
1 5																	
ccg cag aag cgg cct cgc gtg ggg tct cac atc gcg aac aag ggt caa																	163
Pro Gln Lys Arg Pro Arg Val Gly Ser His Ile Ala Asn Lys Gly Gln																	
10 15 20																	
gag act gat atc ggg cga aaa cgc cga gct cga cgc atc aat cgc aca																	211
Glu Thr Asp Ile Gly Arg Lys Arg Arg Ala Arg Arg Ile Asn Arg Thr																	
25 30 35																	
ctc acc gtg gca tat ccg gat gcg cac tgc gaa tta gat ttc acc aat																	259
Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu Leu Asp Phe Thr Asn																	
40 45 50																	
ccg cta gaa ctc acg gtc gcc acc att ttg tcc gcc cag tgc acg gac																	307
Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser Ala Gln Cys Thr Asp																	
55 60 65																	
gtt cgc gtg aac cag gtg acg ccc gcg ttg ttc aag cgc tat ccg acg																	355
Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe Lys Arg Tyr Pro Thr																	
70 75 80 85																	
gcc aca gat tac gcc aac gcc gat cgc acg gaa ttg gag gag ttc atc																	403
Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu Leu Glu Glu Phe Ile																	
90 95 100																	
cgt ccg aca ggc ttt tac cgc aac aag gcc act tct tta atc ggc ctg																	451
Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr Ser Leu Ile Gly Leu																	
105 110 115																	
ggg gag gca cta att tcg ctt cac gac ggc cag gtc ccc ggt acc ctt																	499
Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln Val Pro Gly Thr Leu																	
120 125 130																	
gag cag cta gtt gag ctg ccg ggg gtc ggg cgg aaa acc gcc aac gtg																	547
Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val																	
135 140 145																	
gtg ctg gga aat gct ttc ggt gtt ccg gga atc acg gtg gat aca cac																	595
Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile Thr Val Asp Thr His																	
150 155 160 165																	
ttt ggc agg ttg gtg cgt cgc ctg aag ctc act gat gaa gaa gat ccc																	643

Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr Asp Glu Glu Asp Pro  
 170 175 180

gtc aag gtg gaa aaa gtg atg aac gaa ctc atc gaa aag cct gag tgg 691  
 Val Lys Val Glu Lys Val Met Asn Glu Leu Ile Glu Lys Pro Glu Trp  
 185 190 195

acc atg ttt tca cat agg ctg atc ttc cac gga cgt agg ata tgt cat 739  
 Thr Met Phe Ser His Arg Leu Ile Phe His Gly Arg Arg Ile Cys His  
 200 205 210

agt cga cgc gcc gcc tgt gga gcc tgc atg ctg gca gct gat tgc cca 787  
 Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu Ala Ala Asp Cys Pro  
 215 220 225

tcc ttt ggt ttg gag ggg ccg tca gat cca ttt gag gcg caa aaa ctc 835  
 Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe Glu Ala Gln Lys Leu  
 230 235 240 245

att aaa agt gat gat agg gag cac ctg ctg aaa atg gca gga atg 880  
 Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys Met Ala Gly Met  
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tagaaaacaa atgacaagca gtg 903

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 20 25 30

Arg Ile Asn Arg Thr Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu  
 35 40 45

Leu Asp Phe Thr Asn Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser  
 50 55 60

Ala Gln Cys Thr Asp Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe  
 65 70 75 80

Lys Arg Tyr Pro Thr Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu  
 85 90 95

Leu Glu Glu Phe Ile Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr  
 100 105 110

Ser Leu Ile Gly Leu Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln  
 115 120 125

Val Pro Gly Thr Leu Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg  
 130 135 140

Lys Thr Ala Asn Val Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile  
 145 150 155 160

Thr Val Asp Thr His Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr  
 165 170 175

Asp Glu Glu Asp Pro Val Lys Val Glu Lys Val Met Asn Glu Leu Ile  
 180 185 190

Glu Lys Pro Glu Trp Thr Met Phe Ser His Arg Leu Ile Phe His Gly  
 195 200 205

Arg Arg Ile Cys His Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu  
 210 215 220

Ala Ala Asp Cys Pro Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe  
 225 230 235 240

Glu Ala Gln Lys Leu Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys  
 245 250 255

Met Ala Gly Met  
 260

<210> 11  
 <211> 1740  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1717)  
 <223> RXA02145

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tcattgagcc actcggccct gcattctggg agcgtaagtc atg agt cta gct acc 115  
 Met Ser Leu Ala Thr  
 1 5

gtg gga aac aat ctt gat tcc cgt tac acc atg gcg tcg ggt atc cgt 163  
 Val Gly Asn Asn Leu Asp Ser Arg Tyr Thr Met Ala Ser Gly Ile Arg  
 10 15 20

cgc cag atc aac aag gtc ttc cca act cac tgg tcc ttc atg ctc ggc 211  
 Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp Ser Phe Met Leu Gly  
 25 30 35

gag att gcg ctt tac agc ttc atc gtc ttg ctg ctg act ggt gtc tac 259  
 Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu Leu Thr Gly Val Tyr  
 40 45 50

ctg acc ctg ttc ttc gac cca tca atc acc aag gtc att tat gac ggc 307  
 Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys Val Ile Tyr Asp Gly  
 55 60 65

ggc tac ctc cca ctg aac ggt gtg gag atg tcc cgt gca tac gca act 355  
 Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser Arg Ala Tyr Ala Thr  
 70 75 80 85

gcg ttg gat att tcc ttc gag gtt cgc ggt ggt ctg ttc atc cgc cag 403

Ala Leu Asp Ile Ser Phe Glu Val Arg Gly Gly Leu Phe Ile Arg Gln	
90 95 100	
atg cac cac tgg gca gcc ctg ctg ttc gtt gta tcc atg ctg gtt cac	451
Met His His Trp Ala Ala Leu Leu Phe Val Val Ser Met Leu Val His	
105 110 115	
atg ctc cgt att ttc ttc acc ggt gcg ttc cgt cgc cca cgt gaa gca	499
Met Leu Arg Ile Phe Phe Thr Gly Ala Phe Arg Arg Pro Arg Glu Ala	
120 125 130	
aac tgg atc atc ggt gtt gtt ctg atc atc ctg ggt atg gct gaa ggc	547
Asn Trp Ile Ile Gly Val Val Leu Ile Ile Leu Gly Met Ala Glu Gly	
135 140 145	
ttc atg ggt tac tcc ctg cct gat gac ctg ctc tct ggt gtt ggt ctt	595
Phe Met Gly Tyr Ser Leu Pro Asp Asp Leu Leu Ser Gly Val Gly Leu	
150 155 160 165	
cga atc atg tcc gcc atc atc gtt ggt ctt ccg atc ata ggt acc tgg	643
Arg Ile Met Ser Ala Ile Ile Val Gly Leu Pro Ile Ile Gly Thr Trp	
170 175 180	
atg cac tgg ctg atc ttc ggt gga gac ttc cca tcc gat ctg atg ctg	691
Met His Trp Leu Ile Phe Gly Gly Asp Phe Pro Ser Asp Leu Met Leu	
185 190 195	
gac cgc ttc tac atc gca cac gtt cta atc atc cca gct atc ctg ctt	739
Asp Arg Phe Tyr Ile Ala His Val Leu Ile Ile Pro Ala Ile Leu Leu	
200 205 210	
ggc ttg atc gca gct cac ctg gca ctt gtt tgg tac cag aag cac acc	787
Gly Leu Ile Ala Ala His Leu Ala Leu Val Trp Tyr Gln Lys His Thr	
215 220 225	
cag ttc cca ggc gct ggc cgc act gag aac aac gtg atc ggt atc cga	835
Gln Phe Pro Gly Ala Gly Arg Thr Glu Asn Asn Val Ile Gly Ile Arg	
230 235 240 245	
atc atg cct ctg ttc gca gtt aag gct gtt gct ttc ggc ctc atc gtc	883
Ile Met Pro Leu Phe Ala Val Lys Ala Val Ala Phe Gly Leu Ile Val	
250 255 260	
ttc ggt ttc ctc gca ctg ctt gct ggt gtc acc acc att aac gca att	931
Phe Gly Phe Leu Ala Leu Leu Ala Gly Val Thr Thr Ile Asn Ala Ile	
265 270 275	
tgg aat ctt gga ccg tac aac cct tca cag gtg tct gct ggt tcc cag	979
Trp Asn Leu Gly Pro Tyr Asn Pro Ser Gln Val Ser Ala Gly Ser Gln	
280 285 290	
cct gac gtt tac atg ctg tgg aca gat ggt gct gct cgt gtc atg ccg	1027
Pro Asp Val Tyr Met Leu Trp Thr Asp Gly Ala Ala Arg Val Met Pro	
295 300 305	
gca tgg gag ctc tac ctc ggt aac tac act att cca gca gtc ttc tgg	1075
Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile Pro Ala Val Phe Trp	
310 315 320 325	
gtt gct gtg atg ctg ggt atc ctc gtg gtt ctg ctt gtg act tac cca	1123
Val Ala Val Met Leu Gly Ile Leu Val Val Leu Leu Val Thr Tyr Pro	

330	335	340	
ttc att gag cgt aag ttc acc ggc gac gat gca cac cac aac ttg ctg			1171
Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala His His Asn Leu Leu			
345	350	355	
cag cgt cct cgc gat gtt cca gtc cgc acc tca ctc ggt gtc atg gcg			1219
Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser Leu Gly Val Met Ala			
360	365	370	
ctt gtc ttc tac atc ctg ctt acc gtt tct ggt ggt aac gat gtt tac			1267
Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly Gly Asn Asp Val Tyr			
375	380	385	
gca atg cag ttc cat gtt tca ctg aac gcg atg acc tgg atc ggt cgt			1315
Ala Met Gln Phe His Val Ser Leu Asn Ala Met Thr Trp Ile Gly Arg			
390	395	400	405
atc ggc ctc atc gtt gga cca gct att gca tac ttc atc act tac cga			1363
Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr Phe Ile Thr Tyr Arg			
410	415	420	
ctg tgc atc ggc ttg cag cgc tct gac cgc gag gtc ctg gag cac ggc			1411
Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu Val Leu Glu His Gly			
425	430	435	
atc gag acc ggt atc atc aag cag atg cca aat ggt gcc ttc att gaa			1459
Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn Gly Ala Phe Ile Glu			
440	445	450	
gtt cac cag cca ctt ggc cca gtt gat gac cat ggt cac cca atc cca			1507
Val His Gln Pro Leu Gly Pro Val Asp Asp His Gly His Pro Ile Pro			
455	460	465	
ctg cca tac gct ggc gct gcg gtt cca aag cag atg aac cag ctt ggt			1555
Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln Met Asn Gln Leu Gly			
470	475	480	485
tac gct gag gtt gaa acc cgc ggt gga ttc ttc gga cct gat cca gaa			1603
Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe Gly Pro Asp Pro Glu			
490	495	500	
gac atc cgt gcg aag gct aag gaa att gag cac gca aac cac att gag			1651
Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His Ala Asn His Ile Glu			
505	510	515	
gaa gcg aac act ctt cgt gca ctc aac gag gca aac att gag cgt gac			1699
Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala Asn Ile Glu Arg Asp			
520	525	530	
aag aat gag ggc aag aac tagttttctag gacttcatct ctg			1740
Lys Asn Glu Gly Lys Asn			
535			

&lt;210&gt; 12

&lt;211&gt; 539

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

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 Ser Phe Met Leu Gly Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu  
 35 40 45  
 Leu Thr Gly Val Tyr Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys  
 50 55 60  
 Val Ile Tyr Asp Gly Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser  
 65 70 75 80  
 Arg Ala Tyr Ala Thr Ala Leu Asp Ile Ser Phe Glu Val Arg Gly Gly  
 85 90 95  
 Leu Phe Ile Arg Gln Met His His Trp Ala Ala Leu Leu Phe Val Val  
 100 105 110  
 Ser Met Leu Val His Met Leu Arg Ile Phe Phe Thr Gly Ala Phe Arg  
 115 120 125  
 Arg Pro Arg Glu Ala Asn Trp Ile Ile Gly Val Val Leu Ile Ile Leu  
 130 135 140  
 Gly Met Ala Glu Gly Phe Met Gly Tyr Ser Leu Pro Asp Asp Leu Leu  
 145 150 155 160  
 Ser Gly Val Gly Leu Arg Ile Met Ser Ala Ile Ile Val Gly Leu Pro  
 165 170 175  
 Ile Ile Gly Thr Trp Met His Trp Leu Ile Phe Gly Gly Asp Phe Pro  
 180 185 190  
 Ser Asp Leu Met Leu Asp Arg Phe Tyr Ile Ala His Val Leu Ile Ile  
 195 200 205  
 Pro Ala Ile Leu Leu Gly Leu Ile Ala Ala His Leu Ala Leu Val Trp  
 210 215 220  
 Tyr Gln Lys His Thr Gln Phe Pro Gly Ala Gly Arg Thr Glu Asn Asn  
 225 230 235 240  
 Val Ile Gly Ile Arg Ile Met Pro Leu Phe Ala Val Lys Ala Val Ala  
 245 250 255  
 Phe Gly Leu Ile Val Phe Gly Phe Leu Ala Leu Leu Ala Gly Val Thr  
 260 265 270  
 Thr Ile Asn Ala Ile Trp Asn Leu Gly Pro Tyr Asn Pro Ser Gln Val  
 275 280 285  
 Ser Ala Gly Ser Gln Pro Asp Val Tyr Met Leu Trp Thr Asp Gly Ala  
 290 295 300  
 Ala Arg Val Met Pro Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile  
 305 310 315 320  
 Pro Ala Val Phe Trp Val Ala Val Met Leu Gly Ile Leu Val Val Leu

325										330										335										
Leu	Val	Thr	Tyr	Pro	Phe	Ile	Glu	Arg	Lys	Phe	Thr	Gly	Asp	Asp	Ala															
			340						345					350																
His	His	Asn	Leu	Leu	Gln	Arg	Pro	Arg	Asp	Val	Pro	Val	Arg	Thr	Ser															
		355					360					365																		
Leu	Gly	Val	Met	Ala	Leu	Val	Phe	Tyr	Ile	Leu	Leu	Thr	Val	Ser	Gly															
	370					375					380																			
Gly	Asn	Asp	Val	Tyr	Ala	Met	Gln	Phe	His	Val	Ser	Leu	Asn	Ala	Met															
385					390					395				400																
Thr	Trp	Ile	Gly	Arg	Ile	Gly	Leu	Ile	Val	Gly	Pro	Ala	Ile	Ala	Tyr															
			405						410					415																
Phe	Ile	Thr	Tyr	Arg	Leu	Cys	Ile	Gly	Leu	Gln	Arg	Ser	Asp	Arg	Glu															
		420						425					430																	
Val	Leu	Glu	His	Gly	Ile	Glu	Thr	Gly	Ile	Ile	Lys	Gln	Met	Pro	Asn															
	435					440					445																			
Gly	Ala	Phe	Ile	Glu	Val	His	Gln	Pro	Leu	Gly	Pro	Val	Asp	Asp	His															
	450					455					460																			
Gly	His	Pro	Ile	Pro	Leu	Pro	Tyr	Ala	Gly	Ala	Ala	Val	Pro	Lys	Gln															
465					470				475					480																
Met	Asn	Gln	Leu	Gly	Tyr	Ala	Glu	Val	Glu	Thr	Arg	Gly	Gly	Phe	Phe															
			485					490					495																	
Gly	Pro	Asp	Pro	Glu	Asp	Ile	Arg	Ala	Lys	Ala	Lys	Glu	Ile	Glu	His															
		500						505					510																	
Ala	Asn	His	Ile	Glu	Glu	Ala	Asn	Thr	Leu	Arg	Ala	Leu	Asn	Glu	Ala															
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 Met Ser Leu Ser Ile  
 1 5  
 agt ttt cat aaa att gca ctc tct gcc acc acc ttg ctt ggc gct gtc 163  
 Ser Phe His Lys Ile Ala Leu Ser Ala Thr Thr Leu Leu Gly Ala Val



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Ala Ile Ser Ala Cys Ala Leu Val Thr Gln Ala Pro Pro Ile Asn Ala				
	25	30	35	
gcc ccg gtt act ggc agc agc tca tta agc ttc acc ctc gac ctg ggc				259
Ala Pro Val Thr Gly Ser Ser Ser Leu Ser Phe Thr Leu Asp Leu Gly				
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Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys Leu Thr Gln Gln Ala				
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Gln Asn Gln Ala Ala Pro Arg Val Ala Ala Ser Leu Val Arg Val Val				
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Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly Ala Gln Lys Thr Val				
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Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn Leu Thr Thr Met Leu				
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cgc ggt gcc acc atc aca cta gaa ttt gat tcc acc caa gcc cgc gaa				547
Arg Gly Ala Thr Ile Thr Leu Glu Phe Asp Ser Thr Gln Ala Arg Glu				
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Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp Tyr Thr Lys Gly Asp				
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agc ggt ctt aag ctt gcc aat ttg gaa caa att gcc tca ggc tct gct				643
Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile Ala Ser Gly Ser Ala				
	170	175	180	
gct gaa tac agc ttc gac acc cgc tac aac cac cgc aat att ttc cta				691
Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His Arg Asn Ile Phe Leu				
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cgt gca caa acc ctt gcc aag gca agc agt cta ggt atg tgg ggt				736
Arg Ala Gln Thr Leu Ala Lys Ala Ser Ser Leu Gly Met Trp Gly				
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&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 14

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5

10

15

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Thr Leu Asp Leu Gly Thr Thr Thr Pro Thr Ser Ile Asp Thr Val Lys  
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Leu Val Arg Val Val Asp Gly Asp Thr Ile Val Val Asn Tyr Gln Gly  
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Ala Gln Lys Thr Val Arg Met Ile Gly Ile Asp Ser Pro Glu Thr Lys  
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His Pro Thr Lys Pro Val Gly Phe Tyr Gly Pro Glu Ser Ser Gln Asn  
115 120 125

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Thr Gln Ala Arg Glu Asp Gln Tyr Gly Arg Leu Leu Ala Tyr Val Trp  
145 150 155 160

Tyr Thr Lys Gly Asp Ser Gly Leu Lys Leu Ala Asn Leu Glu Gln Ile  
165 170 175

Ala Ser Gly Ser Ala Ala Glu Tyr Ser Phe Asp Thr Arg Tyr Asn His  
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Met Val Ala Arg Arg  
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Arg Leu Asp Ala Glu Leu Val Arg Arg Lys Ile Ala Arg Ser Arg Glu  
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cac gcg gtt gaa atg atc cgc ggt cgg cgc gtc ttt gtt gca gga atg 211  
 His Ala Val Glu Met Ile Arg Gly Arg Arg Val Phe Val Ala Gly Met  
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 Leu Ala Leu Lys Pro Ala Thr Val Val Glu Pro Glu Val Ser Ile Arg  
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 Val Glu Glu Asp Ala Ser Glu Asp Trp Ala Ser Arg Gly Ala His Lys  
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 Tyr Gly Gln Leu Ile Trp Arg Leu Gln Asn Asp Asp Arg Val Arg Val  
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 Val Asp Arg Thr Asn Ile Arg Tyr Met Thr Leu Glu Asp Thr Gly Gly  
 135 140 145

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 Thr Leu Pro Ala Ile Ala Lys Val Leu Ser Asp Gly Ala Asp Leu Leu  
 170 175 180

ccc atg gtc aag cca caa ttt gaa gtc gga aaa gac cga ttg ggc agt 691  
 Pro Met Val Lys Pro Gln Phe Glu Val Gly Lys Asp Arg Leu Gly Ser  
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 Ala Ser Pro Leu Pro Gly Pro Ser Gly Asn Val Glu Tyr Phe Leu Trp  
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929

942

<213> Corynebacterium glutamicum

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Gly Leu Lys Val Lys Gly Arg Arg Val Leu Asp Ala Gly Ala Ser Thr  
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Gly Gly Phe Thr Asp Val Leu Leu Arg Arg Glu Ala Ser Glu Val Val  
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Asp Arg Val Arg Val Val Asp Arg Thr Asn Ile Arg Tyr Met Thr Leu  
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Ile Ser Leu Lys Leu Thr Leu Pro Ala Ile Ala Lys Val Leu Ser Asp  
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Gly Ala Asp Leu Leu Pro Met Val Lys Pro Gln Phe Glu Val Gly Lys  
180 185 190

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Glu Val Thr Ala Asp Val Ala Lys Phe Ala Ala Thr Leu Gly Leu Ser

Leu Lys His Val Val Ala Ser Pro Leu Pro Gly Pro Ser Gly Asn Va  
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 Met Ile Arg Gly Arg  
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 Arg Val Phe Val Ala Gly Met Leu Ala Leu Lys Pro Ala Thr Val Val  
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 Pro Leu Gly Leu Lys Val Lys Gly Arg Arg Val Leu Asp Ala Gly Ala  
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 Ser Thr Gly Gly Phe Thr Asp Val Leu Leu Arg Arg Glu Ala Ser Glu  
 70 75 80 85  
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 Val Val Ala Val Asp Val Gly Tyr Gly Gln Leu Ile Trp Arg Leu Gln  
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 Asn Asp Asp Arg Val Arg Val Val Asp Arg Thr Asn Ile Arg Tyr Met  
 105 110 115  
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 Thr Leu Glu Asp Thr Gly Gly Glu Cys Asp Met Met Val Gly Asp Leu  
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 Ser Phe Ile Ser Leu Lys Leu Thr Leu Pro Ala Ile Ala Lys Val Leu  
 135 140 145  
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Ser Asp Gly Ala Asp Leu Leu Pro Met Val Lys Pro Gln Phe Glu Val  
 150 155 160 165

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 Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val Arg Ser Pro Glu Leu  
 170 175 180

cgc gca gaa gtt acc gcg gat gtc gcg aaa ttt gcg gcc act ttg ggc 691  
 Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe Ala Ala Thr Leu Gly  
 185 190 195

ctg agc ttg aag cat gtt gtt gca tcc ccg ctg ccc ggc ccg tca ggc 739  
 Leu Ser Leu Lys His Val Val Ala Ser Pro Leu Pro Gly Pro Ser Gly  
 200 205 210

aac gta gaa tac ttc ctg tgg ctg gtt aaa gat ggt ggc gct tca atg 787  
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ccg gat gac cag caa ttg tcg gca atg att gac acg gct gta aag gaa 835  
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 35 40 45

Leu Glu Ser Phe Glu Pro Leu Gly Leu Lys Val Lys Gly Arg Arg Val  
 50 55 60

Leu Asp Ala Gly Ala Ser Thr Gly Gly Phe Thr Asp Val Leu Leu Arg  
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Arg Glu Ala Ser Glu Val Val Ala Val Asp Val Gly Tyr Gly Gln Leu  
 85 90 95

Ile Trp Arg Leu Gln Asn Asp Asp Arg Val Arg Val Val Asp Arg Thr  
 100 105 110

Asn Ile Arg Tyr Met Thr Leu Glu Asp Thr Gly Gly Glu Cys Asp Met  
 115 120 125

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Ile Ala Lys Val Leu Ser Asp Gly Ala Asp Leu Leu Pro Met Val Lys  
 145 150 155 160

Pro Gln Phe Glu Val Gly Lys Asp Arg Leu Gly Ser Gly Gly Val Val  
 165 170 175

Arg Ser Pro Glu Leu Arg Ala Glu Val Thr Ala Asp Val Ala Lys Phe  
 180 185 190

Ala Ala Thr Leu Gly Leu Ser Leu Lys His Val Val Ala Ser Pro Leu  
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Pro Gly Pro Ser Gly Asn Val Glu Tyr Phe Leu Trp Leu Val Lys Asp  
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 Leu Ser Leu Ile Ala Gly Leu Val Val Ile Gly Val Ile Ile Val Leu  
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aac gga tat ttt gtg gct cag gaa ttt gcc tac atg tcc gtt gat cga 211  
 Asn Gly Tyr Phe Val Ala Gln Glu Phe Ala Tyr Met Ser Val Asp Arg  
 25 30 35

aat gag ctg cga gct ctc gct gac tct gga gat aag aag gct cgt cgc 259  
 Asn Glu Leu Arg Ala Leu Ala Asp Ser Gly Asp Lys Lys Ala Arg Arg  
 40 45 50

gct ctc agc atc act aag cgc aca tcc ttt atg ctt tct ggt gcg caa 307  
 Ala Leu Ser Ile Thr Lys Arg Thr Ser Phe Met Leu Ser Gly Ala Gln  
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 Leu Gly Ile Thr Val Thr Gly Leu Leu Val Gly Phe Val Ala Glu Pro  
 70 75 80 85

ctg gtg ggt aac gcg tta ggt gtt ctg cta gga ggg gtg ggg gtt ccc 403  
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Thr Val Val Gln Met Ile Phe Gly Glu Leu Phe Pro Lys Asn Tyr Thr				
	120	125	130	
ctt gcc acg ccg ttg aag tct gcg ctg gcg ctt gcg cct tcg acc acg				547
Leu Ala Thr Pro Leu Lys Ser Ala Leu Ala Leu Ala Pro Ser Thr Thr				
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tgg tat ttg aaa cct cgc tgg ttg gtt gat cac att ctt tgattttgca				596
Trp Tyr Leu Lys Pro Arg Trp Leu Val Asp His Ile Leu				
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 Met Ser Val Asp Arg Asn Glu Leu Arg Ala Leu Ala Asp Ser Gly Asp  
 35 40 45  
 Lys Lys Ala Arg Arg Ala Leu Ser Ile Thr Lys Arg Thr Ser Phe Met  
 50 55 60  
 Leu Ser Gly Ala Gln Leu Gly Ile Thr Val Thr Gly Leu Leu Val Gly  
 65 70 75 80  
 Phe Val Ala Glu Pro Leu Val Gly Asn Ala Leu Gly Val Leu Leu Gly  
 85 90 95  
 Gly Val Gly Val Pro Ala Ala Val Ser Ile Ser Val Gly Thr Val Leu  
 100 105 110  
 Ala Leu Ala Ile Ser Thr Val Val Gln Met Ile Phe Gly Glu Leu Phe  
 115 120 125  
 Pro Lys Asn Tyr Thr Leu Ala Thr Pro Leu Lys Ser Ala Leu Ala Leu  
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Trp	Gln	Ala	Leu	Gly	Val	Met	Val	Tyr	Ala	Leu	Ala	Met	Leu	Gly	Leu	355		
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Phe	Ala	Val	Ser	Ala	Ala	Tyr	His	Arg	Gly	Pro	Trp	Arg	Arg	Leu	His	403		
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 Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile Val Leu Glu Pro Gly  
 120 125 130  
  
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 135 140 145  
  
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 Val Ile Met Asn Met Val Trp Ile Asn His Pro Arg Trp Leu Ser Val  
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 Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala  
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 Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp  
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Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp Met Glu Leu Val Trp  
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Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu Ala Met Leu Gly Leu  
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Phe Ala Val Ser Ala Ala Tyr His Arg Gly Pro Trp Arg Arg Leu His  
90 95 100

acc gtg gcg tgg tgg cgc aaa gct gat cac tcc acc atc gcg gtg ttt 451  
Thr Val Ala Trp Trp Arg Lys Ala Asp His Ser Thr Ile Ala Val Phe  
105 110 115

atc gca gca acc tat acg cca ctg tgc ttg atc gtc tta gag ccc ggt 499  
Ile Ala Ala Thr Tyr Thr Pro Leu Cys Leu Ile Val Leu Glu Pro Gly  
120 125 130

acc gca gca tgg atg tta ggt att gcg tgg gtt ggt gcc att gac agc 547  
Thr Ala Ala Trp Met Leu Gly Ile Ala Trp Val Gly Ala Ile Asp Ser  
135 140 145

gtg atc atg aac atg gtg tgg atc aat cac cca cga tgg ctc agc gtg 595  
Val Ile Met Asn Met Val Trp Ile Asn His Pro Arg Trp Leu Ser Val  
150 155 160 165

ctg gtc tac ttg gcc ttg gga tgg ctc att gtg cca ctt gtc cct caa 643  
Leu Val Tyr Leu Ala Leu Gly Trp Leu Ile Val Pro Leu Val Pro Gln  
170 175 180

ttg tgg tct ggt gct ggc ccc aca gtg gtg tgg ctc ctg ctg gcc gaa 691  
Leu Trp Ser Gly Ala Gly Pro Thr Val Val Trp Leu Leu Leu Ala Glu  
185 190 195

ggc atc gtc tac agc gtt ggc gcg ttg gtg tac ggc ttt 730  
Gly Ile Val Tyr Ser Val Gly Ala Leu Val Tyr Gly Phe  
200 205 210

&lt;210&gt; 26

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 26

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Lys Asp Ser Ser Asp Glu Pro Leu Leu Ala Leu Thr Arg Tyr Val Phe  
20 25 30

Asp Arg Gly Glu Arg Pro Val Thr Arg Gly Leu Phe His Gln Val Ala  
35 40 45

Ala Ile Leu Ser Ile Val Ser Gly Ser Val Leu Ser Thr Tyr Ala Trp  
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Met Glu Leu Val Trp Trp Gln Ala Leu Gly Val Met Val Tyr Ala Leu

65	70	75	80
Ala Met Leu Gly	Leu Phe Ala Val Ser	Ala Ala Tyr His Arg Gly	Pro
	85	90	95
Trp Arg Arg Leu	His Thr Val Ala Trp	Trp Arg Lys Ala Asp	His Ser
	100	105	110
Thr Ile Ala Val	Phe Ile Ala Ala Thr	Tyr Thr Pro Leu	Cys Leu Ile
	115	120	125
Val Leu Glu Pro	Gly Thr Ala Ala Trp	Met Leu Gly Ile	Ala Trp Val
	130	135	140
Gly Ala Ile Asp	Ser Val Ile Met Asn	Met Val Trp Ile	Asn His Pro
	145	150	155
Arg Trp Leu Ser	Val Leu Val Tyr Leu	Ala Leu Gly Trp	Leu Ile Val
	165	170	175
Pro Leu Val Pro	Gln Leu Trp Ser Gly	Ala Gly Pro Thr	Val Val Trp
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Leu Leu Leu Ala	Glu Gly Ile Val Tyr	Ser Val Gly Ala	Leu Val Tyr
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Gly Phe			
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 Leu Ser Ile Ala Thr  
 1 5  
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 Val Val Ala Leu Leu Phe Ser Gly Leu Leu Gly Ala Val Glu Ser Ala  
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 ctt tct tct gtt tcc cgc gcc cgc gtt gaa caa atg ctc aag gat gaa 211  
 Leu Ser Ser Val Ser Arg Ala Arg Val Glu Gln Met Leu Lys Asp Glu  
 25 30 35  
 gcc tcc ggg tcc gcg tcc ttg ctg cga gtc atc gac gaa cgc gca ctc 259  
 Ala Ser Gly Ser Ala Ser Leu Leu Arg Val Ile Asp Glu Arg Ala Leu  
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 cac atc aac atg ctc atc atg ttg cgc acc ttg ctg gat gcc tcc gca 307  
 His Ile Asn Met Leu Ile Met Leu Arg Thr Leu Leu Asp Ala Ser Ala

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Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val Met Asp Ser Trp Ala			
70	75	80	85
tgg ggc atc gtc ctg gcc atc gtg gtg gtt tcc ctc ctg acc ttc gca			403
Trp Gly Ile Val Leu Ala Ile Val Val Val Ser Leu Leu Thr Phe Ala			
	90	95	100
gta gtg ggc gtg ttt ggc cgc acc gtt ggc cgc aaa aac cca tat tca			451
Val Val Gly Val Phe Gly Arg Thr Val Gly Arg Lys Asn Pro Tyr Ser			
	105	110	115
gtg atg ctt cgc tcc gca gtc gtg ctg agc ggt tta gct aaa atc ctt			499
Val Met Leu Arg Ser Ala Val Val Leu Ser Gly Leu Ala Lys Ile Leu			
	120	125	130
ggc ccc att gca cgt ggc ctc atc tgg atc ggc aac atc atc gcg ccc			547
Gly Pro Ile Ala Arg Gly Leu Ile Trp Ile Gly Asn Ile Ile Ala Pro			
	135	140	145
ggc cca ggt ttc cgc aat ggc cct tac gcc act gaa gtg gaa ctg cgt			595
Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr Glu Val Glu Leu Arg			
	150	155	160
gag atg gtc gat atc gcc caa gaa cac ggc atc gtg gaa att gaa gag			643
Glu Met Val Asp Ile Ala Gln Glu His Gly Ile Val Glu Ile Glu Glu			
	170	175	180
cgc cgc atg atc cag tcg gtg ttc gac ctg gca tcc acg acg gtt cgc			691
Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala Ser Thr Thr Val Arg			
	185	190	195
cag gtg atg gtg cca cgt cct gaa atg atc tgg att gaa tct gga aaa			739
Gln Val Met Val Pro Arg Pro Glu Met Ile Trp Ile Glu Ser Gly Lys			
	200	205	210
aca gcc ggg caa gca acc gcg ctg tgc gtg cgc tct ggt cat tcg cgc			787
Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg Ser Gly His Ser Arg			
	215	220	225
atc cca gtc atc ggt gaa aac gtc gac gac atc atc ggc atc gtc tac			835
Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile Ile Gly Ile Val Tyr			
	230	235	240
ctc aaa gac ttg gtc caa aaa acc tac tac gcc act gat ggc gga aag			883
Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala Thr Asp Gly Gly Lys			
	250	255	260
tct gtg ctt gta gac gag gtc atg cgc gaa gct acc ttc gtg cca gac			931
Ser Val Leu Val Asp Glu Val Met Arg Glu Ala Thr Phe Val Pro Asp			
	265	270	275
tcc aag tcc ctt gat gcg ctg ctg cag gaa atg cag gaa gac cac aaa			979
Ser Lys Ser Leu Asp Ala Leu Leu Gln Glu Met Gln Glu Asp His Lys			
	280	285	290
cac atc gca atc ctg gtt gat gaa tac ggc ggc gtg gca ggt ctt att			1027
His Ile Ala Ile Leu Val Asp Glu Tyr Gly Gly Val Ala Gly Leu Ile			
	295	300	305

tcc att gag gat att ttg gaa gaa atc gtc ggt gaa atc gct gat gaa 1075  
 Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Ala Asp Glu  
 310 315 320 325

tat gac gcc cgc gaa gta gcc ccc atc gag aaa atc ggc gac cgc acc 1123  
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 330 335 340

tac cgc gtg gtc tcc cga ctc tcg ctg gaa gat ctc aaa gac cac atc 1171  
 Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp Leu Lys Asp His Ile  
 345 350 355

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 Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly Asp Glu Ile Glu Asp  
 360 365 370

cag gtc gac act gtc ggt ggc ctt att gcc ttt gaa ctt ggc cga gtg 1267  
 Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe Glu Leu Gly Arg Val  
 375 380 385

cct ctg ccg ggt gcc act gtg gaa acc tgc gga cta aag ctc acc gcc 1315  
 Pro Leu Pro Gly Ala Thr Val Glu Thr Cys Gly Leu Lys Leu Thr Ala  
 390 395 400 405

gag gga gcc aag aac cgc cgg ggt cgt ttg cgc atg cat tca gca gtc 1363  
 Glu Gly Ala Lys Asn Arg Arg Gly Arg Leu Arg Met His Ser Ala Val  
 410 415 420

gta gaa gtt ggc gag ccc agc gag gac aac gaa ggt tagtttttta 1409  
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 35 40 45

Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu  
 50 55 60

Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val  
 65 70 75 80

Met Asp Ser Trp Ala Trp Gly Ile Val Leu Ala Ile Val Val Val Ser  
 85 90 95

Leu Leu Thr Phe Ala Val Val Gly Val Phe Gly Arg Thr Val Gly Arg



100	105	110
Lys Asn Pro Tyr Ser Val Met	Leu Arg Ser Ala Val	Val Leu Ser Gly
115	120	125
Leu Ala Lys Ile Leu Gly Pro	Ile Ala Arg Gly Leu	Ile Trp Ile Gly
130	135	140
Asn Ile Ile Ala Pro Gly Pro	Gly Phe Arg Asn Gly Pro	Tyr Ala Thr
145	150	155
Glu Val Glu Leu Arg Glu Met	Val Asp Ile Ala Gln Glu	His Gly Ile
165	170	175
Val Glu Ile Glu Glu Arg Arg	Met Ile Gln Ser Val Phe	Asp Leu Ala
180	185	190
Ser Thr Thr Val Arg Gln Val	Met Val Pro Arg Pro Glu	Met Ile Trp
195	200	205
Ile Glu Ser Gly Lys Thr Ala	Gly Gln Ala Thr Ala Leu	Cys Val Arg
210	215	220
Ser Gly His Ser Arg Ile Pro	Val Ile Gly Glu Asn Val	Asp Asp Ile
225	230	235
Ile Gly Ile Val Tyr Leu Lys	Asp Leu Val Gln Lys Thr	Tyr Tyr Ala
245	250	255
Thr Asp Gly Gly Lys Ser Val	Leu Val Asp Glu Val Met	Arg Glu Ala
260	265	270
Thr Phe Val Pro Asp Ser Lys	Ser Leu Asp Ala Leu Leu	Gln Glu Met
275	280	285
Gln Glu Asp His Lys His Ile	Ala Ile Leu Val Asp Glu	Tyr Gly Gly
290	295	300
Val Ala Gly Leu Ile Ser Ile	Glu Asp Ile Leu Glu Glu	Ile Val Gly
305	310	315
Glu Ile Ala Asp Glu Tyr Asp	Ala Arg Glu Val Ala Pro	Ile Glu Lys
325	330	335
Ile Gly Asp Arg Thr Tyr Arg	Val Val Ser Arg Leu Ser	Leu Glu Asp
340	345	350
Leu Lys Asp His Ile Glu Glu	Glu Leu Asp Leu Glu Ile	Glu Phe Gly
355	360	365
Asp Glu Ile Glu Asp Gln Val	Asp Thr Val Gly Gly Leu	Ile Ala Phe
370	375	380
Glu Leu Gly Arg Val Pro Leu	Pro Gly Ala Thr Val Glu	Thr Cys Gly
385	390	395
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gtc	gtt	gcg	ttg	ctc	ttc	tcc	ggt	tta	tta	ggt	gcg	gtt	gaa	tct	gcg	163			
Val	Val	Ala	Leu	Leu	Phe	Ser	Gly	Leu	Leu	Gly	Ala	Val	Glu	Ser	Ala				
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ctt	tct	tct	gtt	tcc	cgc	gcc	cgc	gtt	gaa	caa	atg	ctc	aag	gat	gaa	211			
Leu	Ser	Ser	Val	Ser	Arg	Ala	Arg	Val	Glu	Gln	Met	Leu	Lys	Asp	Glu				
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gcc	tcc	ggg	tcc	gcg	tcc	ttg	ctg	cga	gtc	atc	gac	gaa	cgc	gca	ctc	259			
Ala	Ser	Gly	Ser	Ala	Ser	Leu	Leu	Arg	Val	Ile	Asp	Glu	Arg	Ala	Leu				
				40					45							50			
cac	atc	aac	atg	ctc	atc	atg	ttg	cgc	acc	ttg	ctg	gat	gcc	tcc	gca	307			
His	Ile	Asn	Met	Leu	Ile	Met	Leu	Arg	Thr	Leu	Leu	Asp	Ala	Ser	Ala				
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gca	gtc	ttc	gcc	ggg	gca	atc	gca	gtc	aat	gtg	atg	gac	agc	tgg	gcg	355			
Ala	Val	Phe	Ala	Gly	Ala	Ile	Ala	Val	Asn	Val	Met	Asp	Ser	Trp	Ala				
				70					75					80			85		
tgg	ggc	atc	gtc	ctg	gcc	atc	gtg	gtg	gtt	tcc	ctc	ctg	acc	ttc	gca	403			
Trp	Gly	Ile	Val	Leu	Ala	Ile	Val	Val	Val	Ser	Leu	Leu	Thr	Phe	Ala				
				90					95							100			
gta	gtg	ggc	gtg	ttt	ggc	cgc	acc	gtt	ggc	cgc	aaa	aac	cca	tat	tca	451			
Val	Val	Gly	Val	Phe	Gly	Arg	Thr	Val	Gly	Arg	Lys	Asn	Pro	Tyr	Ser				
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gtg	atg	ctt	cgc	tcc	gca	gtc	gtg	ctg	agc	ggt	tta	gct	aaa	atc	ctt	499			
Val	Met	Leu	Arg	Ser	Ala	Val	Val	Leu	Ser	Gly	Leu	Ala	Lys	Ile	Leu				
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ggc	ccc	att	gca	cgt	ggc	ctc	atc	tgg	atc	ggc	aac	atc	atc	gcg	ccc	547			
Gly	Pro	Ile	Ala	Arg	Gly	Leu	Ile	Trp	Ile	Gly	Asn	Ile	Ile	Ala	Pro				
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cgc cgc atg atc cag tcg gtg ttc gac ctg gca tcc acg acg gtt cgc 691  
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 185 190 195

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 Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile Ile Gly Ile Val Tyr  
 230 235 240 245

ctc aaa gac ttg gtc caa aaa acc tac tac gcc act gat ggc gga aag 883  
 Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala Thr Asp Gly Gly Lys  
 250 255 260

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 Ser Val Leu Val Asp Glu Val Met Arg Glu Ala Thr Phe Val Pro Asp  
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cac atc gca atc ctg gtt gat gaa tac ggc ggc gtg gca ggt ctt att 1027  
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 295 300 305

tcc att gag gat att ttg gaa gaa atc gtc ggt gaa atc gct gat gaa 1075  
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 310 315 320 325

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 Tyr Arg Val Val Ser Arg Leu Ser Leu Glu Asp Leu Lys Asp His Ile  
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 35 40 45  
 Asp Glu Arg Ala Leu His Ile Asn Met Leu Ile Met Leu Arg Thr Leu  
 50 55 60  
 Leu Asp Ala Ser Ala Ala Val Phe Ala Gly Ala Ile Ala Val Asn Val  
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 Met Asp Ser Trp Ala Trp Gly Ile Val Leu Ala Ile Val Val Val Ser  
 85 90 95  
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 Lys Asn Pro Tyr Ser Val Met Leu Arg Ser Ala Val Val Leu Ser Gly  
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 Asn Ile Ile Ala Pro Gly Pro Gly Phe Arg Asn Gly Pro Tyr Ala Thr  
 145 150 155 160  
 Glu Val Glu Leu Arg Glu Met Val Asp Ile Ala Gln Glu His Gly Ile  
 165 170 175  
 Val Glu Ile Glu Glu Arg Arg Met Ile Gln Ser Val Phe Asp Leu Ala  
 180 185 190  
 Ser Thr Thr Val Arg Gln Val Met Val Pro Arg Pro Glu Met Ile Trp  
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 Ile Glu Ser Gly Lys Thr Ala Gly Gln Ala Thr Ala Leu Cys Val Arg  
 210 215 220  
 Ser Gly His Ser Arg Ile Pro Val Ile Gly Glu Asn Val Asp Asp Ile  
 225 230 235 240  
 Ile Gly Ile Val Tyr Leu Lys Asp Leu Val Gln Lys Thr Tyr Tyr Ala

245 250 255  
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 260 265 270  
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 275 280 285  
 Gln Glu Asp His Lys His Ile Ala Ile Leu Val Asp Glu Tyr Gly Gly  
 290 295 300  
 Val Ala Gly Leu Ile Ser Ile Glu Asp Ile Leu Glu Glu Ile Val Gly  
 305 310 315 320  
 Glu Ile Ala Asp Glu Tyr Asp Ala Arg Glu Val Ala Pro Ile Glu Lys  
 325 330 335  
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 340 345 350  
 Leu Lys Asp His Ile Glu Glu Glu Leu Asp Leu Glu Ile Glu Phe Gly  
 355 360 365  
 Asp Glu Ile Glu Asp Gln Val Asp Thr Val Gly Gly Leu Ile Ala Phe  
 370 375 380  
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 Met Glu Cys Met Ser  
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Asp Pro Thr Leu Ser Thr Glu Phe Asp Glu Val His Arg Trp Val Asp	
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Trp Pro Tyr Asn Gly Gly Thr Met Asp Thr Gly Ile Asp Leu Val Ala	
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tat aac aag gac gat gat gct tat acg gcg atc cag tgc aag ttt tat	355
Tyr Asn Lys Asp Asp Asp Ala Tyr Thr Ala Ile Gln Cys Lys Phe Tyr	
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Leu Pro Thr Thr Ser Leu Ala Lys Gly Gln Leu Asp Ser Phe Phe Glu	
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Ala Ser Gly Arg Thr Phe Glu Thr Pro Glu Gly Thr Arg Ser Phe Ser	
105 110 115	
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Asn Arg Leu Val Ile Ser Thr Thr Asp Lys Trp Ser Ser Asn Ala Glu	
120 125 130	
aag atg ttg gag aac caa acc att cca act aac cgc att ggt cta tct	547
Lys Met Leu Glu Asn Gln Thr Ile Pro Thr Asn Arg Ile Gly Leu Ser	
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Ala Ile Ala Glu Ser Pro Ile Asp Trp Asp Ile Ala Tyr Pro Gly Ser	
150 155 160 165	
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Glu Leu Thr Ile Asn Leu Gln Leu Lys Glu Pro Tyr Ser Pro Arg Pro	
170 175 180	
cac cag caa act gct att gaa aaa gca att gaa ggc ttc caa act cat	691
His Gln Gln Thr Ala Ile Glu Lys Ala Ile Glu Gly Phe Gln Thr His	
185 190 195	
gac cgt ggc aag ctc atc atg gct tgc ggt acc gga aaa acc ttt act	739
Asp Arg Gly Lys Leu Ile Met Ala Cys Gly Thr Gly Lys Thr Phe Thr	
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215 220 225	
cgc att ctt ttt cta gtc cct tcc atc agc ttg ctt tcg caa aca ctc	835
Arg Ile Leu Phe Leu Val Pro Ser Ile Ser Leu Leu Ser Gln Thr Leu	
230 235 240 245	
aaa gag tgg act gca caa aag aca atg gat ctt cgt cct gtc gcc gta	883
Lys Glu Trp Thr Ala Gln Lys Thr Met Asp Leu Arg Pro Val Ala Val	
250 255 260	
tgt tct gac tcc aag gtc tcc aag gct gca gaa gat att gct gct tat	931
Cys Ser Asp Ser Lys Val Ser Lys Ala Ala Glu Asp Ile Ala Ala Tyr	
265 270 275	
gat ctt gaa gtt ccg gta agt act gat ggt gca ttg att gcg gaa aaa	979

Asp	Leu	Glu	Val	Pro	Val	Ser	Thr	Asp	Gly	Ala	Leu	Ile	Ala	Glu	Lys		
	280						285					290					
ctg	gag	cat	cgt	aag	cga	gca	gca	gga	ttg	acc	gtg	gtg	ttc	tct	act	1027	
Leu	Glu	His	Arg	Lys	Arg	Ala	Ala	Gly	Leu	Thr	Val	Val	Phe	Ser	Thr		
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tac	cag	tcc	ctt	cct	gct	gtt	cac	gcg	gct	caa	gaa	gct	ggg	gct	gag	1075	
Tyr	Gln	Ser	Leu	Pro	Ala	Val	His	Ala	Ala	Gln	Glu	Ala	Gly	Ala	Glu		
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ccc	ttt	gat	ctt	gtc	atc	tgc	gat	gaa	gcc	cac	cgc	acc	aca	ggc	atc	1123	
Pro	Phe	Asp	Leu	Val	Ile	Cys	Asp	Glu	Ala	His	Arg	Thr	Thr	Gly	Ile		
				330					335					340			
acc	ttg	gct	gga	gaa	gac	cct	tca	aac	ttc	acc	cgc	att	cat	gac	gct	1171	
Thr	Leu	Ala	Gly	Glu	Asp	Pro	Ser	Asn	Phe	Thr	Arg	Ile	His	Asp	Ala		
			345					350					355				
tct	tat	atc	aag	gca	gca	aag	cgg	ctg	tac	atg	acg	gca	acc	cca	agg	1219	
Ser	Tyr	Ile	Lys	Ala	Ala	Lys	Arg	Leu	Tyr	Met	Thr	Ala	Thr	Pro	Arg		
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ctt	ttc	gac	gac	tcc	gtg	aag	ggc	aag	gct	gca	gat	cat	tca	gct	gaa	1267	
Leu	Phe	Asp	Asp	Ser	Val	Lys	Gly	Lys	Ala	Ala	Asp	His	Ser	Ala	Glu		
		375				380					385						
gtt	tct	tcc	atg	gat	gat	gaa	gca	atc	tac	gga	ccc	gaa	ttt	cac	cgg	1315	
Val	Ser	Ser	Met	Asp	Asp	Glu	Ala	Ile	Tyr	Gly	Pro	Glu	Phe	His	Arg		
390					395					400					405		
ctg	ggt	ttt	ggg	gaa	gca	gta	gaa	aaa	ggc	ctg	ctt	act	gac	tac	aaa	1363	
Leu	Gly	Phe	Gly	Glu	Ala	Val	Glu	Lys	Gly	Leu	Leu	Thr	Asp	Tyr	Lys		
			410						415					420			
gtt	gta	gtg	atg	aca	gtt	gat	gag	caa	gtt	gca	gcc	agt	gcc	tta	act	1411	
Val	Val	Val	Met	Thr	Val	Asp	Glu	Gln	Val	Ala	Ala	Ser	Ala	Leu	Thr		
			425					430					435				
gtt	ttg	ggt	tca	aca	cct	ggt	gaa	gaa	ctc	act	ctg	gac	atg	act	tcc	1459	
Val	Leu	Gly	Ser	Thr	Pro	Gly	Glu	Glu	Leu	Thr	Leu	Asp	Met	Thr	Ser		
		440					445					450					
gca	att	att	ggc	gcg	tgg	aat	ggc	ttg	gca	aag	cgt	tcg	ggt	aaa	gag	1507	
Ala	Ile	Ile	Gly	Ala	Trp	Asn	Gly	Leu	Ala	Lys	Arg	Ser	Gly	Lys	Glu		
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caa	gac	acc	aag	act	ggt	ttc	tca	agc	tct	gac	gca	gca	atg	gaa	cga	1555	
Gln	Asp	Thr	Lys	Thr	Gly	Phe	Ser	Ser	Ser	Asp	Ala	Ala	Met	Glu	Arg		
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gct	gtt	gca	ttt	gcg	cga	gac	att	aag	act	tct	cag	caa	atc	gcg	gag	1603	
Ala	Val	Ala	Phe	Ala	Arg	Asp	Ile	Lys	Thr	Ser	Gln	Gln	Ile	Ala	Glu		
				490				495						500			
tct	ttt	cca	cga	gtt	gtc	aat	gct	tat	acg	act	gag	ctt	gag	gtt	aaa	1651	
Ser	Phe	Pro	Arg	Val	Val	Asn	Ala	Tyr	Thr	Thr	Glu	Leu	Glu	Val	Lys		
			505					510					515				
aac	gat	gac	gta	gat	gag	cac	aac	ctc	aat	ttg	agc	gtg	gca	tgc	cag	1699	
Asn	Asp	Asp	Val	Asp	Glu	His	Asn	Leu	Asn	Leu	Ser	Val	Ala	Cys	Gln		

520	525	530	
cat gtc gat gga tca atg aat gcg ctg gaa cga aac tct cgt tta act			1747
His Val Asp Gly Ser Met Asn Ala Leu Glu Arg Asn Ser Arg Leu Thr			
535	540	545	
tgg ctt aaa gct cct acc cag tca atg gaa acc aag att ctt act aac			1795
Trp Leu Lys Ala Pro Thr Gln Ser Met Glu Thr Lys Ile Leu Thr Asn			
550	555	560	565
gcg cgc tgc ctt tct gag ggt gtc gat gta ccg gct ttg gat tcc gta			1843
Ala Arg Cys Leu Ser Glu Gly Val Asp Val Pro Ala Leu Asp Ser Val			
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atc ttc ttt aat ccc cgt aat tcc atg gtg gat gtg gtt cag tcg gtt			1891
Ile Phe Phe Asn Pro Arg Asn Ser Met Val Asp Val Val Gln Ser Val			
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ggc cga gtt atg cgt aaa tct cca ggt aag aat tac gga tat atc atc			1939
Gly Arg Val Met Arg Lys Ser Pro Gly Lys Asn Tyr Gly Tyr Ile Ile			
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ttg cca gtt gct gtt ccc cca ggt gtt gca cca tca gct gcg tta aat			1987
Leu Pro Val Ala Val Pro Pro Gly Val Ala Pro Ser Ala Ala Leu Asn			
615	620	625	
gat tca cgc cgc ttc aag gtt gta tgg cag gtt ctt aac gcc ctt cgt			2035
Asp Ser Arg Arg Phe Lys Val Val Trp Gln Val Leu Asn Ala Leu Arg			
630	635	640	645
gct cac gat gac cgt ttt aac gca atg gtg aac tcc att gcg ctc aat			2083
Ala His Asp Asp Arg Phe Asn Ala Met Val Asn Ser Ile Ala Leu Asn			
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gag gga aat att aag gat cta cct gtt gag act gag cat act ggc cct			2131
Glu Gly Asn Ile Lys Asp Leu Pro Val Glu Thr Glu His Thr Gly Pro			
665	670	675	
aca agt aaa gat aga gat aac gca ccc tat gac agt gct gaa tcc gct			2179
Thr Ser Lys Asp Arg Asp Asn Ala Pro Tyr Asp Ser Ala Glu Ser Ala			
680	685	690	
aca caa tac gta ctg ttc tct tta gaa cag tgg caa gaa gcg atc tac			2227
Thr Gln Tyr Val Leu Phe Ser Leu Glu Gln Trp Gln Glu Ala Ile Tyr			
695	700	705	
acc aag ctt gta gat aaa gtt ggt acc cga acc tac tgg gaa gat tgg			2275
Thr Lys Leu Val Asp Lys Val Gly Thr Arg Thr Tyr Trp Glu Asp Trp			
710	715	720	725
gca gat gat gtt gct gac atc gcc caa gca caa ata acc cgt att aaa			2323
Ala Asp Asp Val Ala Asp Ile Ala Gln Ala Gln Ile Thr Arg Ile Lys			
730	735	740	
gcg ctc tta gac aat gct tca cca acg atc aaa gaa gag ttc gag cga			2371
Ala Leu Leu Asp Asn Ala Ser Pro Thr Ile Lys Glu Glu Phe Glu Arg			
745	750	755	
ttt gtt gaa ggt cta cgt ggc aac ctc aat gag tcc atc tct gac gac			2419
Phe Val Glu Gly Leu Arg Gly Asn Leu Asn Glu Ser Ile Ser Asp Asp			
760	765	770	



gag gca atc agc atg ttg tca cag cat ctg atc acc gca cca gtg ttt	2467
Glu Ala Ile Ser Met Leu Ser Gln His Leu Ile Thr Ala Pro Val Phe	
775 780 785	
gac gct cta ttt gct gaa tca agc ttc gct aag caa aac cct gtt tcc	2515
Asp Ala Leu Phe Ala Glu Ser Ser Phe Ala Lys Gln Asn Pro Val Ser	
790 795 800 805	
cag gtt atg caa cgc atg gca gat gct ctt aat agt gct gaa ctt aac	2563
Gln Val Met Gln Arg Met Ala Asp Ala Leu Asn Ser Ala Glu Leu Asn	
810 815 820	
tct gaa acg gaa aaa ctt gag aag ttc tat gac tct gtt cgt atc cgt	2611
Ser Glu Thr Glu Lys Leu Glu Lys Phe Tyr Asp Ser Val Arg Ile Arg	
825 830 835	
gct gct gaa gta agc tcc gca gct ggt aaa caa gca gta att aaa gac	2659
Ala Ala Glu Val Ser Ser Ala Ala Gly Lys Gln Ala Val Ile Lys Asp	
840 845 850	
ctc tac gaa cga ttc ttt aaa aag gcc ttt aaa aag caa tct gaa gct	2707
Leu Tyr Glu Arg Phe Phe Lys Lys Ala Phe Lys Lys Gln Ser Glu Ala	
855 860 865	
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Leu Gly Ile Val Tyr Thr Pro Val Glu Ile Val Asp Phe Ile Leu Arg	
870 875 880 885	
gct gcc gat gat gtg tcc aag aag cat ttt ggt cgt ggc tta agc gat	2803
Ala Ala Asp Asp Val Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp	
890 895 900	
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Lys Asp Val His Val Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met	
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Val Arg Leu Leu Gln Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg	
920 925 930	
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Lys Tyr Ala Asn Glu Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr	
935 940 945	
tat gtt gcg gcc gtt aac att gag acc act tat ttt ggt ctc gag gga	2995
Tyr Val Ala Ala Val Asn Ile Glu Thr Thr Tyr Phe Gly Leu Glu Gly	
950 955 960 965	
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Glu Arg Ala Leu Arg Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe	
970 975 980	
gat ggc att gtg ttg ggt gat acc ttc cag atg tat gaa gac gat gac	3091
Asp Gly Ile Val Leu Gly Asp Thr Phe Gln Met Tyr Glu Asp Asp Asp	
985 990 995	
aaa ctc gat cta gat gtt ttt act gct aac aat gac cgt atg gag cgt	3139
Lys Leu Asp Leu Asp Val Phe Thr Ala Asn Asn Asp Arg Met Glu Arg	
1000 1005 1010	

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 Arg Thr Gly Gly Asp Leu Ala Lys Arg Glu Gly Gly Asn Val Phe Asn  
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cct caa cag aca tac ttc cat gtt tca ttg aac cag cgt cga tac cag 4147  
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 1480 1485 1490

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 Met Asp Leu His Ile Asn Tyr Glu Asp Val Glu Pro Trp Asp Val Glu  
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 Val Lys Val Lys Glu Lys Ala Asp Pro Thr Asp Arg Glu Thr Trp Arg  
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 Ser Gly Ile Pro Glu Glu Ala Glu Asn Tyr Gln Leu Gly Ser Arg Ser  
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 1625                      1630                      1635  
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 20                      25                      30  
 Asn Phe Ile Lys Ser Asp Pro Thr Leu Ser Thr Glu Phe Asp Glu Val  
 35                      40                      45  
 His Arg Trp Val Asp Trp Pro Tyr Asn Gly Gly Thr Met Asp Thr Gly  
 50                      55                      60  
 Ile Asp Leu Val Ala Tyr Asn Lys Asp Asp Ala Tyr Thr Ala Ile  
 65                      70                      75                      80

Gln	Cys	Lys	Phe	Tyr	Leu	Pro	Thr	Thr	Ser	Leu	Ala	Lys	Gly	Gln	Leu	
				85					90					95		
Asp	Ser	Phe	Phe	Glu	Ala	Ser	Gly	Arg	Thr	Phe	Glu	Thr	Pro	Glu	Gly	
				100					105					110		
Thr	Arg	Ser	Phe	Ser	Asn	Arg	Leu	Val	Ile	Ser	Thr	Thr	Asp	Lys	Trp	
				115					120					125		
Ser	Ser	Asn	Ala	Glu	Lys	Met	Leu	Glu	Asn	Gln	Thr	Ile	Pro	Thr	Asn	
				130					135					140		
Arg	Ile	Gly	Leu	Ser	Ala	Ile	Ala	Glu	Ser	Pro	Ile	Asp	Trp	Asp	Ile	
				145					150					155		
Ala	Tyr	Pro	Gly	Ser	Glu	Leu	Thr	Ile	Asn	Leu	Gln	Leu	Lys	Glu	Pro	
				165					170					175		
Tyr	Ser	Pro	Arg	Pro	His	Gln	Gln	Thr	Ala	Ile	Glu	Lys	Ala	Ile	Glu	
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Gly	Phe	Gln	Thr	His	Asp	Arg	Gly	Lys	Leu	Ile	Met	Ala	Cys	Gly	Thr	
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Gly	Lys	Thr	Phe	Thr	Ala	Leu	Arg	Leu	Ser	Glu	Glu	Val	Ala	Arg	Leu	
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Asn	Gly	Asn	Lys	Ala	Arg	Ile	Leu	Phe	Leu	Val	Pro	Ser	Ile	Ser	Leu	
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Leu	Ser	Gln	Thr	Leu	Lys	Glu	Trp	Thr	Ala	Gln	Lys	Thr	Met	Asp	Leu	
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Arg	Pro	Val	Ala	Val	Cys	Ser	Asp	Ser	Lys	Val	Ser	Lys	Ala	Ala	Glu	
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Asp	Ile	Ala	Ala	Tyr	Asp	Leu	Glu	Val	Pro	Val	Ser	Thr	Asp	Gly	Ala	
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				290					295					300		
Val	Val	Phe	Ser	Thr	Tyr	Gln	Ser	Leu	Pro	Ala	Val	His	Ala	Ala	Gln	
				305					310					315		
Glu	Ala	Gly	Ala	Glu	Pro	Phe	Asp	Leu	Val	Ile	Cys	Asp	Glu	Ala	His	
				325					330					335		
Arg	Thr	Thr	Gly	Ile	Thr	Leu	Ala	Gly	Glu	Asp	Pro	Ser	Asn	Phe	Thr	
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Arg	Ile	His	Asp	Ala	Ser	Tyr	Ile	Lys	Ala	Ala	Lys	Arg	Leu	Tyr	Met	
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Thr	Ala	Thr	Pro	Arg	Leu	Phe	Asp	Asp	Ser	Val	Lys	Gly	Lys	Ala	Ala	
				370					375					380		
Asp	His	Ser	Ala	Glu	Val	Ser	Ser	Met	Asp	Asp	Glu	Ala	Ile	Tyr	Gly	
				385					390					395		

Pro Glu Phe His Arg Leu Gly Phe Gly Glu Ala Val Glu Lys Gly Leu  
 405 410 415  
 Leu Thr Asp Tyr Lys Val Val Val Met Thr Val Asp Glu Gln Val Ala  
 420 425 430  
 Ala Ser Ala Leu Thr Val Leu Gly Ser Thr Pro Gly Glu Glu Leu Thr  
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 Leu Asp Met Thr Ser Ala Ile Ile Gly Ala Trp Asn Gly Leu Ala Lys  
 450 455 460  
 Arg Ser Gly Lys Glu Gln Asp Thr Lys Thr Gly Phe Ser Ser Ser Asp  
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 485 490 495  
 Gln Gln Ile Ala Glu Ser Phe Pro Arg Val Val Asn Ala Tyr Thr Thr  
 500 505 510  
 Glu Leu Glu Val Lys Asn Asp Asp Val Asp Glu His Asn Leu Asn Leu  
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 Ser Val Ala Cys Gln His Val Asp Gly Ser Met Asn Ala Leu Glu Arg  
 530 535 540  
 Asn Ser Arg Leu Thr Trp Leu Lys Ala Pro Thr Gln Ser Met Glu Thr  
 545 550 555 560  
 Lys Ile Leu Thr Asn Ala Arg Cys Leu Ser Glu Gly Val Asp Val Pro  
 565 570 575  
 Ala Leu Asp Ser Val Ile Phe Phe Asn Pro Arg Asn Ser Met Val Asp  
 580 585 590  
 Val Val Gln Ser Val Gly Arg Val Met Arg Lys Ser Pro Gly Lys Asn  
 595 600 605  
 Tyr Gly Tyr Ile Ile Leu Pro Val Ala Val Pro Pro Gly Val Ala Pro  
 610 615 620  
 Ser Ala Ala Leu Asn Asp Ser Arg Arg Phe Lys Val Val Trp Gln Val  
 625 630 635 640  
 Leu Asn Ala Leu Arg Ala His Asp Asp Arg Phe Asn Ala Met Val Asn  
 645 650 655  
 Ser Ile Ala Leu Asn Glu Gly Asn Ile Lys Asp Leu Pro Val Glu Thr  
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 Glu His Thr Gly Pro Thr Ser Lys Asp Arg Asp Asn Ala Pro Tyr Asp  
 675 680 685  
 Ser Ala Glu Ser Ala Thr Gln Tyr Val Leu Phe Ser Leu Glu Gln Trp  
 690 695 700  
 Gln Glu Ala Ile Tyr Thr Lys Leu Val Asp Lys Val Gly Thr Arg Thr  
 705 710 715 720  
 Tyr Trp Glu Asp Trp Ala Asp Asp Val Ala Asp Ile Ala Gln Ala Gln

	725	730	735
Ile Thr Arg Ile Lys Ala Leu Leu Asp Asn Ala Ser Pro Thr Ile Lys 740                    745                    750			
Glu Glu Phe Glu Arg Phe Val Glu Gly Leu Arg Gly Asn Leu Asn Glu 755                        760                    765			
Ser Ile Ser Ser Asp Asp Glu Ala Ile Ser Met Leu Ser Gln His Leu Ile 770                              775                    780			
Thr Ala Pro Val Phe Asp Ala Leu Phe Ala Glu Ser Ser Phe Ala Lys 785                              790                    795                    800			
Gln Asn Pro Val Ser Gln Val Met Gln Arg Met Ala Asp Ala Leu Asn 805                    810                    815			
Ser Ala Glu Leu Asn Ser Glu Thr Glu Lys Leu Glu Lys Phe Tyr Asp 820                    825                    830			
Ser Val Arg Ile Arg Ala Ala Glu Val Ser Ser Ala Ala Gly Lys Gln 835                    840                    845			
Ala Val Ile Lys Asp Leu Tyr Glu Arg Phe Phe Lys Lys Ala Phe Lys 850                              855                    860			
Lys Gln Ser Glu Ala Leu Gly Ile Val Tyr Thr Pro Val Glu Ile Val 865                              870                    875                    880			
Asp Phe Ile Leu Arg Ala Ala Asp Asp Val Ser Lys Lys His Phe Gly 885                    890                    895			
Arg Gly Leu Ser Asp Lys Asp Val His Val Leu Asp Pro Phe Thr Gly 900                    905                    910			
Thr Gly Thr Phe Met Val Arg Leu Leu Gln Ser Gly Leu Ile Lys Pro 915                              920                    925			
Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu Leu His Ala Thr Glu Ile 930                              935                    940			
Met Leu Leu Ala Tyr Tyr Val Ala Ala Val Asn Ile Glu Thr Thr Tyr 945                              950                    955                    960			
Phe Gly Leu Glu Gly Glu Arg Ala Leu Arg Asn Gly Glu Asp Ala Pro 965                    970                    975			
Val Tyr Glu Pro Phe Asp Gly Ile Val Leu Gly Asp Thr Phe Gln Met 980                    985                    990			
Tyr Glu Asp Asp Asp Lys Leu Asp Leu Asp Val Phe Thr Ala Asn Asn 995                    1000                    1005			
Asp Arg Met Glu Arg Gln Arg Leu Thr Pro Val Gln Val Ile Val Gly 1010                              1015                    1020			
Asn Pro Pro Tyr Ser Val Gly Gln Ser Ser Ala Asn Asp Asn Asn Ala 1025                              1030                    1035                    1040			
Asn Leu Lys Tyr Pro Thr Leu Asp Arg Arg Ile Glu Asp Ser Tyr Ala 1045                    1050                    1055			

Lys Tyr Ser Thr Ala Thr Asn Lys Asn Ser Leu Tyr Asp Ser Tyr Leu  
1060 1065 1070

Arg Ala Phe Arg Trp Ala Thr Asp Arg Ile His Thr Gln Gly Val Val  
1075 1080 1085

Ala Phe Val Ser Asn Asn Gly Trp Val Asp Gly Asn Thr Ala Asp Gly  
1090 1095 1100

Val Arg Leu Ser Leu Ala Gln Asp Phe Ser Glu Ile Tyr Val Phe Asn  
1105 1110 1115 1120

Leu Arg Gly Asn Ser Arg Thr Gly Gly Asp Leu Ala Lys Arg Glu Gly  
1125 1130 1135

Gly Asn Val Phe Asn Val Arg Val Gly Thr Gln Ile Ile Val Ala Val  
1140 1145 1150

Lys Asn Pro Gln Leu Ser Gly Cys Arg Ile Leu Tyr Lys Asp Ile Gly  
1155 1160 1165

Asp Asn Leu Ser Ala Asp Ala Lys Leu Asn Glu Ile Ala Val Ala Thr  
1170 1175 1180

Ile Glu Gly Ala Glu Trp Gln Thr Ile Ser Pro Asn Glu Tyr Gly Asp  
1185 1190 1195 1200

Trp Ile Ser Gln Arg Ser Val Asp Phe Asp Thr Trp Pro Val Leu Gly  
1205 1210 1215

Asp Lys Lys Asn Lys Ser Ala Leu Lys Val Phe Gln Thr Phe Ser Ala  
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Gly Leu Lys Thr Gly Arg Asp Ala Trp Cys Tyr Gly Pro Thr Ser Ala  
1235 1240 1245

Gln Val Lys Thr Asn Ile Thr Arg Leu Leu Glu Thr Tyr Glu Gln Ala  
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Gln Gln Arg Phe Asn Ser Trp Val Val Asp Asn Gly Val Thr Ser Pro  
1265 1270 1275 1280

Lys Glu Ala Asp Val Asn Gln Phe Leu Lys Gln Asn Pro Asp Leu Ala  
1285 1290 1295

Asp Ser Lys Lys Ile Ser Trp Asp Ser Asn Leu Lys Met Ser Leu Ser  
1300 1305 1310

Arg Gly Asp Thr Phe Ser Phe Asp Pro Ser Ser Ile Gln Met Ser Leu  
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Tyr Arg Pro Phe Phe Pro Gln Gln Thr Tyr Phe His Val Ser Leu Asn  
1330 1335 1340

Gln Arg Arg Tyr Gln Leu Pro Ser Met Phe Pro Thr Pro Glu His Asp  
1345 1350 1355 1360

Asn Gln Gly Phe Tyr Ile Val Asn Pro Gly Ser Ala Lys Pro Phe Ser  
1365 1370 1375



Thr Leu Ala Thr Asn Leu Leu Pro Asp Leu Ala Met Trp Gly Ser Asn  
 1380 1385 1390  
 Ala Gly Gln Phe Phe Thr Arg Trp Thr Trp Glu Pro Ile Glu Thr Arg  
 1395 1400 1405  
 Glu Gly Glu Leu Asp Phe Gly Asn Gly Leu Phe Ser Thr Thr Pro Lys  
 1410 1415 1420  
 Lys Gly Val Glu Gly Glu Ile Leu Asp Gly Tyr Arg Arg Val Asp Asn  
 1425 1430 1435 1440  
 Ile Thr Asp Glu Ile Leu Lys Leu Tyr Gln Ser Ser Leu Gly Glu Asp  
 1445 1450 1455  
 Val Thr Lys Asp Asp Ile Phe Tyr Phe Val Tyr Ala Gln Leu His Asp  
 1460 1465 1470  
 Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp Leu Lys Lys Met Leu Pro  
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 His Ile Glu Thr Pro Thr Asp Arg Ala Arg Phe Asp His Phe Val Thr  
 1490 1495 1500  
 Ala Gly Lys Glu Leu Met Asp Leu His Ile Asn Tyr Glu Asp Val Glu  
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 Arg Glu Thr Trp Arg Val Thr Lys Met Lys Trp Ala Lys Val Arg Asp  
 1540 1545 1550  
 Pro Glu Thr Lys Lys Leu Val Glu Asp His Thr Thr Leu Ile Tyr Asn  
 1555 1560 1565  
 Ser Ser Ile Thr Ile Ser Gly Ile Pro Glu Glu Ala Glu Asn Tyr Gln  
 1570 1575 1580  
 Leu Gly Ser Arg Ser Ala Ile Ala Trp Leu Ile Asp Arg Tyr Gln Val  
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 Lys Lys Asp Lys Ala Ser Gly Ile Val Asn Asp Pro Asn Asp Trp Ala  
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acc cct gtt gag atc gtg gac ttt att ctg cga gct gcc gat gat gtg	96
Thr Pro Val Glu Ile Val Asp Phe Ile Leu Arg Ala Ala Asp Asp Val	
20 25 30	
tcc aag aag cat ttt ggt cgt ggc tta agc gat aaa gat gtc cat gtt	144
Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp Lys Asp Val His Val	
35 40 45	
ctt gat cct ttc acc ggt acg ggt act ttt atg gtg cgt tta ttg cag	192
Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met Val Arg Leu Leu Gln	
50 55 60	
tca ggt cta att aag cct gaa gat ttg gcc cgt aaa tat gcc aat gag	240
Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu	
65 70 75 80	
ctg cac gct act gag atc atg ttg ctt gcc tat tat gtt gcg gcc gtt	288
Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr Tyr Val Ala Ala Val	
85 90 95	
aac att gag acc act tat ttt ggt ctc gag gga gag cgt gct ctg cgt	336
Asn Ile Glu Thr Tyr Phe Gly Leu Glu Gly Glu Arg Ala Leu Arg	
100 105 110	
aat ggt gaa gat gcg ccg gtc tat gag ccg ttt gat ggc att gtg ttg	384
Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe Asp Gly Ile Val Leu	
115 120 125	
ggt gat acc ttc cag atg tat gaa gac gat gac aaa ctc gat cta gat	432
Gly Asp Thr Phe Gln Met Tyr Glu Asp Asp Asp Lys Leu Asp Leu Asp	
130 135 140	
gtt ttt act gct aac aat gac cgt atg gag cgt cag aga ctt act cct	480
Val Phe Thr Ala Asn Asn Asp Arg Met Glu Arg Gln Arg Leu Thr Pro	
145 150 155 160	
gta cag gtt att gtg ggt aac ccg cct tac tct gtg ggg caa tcg agt	528
Val Gln Val Ile Val Gly Asn Pro Pro Tyr Ser Val Gly Gln Ser Ser	
165 170 175	
gcg aat gac aat aac gca aac ctc aag tac ccc act ctt gat cga cgt	576
Ala Asn Asp Asn Asn Ala Asn Leu Lys Tyr Pro Thr Leu Asp Arg Arg	
180 185 190	
att gaa gat tct tat gcg aag tat tcg acc gca aca aat aag aac tct	624
Ile Glu Asp Ser Tyr Ala Lys Tyr Ser Thr Ala Thr Asn Lys Asn Ser	
195 200 205	
ctg tac gac tcc tat tta cgt gct ttc cgg tgg gca aca gat cgt att	672
Leu Tyr Asp Ser Tyr Leu Arg Ala Phe Arg Trp Ala Thr Asp Arg Ile	
210 215 220	
cac aca caa ggg gtt gtt gct ttt gtt tct aac aac ggt tgg gtt gac	720
His Thr Gln Gly Val Val Ala Phe Val Ser Asn Asn Gly Trp Val Asp	
225 230 235 240	

ggc aat acc gct gat ggt gtg cgc cta agt ttg gca cag gac ttc tcc 768  
 Gly Asn Thr Ala Asp Gly Val Arg Leu Ser Leu Ala Gln Asp Phe Ser  
 245 250 255

gag att tat gtt ttc aac ctt cgt ggc aat tcc cga aca ggt ggt gat 816  
 Glu Ile Tyr Val Phe Asn Leu Arg Gly Asn Ser Arg Thr Gly Gly Asp  
 260 265 270

ttg gct aag cgc gag ggc ggc aac gtc ttt aat gtc cgt gtg ggt act 864  
 Leu Ala Lys Arg Glu Gly Gly Asn Val Phe Asn Val Arg Val Gly Thr  
 275 280 285

caa atc att gtt gcc gtg aaa aac cca caa ttg tct ggt tgc agg att 912  
 Gln Ile Ile Val Ala Val Lys Asn Pro Gln Leu Ser Gly Cys Arg Ile  
 290 295 300

ctt tat aaa gat att ggt gac aat ctc agc gcg gat gcg aag ttg aac 960  
 Leu Tyr Lys Asp Ile Gly Asp Asn Leu Ser Ala Asp Ala Lys Leu Asn  
 305 310 315 320

gag att gcc gtt gcc aca att gag ggc gct gag tgg cag act att tcg 1008  
 Glu Ile Ala Val Ala Thr Ile Glu Gly Ala Glu Trp Gln Thr Ile Ser  
 325 330 335

cct aat gaa tat gga gat tgg atc agc cag cgc tct gta gat ttt gat 1056  
 Pro Asn Glu Tyr Gly Asp Trp Ile Ser Gln Arg Ser Val Asp Phe Asp  
 340 345 350

acc tgg cct gta ctc ggt gat aag aaa aac aaa tct gca tta aag gtt 1104  
 Thr Trp Pro Val Leu Gly Asp Lys Lys Asn Lys Ser Ala Leu Lys Val  
 355 360 365

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 370 375 380

tat ggg cca aca tct gcg cag gta aaa act aat atc acc cgg tta tta 1200  
 Tyr Gly Pro Thr Ser Ala Gln Val Lys Thr Asn Ile Thr Arg Leu Leu  
 385 390 395 400

gaa acc tat gaa caa gct cag caa cgg ttt aat tcg tgg gtt gtg gat 1248  
 Glu Thr Tyr Glu Gln Ala Gln Gln Arg Phe Asn Ser Trp Val Val Asp  
 405 410 415

aac gga gtg aca tct cct aag gaa gct gac gtt aat caa ttc ctt aag 1296  
 Asn Gly Val Thr Ser Pro Lys Glu Ala Asp Val Asn Gln Phe Leu Lys  
 420 425 430

cag aac cct gat tta gcg gat agc aag aaa ata tcc tgg gat tcc aat 1344  
 Gln Asn Pro Asp Leu Ala Asp Ser Lys Lys Ile Ser Trp Asp Ser Asn  
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cta aaa atg tcc ttg tca cgc ggt gat act ttt tct ttt gat cca agc 1392  
 Leu Lys Met Ser Leu Ser Arg Gly Asp Thr Phe Ser Phe Asp Pro Ser  
 450 455 460

agc atc caa atg tcc ttg tat cgt cca ttt ttc cct caa cag aca tac 1440  
 Ser Ile Gln Met Ser Leu Tyr Arg Pro Phe Phe Pro Gln Gln Thr Tyr  
 465 470 475 480

ttc cat gtt tca ttg aac cag cgt cga tac cag tta ccg tca atg ttc	1488
Phe His Val Ser Leu Asn Gln Arg Arg Tyr Gln Leu Pro Ser Met Phe	
485 490 495	
ccg acc ccg gaa cat gac aac cag ggc ttt tat atc gtc aac cca ggt	1536
Pro Thr Pro Glu His Asp Asn Gln Gly Phe Tyr Ile Val Asn Pro Gly	
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agt gcc aag cca ttc tct acc ctt gca aca aat cta ctt cca gat ctt	1584
Ser Ala Lys Pro Phe Ser Thr Leu Ala Thr Asn Leu Leu Pro Asp Leu	
515 520 525	
gct atg tgg ggt tct aac gcc gga cag ttc ttt acc cga tgg act tgg	1632
Ala Met Trp Gly Ser Asn Ala Gly Gln Phe Phe Thr Arg Trp Thr Trp	
530 535 540	
gaa ccc atc gaa act cga gaa ggc gaa tta gac ttc ggt aat gga ctt	1680
Glu Pro Ile Glu Thr Arg Glu Gly Glu Leu Asp Phe Gly Asn Gly Leu	
545 550 555 560	
ttc tcc aca acc cca aaa aag gga gtt gaa ggc gag atc ctt gac ggt	1728
Phe Ser Thr Thr Pro Lys Lys Gly Val Glu Gly Glu Ile Leu Asp Gly	
565 570 575	
tac cgg cgc gtc gat aac atc acc gac gag atc tta aag ctc tac caa	1776
Tyr Arg Arg Val Asp Asn Ile Thr Asp Glu Ile Leu Lys Leu Tyr Gln	
580 585 590	
tca agc ttg ggt gag gat gtc acc aag gat gac atc ttc tac ttt gtt	1824
Ser Ser Leu Gly Glu Asp Val Thr Lys Asp Asp Ile Phe Tyr Phe Val	
595 600 605	
tat gca cag ttg cat gat cct gcc tat cgt gag gcc tat gcg gct gat	1872
Tyr Ala Gln Leu His Asp Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp	
610 615 620	
cta aag aag atg ctg cca cat att gaa acc cct act gat cgc gca cgc	1920
Leu Lys Lys Met Leu Pro His Ile Glu Thr Pro Thr Asp Arg Ala Arg	
625 630 635 640	
ttt gat cac ttt gtg aca gcc ggc aag gaa ttg atg gat ctt cat atc	1968
Phe Asp His Phe Val Thr Ala Gly Lys Glu Leu Met Asp Leu His Ile	
645 650 655	
aac tat gaa gat gtt gaa cca tgg gat gtg gag gta aag gtc aaa gaa	2016
Asn Tyr Glu Asp Val Glu Pro Trp Asp Val Glu Val Lys Val Lys Glu	
660 665 670	
aaa gct gat ccc acg gat cgt gag acc tgg cgt gtt acc aag atg aag	2064
Lys Ala Asp Pro Thr Asp Arg Glu Thr Trp Arg Val Thr Lys Met Lys	
675 680 685	
tgg gct aag gtt cgt gat cca gag acc aag aaa ttg gtg gag gac cat	2112
Trp Ala Lys Val Arg Asp Pro Glu Thr Lys Lys Leu Val Glu Asp His	
690 695 700	
acc acc ttg att tac aac agc tca atc acc atc agc ggc atc ccc gaa	2160
Thr Thr Leu Ile Tyr Asn Ser Ser Ile Thr Ile Ser Gly Ile Pro Glu	
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Ser Lys Lys His Phe Gly Arg Gly Leu Ser Asp Lys Asp Val His Val
          35             40             45

Leu Asp Pro Phe Thr Gly Thr Gly Thr Phe Met Val Arg Leu Leu Gln
          50             55             60

Ser Gly Leu Ile Lys Pro Glu Asp Leu Ala Arg Lys Tyr Ala Asn Glu
          65             70             75             80

Leu His Ala Thr Glu Ile Met Leu Leu Ala Tyr Tyr Val Ala Ala Val
          85             90             95

Asn Ile Glu Thr Thr Tyr Phe Gly Leu Glu Gly Glu Arg Ala Leu Arg
          100             105             110

Asn Gly Glu Asp Ala Pro Val Tyr Glu Pro Phe Asp Gly Ile Val Leu
          115             120             125

Gly Asp Thr Phe Gln Met Tyr Glu Asp Asp Asp Lys Leu Asp Leu Asp
          130             135             140

Val Phe Thr Ala Asn Asn Asp Arg Met Glu Arg Gln Arg Leu Thr Pro
          145             150             155             160

Val Gln Val Ile Val Gly Asn Pro Pro Tyr Ser Val Gly Gln Ser Ser
          165             170             175

Ala Asn Asp Asn Asn Ala Asn Leu Lys Tyr Pro Thr Leu Asp Arg Arg
          180             185             190

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Ile Glu Asp Ser Tyr Ala Lys Tyr Ser Thr Ala Thr Asn Lys Asn Ser  
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 Leu Tyr Asp Ser Tyr Leu Arg Ala Phe Arg Trp Ala Thr Asp Arg Ile  
 210 215 220  
 His Thr Gln Gly Val Val Ala Phe Val Ser Asn Asn Gly Trp Val Asp  
 225 230 235 240  
 Gly Asn Thr Ala Asp Gly Val Arg Leu Ser Leu Ala Gln Asp Phe Ser  
 245 250 255  
 Glu Ile Tyr Val Phe Asn Leu Arg Gly Asn Ser Arg Thr Gly Gly Asp  
 260 265 270  
 Leu Ala Lys Arg Glu Gly Gly Asn Val Phe Asn Val Arg Val Gly Thr  
 275 280 285  
 Gln Ile Ile Val Ala Val Lys Asn Pro Gln Leu Ser Gly Cys Arg Ile  
 290 295 300  
 Leu Tyr Lys Asp Ile Gly Asp Asn Leu Ser Ala Asp Ala Lys Leu Asn  
 305 310 315 320  
 Glu Ile Ala Val Ala Thr Ile Glu Gly Ala Glu Trp Gln Thr Ile Ser  
 325 330 335  
 Pro Asn Glu Tyr Gly Asp Trp Ile Ser Gln Arg Ser Val Asp Phe Asp  
 340 345 350  
 Thr Trp Pro Val Leu Gly Asp Lys Lys Asn Lys Ser Ala Leu Lys Val  
 355 360 365  
 Phe Gln Thr Phe Ser Ala Gly Leu Lys Thr Gly Arg Asp Ala Trp Cys  
 370 375 380  
 Tyr Gly Pro Thr Ser Ala Gln Val Lys Thr Asn Ile Thr Arg Leu Leu  
 385 390 395 400  
 Glu Thr Tyr Glu Gln Ala Gln Gln Arg Phe Asn Ser Trp Val Val Asp  
 405 410 415  
 Asn Gly Val Thr Ser Pro Lys Glu Ala Asp Val Asn Gln Phe Leu Lys  
 420 425 430  
 Gln Asn Pro Asp Leu Ala Asp Ser Lys Lys Ile Ser Trp Asp Ser Asn  
 435 440 445  
 Leu Lys Met Ser Leu Ser Arg Gly Asp Thr Phe Ser Phe Asp Pro Ser  
 450 455 460  
 Ser Ile Gln Met Ser Leu Tyr Arg Pro Phe Phe Pro Gln Gln Thr Tyr  
 465 470 475 480  
 Phe His Val Ser Leu Asn Gln Arg Arg Tyr Gln Leu Pro Ser Met Phe  
 485 490 495  
 Pro Thr Pro Glu His Asp Asn Gln Gly Phe Tyr Ile Val Asn Pro Gly  
 500 505 510

Ser Ala Lys Pro Phe Ser Thr Leu Ala Thr Asn Leu Leu Pro Asp Leu  
 515 520 525  
 Ala Met Trp Gly Ser Asn Ala Gly Gln Phe Phe Thr Arg Trp Thr Trp  
 530 535 540  
 Glu Pro Ile Glu Thr Arg Glu Gly Glu Leu Asp Phe Gly Asn Gly Leu  
 545 550 555 560  
 Phe Ser Thr Thr Pro Lys Lys Gly Val Glu Gly Glu Ile Leu Asp Gly  
 565 570 575  
 Tyr Arg Arg Val Asp Asn Ile Thr Asp Glu Ile Leu Lys Leu Tyr Gln  
 580 585 590  
 Ser Ser Leu Gly Glu Asp Val Thr Lys Asp Asp Ile Phe Tyr Phe Val  
 595 600 605  
 Tyr Ala Gln Leu His Asp Pro Ala Tyr Arg Glu Ala Tyr Ala Ala Asp  
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 Phe Asp His Phe Val Thr Ala Gly Lys Glu Leu Met Asp Leu His Ile  
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 Asn Tyr Glu Asp Val Glu Pro Trp Asp Val Glu Val Lys Val Lys Glu  
 660 665 670  
 Lys Ala Asp Pro Thr Asp Arg Glu Thr Trp Arg Val Thr Lys Met Lys  
 675 680 685  
 Trp Ala Lys Val Arg Asp Pro Glu Thr Lys Lys Leu Val Glu Asp His  
 690 695 700  
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 Glu Ala Glu Asn Tyr Gln Leu Gly Ser Arg Ser Ala Ile Ala Trp Leu  
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 Asp Pro Asn Asp Trp Ala Asp Glu Val Gly Asn Pro Arg Tyr Ile Val  
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&lt;211&gt; 4923

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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&lt;221&gt; CDS

&lt;222&gt; (101)..(4900)

&lt;223&gt; RXA02363

&lt;400&gt; 35

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Lys Lys Ser Phe Ser Asp Phe Phe Ser Pro Leu Ala Thr Glu Thr Glu
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aca act att acg ctc tcg gca att gag gta gag aaa gtc aat gcc aag 211
Thr Thr Ile Thr Leu Ser Ala Ile Glu Val Glu Lys Val Asn Ala Lys
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act gaa gtc act cga aat att gat cca gtc gaa gca gca gaa caa atc 259
Thr Glu Val Thr Arg Asn Ile Asp Pro Val Glu Ala Ala Glu Gln Ile
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agc cgc gac tac cgc cgc tac ctg aaa aca ctt att agc ccc agt aat 307
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aag aca att gcg gca gaa ttc aac cga gag att gat gag tcc gaa aac 355
Lys Thr Ile Ala Ala Glu Phe Asn Arg Glu Ile Asp Glu Ser Glu Asn
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ctt gtc tac gga cca att ttg cag ctg act ccg cct tat gca cca ggt 403
Leu Val Tyr Gly Pro Ile Leu Gln Leu Thr Pro Pro Tyr Ala Pro Gly
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aag tcc cct gct caa tta att gat gag gga gtc ctt tct cca aac ttc 451
Lys Ser Pro Ala Gln Leu Ile Asp Glu Gly Val Leu Ser Pro Asn Phe
                      105                      110                      115

tca cgt ctc gat gcc gca cta ccc aaa gat cgc ccg ctt tat cag cat 499
Ser Arg Leu Asp Ala Ala Leu Pro Lys Asp Arg Pro Leu Tyr Gln His
                      120                      125                      130

cag gaa gac gct ctg cga aaa atc gct agt ggc cga aac tta atc gtt 547
Gln Glu Asp Ala Leu Arg Lys Ile Ala Ser Gly Arg Asn Leu Ile Val
                      135                      140                      145

tca acc ggt aca gga tct gga aaa aca gag tct ttc ctc atc ccg atc 595
Ser Thr Gly Thr Gly Ser Gly Lys Thr Glu Ser Phe Leu Ile Pro Ile
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Phe Asp Gln Leu Leu Arg Gln Gln Gln Ala Gly Glu Leu Asn Pro Gly
                      170                      175                      180

gtc aga gca ttg ctt ctt tac cct atg aat gct ctt gca aat gat cag 691
Val Arg Ala Leu Leu Leu Tyr Pro Met Asn Ala Leu Ala Asn Asp Gln
                      185                      190                      195

gag aaa cgt ctc cgc gaa tta ttg gca gac acc ccg gaa att act ttt 739
Glu Lys Arg Leu Arg Glu Leu Leu Ala Asp Thr Pro Glu Ile Thr Phe

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cta att agc cgt gat gag atg cag gaa aat cca cct cat atc ttg ctc Leu Ile Ser Arg Asp Glu Met Gln Glu Asn Pro Pro His Ile Leu Leu 250 255 260			883
acc aac tac gca atg ttg gaa tac ctc ctg ctt cgt cct gca gac aac Thr Asn Tyr Ala Met Leu Glu Tyr Leu Leu Leu Arg Pro Ala Asp Asn 265 270 275			931
gca ttc ttc gat gat gca tat tcc aat aat tgg aag ttc ctt gtt ctt Ala Phe Phe Asp Asp Ala Tyr Ser Asn Asn Trp Lys Phe Leu Val Leu 280 285 290			979
gat gaa gct cat gtc tac gcc gga gca caa ggc act gaa gtc ggc atg Asp Glu Ala His Val Tyr Ala Gly Ala Gln Gly Thr Glu Val Gly Met 295 300 305			1027
ctg atg agg cgc ctg aaa gat cgt gtc caa cga gga aat ccc ctc cag Leu Met Arg Arg Leu Lys Asp Arg Val Gln Arg Gly Asn Pro Leu Gln 310 315 320 325			1075
tgc atc gct aca agt gct tct ttg gaa gga act aaa gaa gcc atc atg Cys Ile Ala Thr Ser Ala Ser Leu Glu Gly Thr Lys Glu Ala Ile Met 330 335 340			1123
acc ttt gga caa gac ctc ttt ggt gaa cct ttt gag ttt gtc aac gaa Thr Phe Gly Gln Asp Leu Phe Gly Glu Pro Phe Glu Phe Val Asn Glu 345 350 355			1171
gat ccc tcg cgc cag gat ttg gta tcc gcg cat cgg aga aaa cta cca Asp Pro Ser Arg Gln Asp Leu Val Ser Ala His Arg Arg Lys Leu Pro 360 365 370			1219
aaa acc ttt acg tgg tcc cta cca gat gag ctc ttt gac cag cct tta Lys Thr Phe Thr Trp Ser Leu Pro Asp Glu Leu Phe Asp Gln Pro Leu 375 380 385			1267
gaa agt gat ggt ctt ttc caa gca cta caa gag cgc ggt gga gat caa Glu Ser Asp Gly Leu Phe Gln Ala Leu Gln Glu Arg Gly Gly Asp Gln 390 395 400 405			1315
tac gaa gag ctc tcc aaa gaa gaa cac atc gta aaa ctc cgc gaa cta Tyr Glu Glu Leu Ser Lys Glu Glu His Ile Val Lys Leu Arg Glu Leu 410 415 420			1363
toc cag caa tca agc act cga gtt gaa gac atc ggc aag ggt ctt tgg Ser Gln Gln Ser Ser Thr Arg Val Glu Asp Ile Gly Lys Gly Leu Trp 425 430 435			1411
cca aat gtt act gat aaa gca tca atg cac cgc aca cat atg ctg gtg Pro Asn Val Thr Asp Lys Ala Ser Met His Arg Thr His Met Leu Val 440 445 450			1459

aat tta ggc agt ggc gtt cta tcc cat gat gga gta cca gct ctg tcc 1507  
 Asn Leu Gly Ser Gly Val Leu Ser His Asp Gly Val Pro Ala Leu Ser  
 455 460 465

gcg cgt tat cac atg ttt gtc cgc gca gtt gaa ggc gct ttt ctt ggg 1555  
 Ala Arg Tyr His Met Phe Val Arg Ala Val Glu Gly Ala Phe Leu Gly  
 470 475 480 485

tat aca gag caa gga aag cca atc gtg tcc ttg gac cgg caa gtg aca 1603  
 Tyr Thr Glu Gln Gly Lys Pro Ile Val Ser Leu Asp Arg Gln Val Thr  
 490 495 500

tta ggc gac aca gct cga cca atg tat gaa atg ggt gct tgc atc aaa 1651  
 Leu Gly Asp Thr Ala Arg Pro Met Tyr Glu Met Gly Ala Cys Ile Lys  
 505 510 515

tgt gga acc gtt cat atc agc gcc cat aat gat tct ggt ttc ctt gtg 1699  
 Cys Gly Thr Val His Ile Ser Ala His Asn Asp Ser Gly Phe Leu Val  
 520 525 530

cct cca gag aat tcc tca aat ttc gac gaa caa cag ctc aaa tgg gta 1747  
 Pro Pro Glu Asn Ser Ser Asn Phe Asp Glu Gln Gln Leu Lys Trp Val  
 535 540 545

gtc ctc acc gat gat ttc gaa aca gca gac atc gac gaa gat gac cta 1795  
 Val Leu Thr Asp Asp Phe Glu Thr Ala Asp Ile Asp Glu Asp Asp Leu  
 550 555 560 565

gaa act gat gct gac gag aac gtc aaa gtc ctt gag cta caa aaa tta 1843  
 Glu Thr Asp Ala Asp Glu Asn Val Lys Val Leu Glu Leu Gln Lys Leu  
 570 575 580

tgt acg gcc tgc gga aaa cta aac gga aag aac tct ctt ctc tgc tcc 1891  
 Cys Thr Ala Cys Gly Lys Leu Asn Gly Lys Asn Ser Leu Leu Cys Ser  
 585 590 595

gga tgc tca tca cat cat gac cag ttt att gat gta aag atc ttg gaa 1939  
 Gly Cys Ser Ser His His Asp Gln Phe Ile Asp Val Lys Ile Leu Glu  
 600 605 610

ccc cgg aat ggt agc caa tta aca tgc act cga tgc ggt ggc cga gaa 1987  
 Pro Arg Asn Gly Ser Gln Leu Thr Cys Thr Arg Cys Gly Gly Arg Glu  
 615 620 625

aag aac ctg att cga cga ctc cga acc gat tca aat gct gca cct tct 2035  
 Lys Asn Leu Ile Arg Arg Leu Arg Thr Asp Ser Asn Ala Ala Pro Ser  
 630 635 640 645

gtc ctc acc aca tca ttg ttc caa ctg ttg cca gaa tca gct gat caa 2083  
 Val Leu Thr Thr Ser Leu Phe Gln Leu Leu Pro Glu Ser Ala Asp Gln  
 650 655 660

gat aca tca cgc aag atc ggt gct gga cgc aaa cta ctc acg ttt tct 2131  
 Asp Thr Ser Arg Lys Ile Gly Ala Gly Arg Lys Leu Leu Thr Phe Ser  
 665 670 675

gac tcc cgc cag gct gcc gct tac gca gca cca tat ttg caa gca agt 2179  
 Asp Ser Arg Gln Ala Ala Tyr Ala Ala Pro Tyr Leu Gln Ala Ser  
 680 685 690

tac acc agg ttg cta gag cga aga atc ctc att gag acc ctg cgg gat	2227
Tyr Thr Arg Leu Leu Glu Arg Arg Ile Leu Ile Glu Thr Leu Arg Asp	
695 700 705	
gaa gaa ttt act gaa ggc gca tcc att gaa cga tgg att tcc cgc gca	2275
Glu Glu Phe Thr Glu Gly Ala Ser Ile Glu Arg Trp Ile Ser Arg Ala	
710 715 720 725	
agt gaa gtg gcg aaa aac aat cga gtc ctc gct aac aac ttg aac cca	2323
Ser Glu Val Ala Lys Asn Asn Arg Val Leu Ala Asn Asn Leu Asn Pro	
730 735 740	
cgc gaa aca cta gaa cag aca ggt aac tgg gta ttc gca gat ctt gct	2371
Arg Glu Thr Leu Glu Gln Thr Gly Asn Trp Val Phe Ala Asp Leu Ala	
745 750 755	
tcg aca gtc cga agt agt tcg act gaa ggg ctt gga cta gcc aaa att	2419
Ser Thr Val Arg Ser Ser Ser Thr Glu Gly Leu Gly Leu Ala Lys Ile	
760 765 770	
gaa ctg acc cct gag gct ttg tcg caa ctc agt ttc aga aaa cca ctt	2467
Glu Leu Thr Pro Glu Ala Leu Ser Gln Leu Ser Phe Arg Lys Pro Leu	
775 780 785	
ggc gag atg ttt ggg gat ccg gat gcc gcc gac gcc ttt ttt aat ctc	2515
Gly Glu Met Phe Gly Asp Pro Asp Ala Ala Asp Ala Phe Phe Asn Leu	
790 795 800 805	
ttc gct caa gaa ttc cgt cac aag ggc gca atc aat tgc cct gac tac	2563
Phe Ala Gln Glu Phe Arg His Lys Gly Ala Ile Asn Cys Pro Asp Tyr	
810 815 820	
gtc aat ctt gag gat gaa cgc ttt ggc cct cgt cgt ggg cag cac ttt	2611
Val Asn Leu Glu Asp Glu Arg Phe Gly Pro Arg Arg Gly Gln His Phe	
825 830 835	
ttc acc aaa gat ggt gga aga aaa tca aca cga cgc ctc tac tca tgg	2659
Phe Thr Lys Asp Gly Gly Arg Lys Ser Thr Arg Arg Leu Tyr Ser Trp	
840 845 850	
att ccg caa cga gga acc aac aat cgc aag gac ttc att aca aaa gtc	2707
Ile Pro Gln Arg Gly Thr Asn Asn Arg Lys Asp Phe Ile Thr Lys Val	
855 860 865	
ttg aac cgc atc gga caa gca ggt gac gaa ggt gaa aat att acg acg	2755
Leu Asn Arg Ile Gly Gln Ala Gly Asp Glu Gly Glu Asn Ile Thr Thr	
870 875 880 885	
ctt ctc cat cac cta tgg aat gac tac act aat tcc gaa att ttg aag	2803
Leu Leu His His Leu Trp Asn Asp Tyr Thr Asn Ser Glu Ile Leu Lys	
890 895 900	
gtc cca ggc gaa aag gcc gaa ggc tac aca ctt aac tac aac tca ctg	2851
Val Pro Gly Glu Lys Ala Glu Gly Tyr Thr Leu Asn Tyr Asn Ser Leu	
905 910 915	
caa gta agc cct gga aaa caa cat tcc tgg tat gaa tgt gac act tgt	2899
Gln Val Ser Pro Gly Lys Gln His Ser Trp Tyr Glu Cys Asp Thr Cys	
920 925 930	
aga aat aca acg cca ttt aat gtt ctc ggg ctg tgt cca cat ggg ttc	2947

Arg	Asn	Thr	Thr	Pro	Phe	Asn	Val	Leu	Gly	Leu	Cys	Pro	His	Gly	Phe		
935						940					945						
tgt	aaa	ggc	aag	cta	aaa	gaa	atc	gat	act	ttc	tta	ccg	gag	tat	gcc	2995	
Cys	Lys	Gly	Lys	Leu	Lys	Glu	Ile	Asp	Thr	Phe	Leu	Pro	Glu	Tyr	Ala		
950					955					960					965		
acc	aat	cat	tat	cgg	aag	ttg	gca	aca	tcg	ctt	gaa	att	ctt	ccg	ctt	3043	
Thr	Asn	His	Tyr	Arg	Lys	Leu	Ala	Thr	Ser	Leu	Glu	Ile	Leu	Pro	Leu		
				970					975						980		
tca	gcc	aaa	gag	cac	act	gct	caa	tgg	acg	cca	acg	gag	gct	gca	gag	3091	
Ser	Ala	Lys	Glu	His	Thr	Ala	Gln	Trp	Thr	Pro	Thr	Glu	Ala	Ala	Glu		
			985					990					995				
gtt	cag	aaa	gaa	ttc	atc	gaa	gga	aaa	atc	aat	gtc	cta	agc	tgt	tct	3139	
Val	Gln	Lys	Glu	Phe	Ile	Glu	Gly	Lys	Ile	Asn	Val	Leu	Ser	Cys	Ser		
	1000						1005						1010				
act	acg	ttt	gag	ctt	gga	gtt	gac	gtt	ggt	gat	ctg	cag	tca	gta	atg	3187	
Thr	Thr	Phe	Glu	Leu	Gly	Val	Asp	Val	Gly	Asp	Leu	Gln	Ser	Val	Met		
	1015					1020					1025						
atg	cgc	aac	gta	ccg	cca	cgt	acg	gct	aac	tat	gtg	caa	cgt	gcg	gga	3235	
Met	Arg	Asn	Val	Pro	Pro	Arg	Thr	Ala	Asn	Tyr	Val	Gln	Arg	Ala	Gly		
1030					1035					1040					1045		
cgt	gcg	gga	cgc	cga	tca	ggt	tca	gca	gct	ttt	gtg	ctt	acc	ttt	gct	3283	
Arg	Ala	Gly	Arg	Arg	Ser	Gly	Ser	Ala	Ala	Phe	Val	Leu	Thr	Phe	Ala		
				1050				1055						1060			
aag	cga	tct	tct	cat	gac	ttg	gct	gta	ttt	aag	aac	cca	acc	cag	atg	3331	
Lys	Arg	Ser	Ser	His	Asp	Leu	Ala	Val	Phe	Lys	Asn	Pro	Thr	Gln	Met		
				1065				1070						1075			
att	gat	ggc	gaa	atg	aca	gtg	cca	ttt	ttg	cac	att	aac	aat	gcc	cga	3379	
Ile	Asp	Gly	Glu	Met	Thr	Val	Pro	Phe	Leu	His	Ile	Asn	Asn	Ala	Arg		
	1080					1085						1090					
atc	gcc	cgt	cgt	cac	acc	tat	tca	atc	gct	ctc	gcc	gca	ttt	ttc	cga	3427	
Ile	Ala	Arg	Arg	His	Thr	Tyr	Ser	Ile	Ala	Leu	Ala	Ala	Phe	Phe	Arg		
	1095					1100					1105						
gag	cag	gct	gcc	caa	aat	cgg	ttc	tgg	aaa	aag	gcc	gga	gag	ttc	ttc	3475	
Glu	Gln	Ala	Ala	Gln	Asn	Arg	Phe	Trp	Lys	Lys	Ala	Gly	Glu	Phe	Phe		
1110					1115					1120				1125			
ctt	ggc	act	gat	gca	gct	cca	tac	ctt	agg	cct	gct	gtc	gca	gag	caa	3523	
Leu	Gly	Thr	Asp	Ala	Ala	Pro	Tyr	Leu	Arg	Pro	Ala	Val	Ala	Glu	Gln		
				1130					1135					1140			
gag	gca	acg	gag	atc	ctc	gaa	gag	ttt	ctc	tcc	cct	gtt	cct	aat	tac	3571	
Glu	Ala	Thr	Glu	Ile	Leu	Glu	Glu	Phe	Leu	Ser	Pro	Val	Pro	Asn	Tyr		
			1145					1150						1155			
atc	act	gaa	gcc	ctc	cgt	cgc	gta	ttc	cct	gag	tcc	ctg	cat	gag	gat	3619	
Ile	Thr	Glu	Ala	Leu	Arg	Arg	Val	Phe	Pro	Glu	Ser	Leu	His	Glu	Asp		
		1160					1165					1170					
ctg	gat	att	gaa	aat	caa	ggt	tgg	gtt	aaa	caa	ttc	ctt	gaa	att	ttc	3667	
Leu	Asp	Ile	Glu	Asn	Gln	Gly	Trp	Val	Lys	Gln	Phe	Leu	Glu	Ile	Phe		

1175	1180	1185	
gat aca act cgt cag gag atc tcc gaa gat ttc caa acg ctt aaa aag			3715
Asp Thr Thr Arg Gln Glu Ile Ser Glu Asp Phe Gln Thr Leu Lys Lys			
1190	1195	1200	1205
atg caa ggg cga gcg ctg ggc agt gaa caa ggc aaa aag gca gat gcc			3763
Met Gln Gly Arg Ala Leu Gly Ser Glu Gln Gly Lys Lys Ala Asp Ala			
1210	1215	1220	
ttc aaa cgc aca atc aca act ctg atg gac caa gat ctt ttg gga tac			3811
Phe Lys Arg Thr Ile Thr Thr Leu Met Asp Gln Asp Leu Leu Gly Tyr			
1225	1230	1235	
ttg gcc aag aag aac atg ctg ccc aag tac agc ttc cct gtc gat aca			3859
Leu Ala Lys Lys Asn Met Leu Pro Lys Tyr Ser Phe Pro Val Asp Thr			
1240	1245	1250	
gta gat ctt caa aca aac ttc agt gaa gct gga aat aag gtg agc ttg			3907
Val Asp Leu Gln Thr Asn Phe Ser Glu Ala Gly Asn Lys Val Ser Leu			
1255	1260	1265	
tca cga gat ctt cag cta gcg att acc gac tat gct cct ggt gcg gag			3955
Ser Arg Asp Leu Gln Leu Ala Ile Thr Asp Tyr Ala Pro Gly Ala Glu			
1270	1275	1280	1285
tta gta gca ggc gga aaa ttg tgg aaa tcc gct ggc att cga cac cta			4003
Leu Val Ala Gly Gly Lys Leu Trp Lys Ser Ala Gly Ile Arg His Leu			
1290	1295	1300	
gcc ggt aaa aag gtg gaa act ttt tat tgg aca acg tgt act gag tgt			4051
Ala Gly Lys Lys Val Glu Thr Phe Tyr Trp Thr Thr Cys Thr Glu Cys			
1305	1310	1315	
aaa cat act gaa acc tct cgt ttt gga ttt aca tct gaa gat gtc tgt			4099
Lys His Thr Glu Thr Ser Arg Phe Gly Phe Thr Ser Glu Asp Val Cys			
1320	1325	1330	
tct cag tgc tct gca cca ata tcg ctg ggt aaa gag aac aag ttc ctt			4147
Ser Gln Cys Ser Ala Pro Ile Ser Leu Gly Lys Glu Asn Lys Phe Leu			
1335	1340	1345	
atc cct cgt ttt ggt ttc gtt gca gac cca aat cca act gaa gtg ggc			4195
Ile Pro Arg Phe Gly Phe Val Ala Asp Pro Asn Pro Thr Glu Val Gly			
1350	1355	1360	1365
act gct ccc ccg gtc cga tcc tct aat cga ctt gaa ttt gta aag cag			4243
Thr Ala Pro Pro Val Arg Ser Ser Asn Arg Leu Glu Phe Val Lys Gln			
1370	1375	1380	
ttc ggt gtc aaa gat gac agt gaa gag ttc tca aat tca gat ggg aca			4291
Phe Gly Val Lys Asp Asp Ser Glu Glu Phe Ser Asn Ser Asp Gly Thr			
1385	1390	1395	
gca act gcg caa gta ctt act tct tct tgg agt cgg acg gag atg gga			4339
Ala Thr Ala Gln Val Leu Thr Ser Ser Trp Ser Arg Thr Glu Met Gly			
1400	1405	1410	
gcg ctt gaa aca ggt cct aac aag aat gga ttt tgg tat tgc caa aca			4387
Ala Leu Glu Thr Gly Pro Asn Lys Asn Gly Phe Trp Tyr Cys Gln Thr			
1415	1420	1425	

tgc gga ttc ggc act ccc aat ggc gcc gaa atc cct aaa agc cat cga 4435  
 Cys Gly Phe Gly Thr Pro Asn Gly Ala Glu Ile Pro Lys Ser His Arg  
 1430 1435 1440 1445  
  
 aac ccc aga act aag cag cag tgt ggc acc tac tac tta gaa ccc cac 4483  
 Asn Pro Arg Thr Lys Gln Gln Cys Gly Thr Tyr Tyr Leu Glu Pro His  
 1450 1455 1460  
  
 tct ttg ggt cac acc tac caa act gac atc gcg aca gtt gcc gtt cct 4531  
 Ser Leu Gly His Thr Tyr Gln Thr Asp Ile Ala Thr Val Ala Val Pro  
 1465 1470 1475  
  
 tct tat aca aat ctt gac ttc gaa ggg tgg cgc tct gga atg tac gcc 4579  
 Ser Tyr Thr Asn Leu Asp Phe Glu Gly Trp Arg Ser Gly Met Tyr Ala  
 1480 1485 1490  
  
 atc atc gag gca gct gct gaa tgt tta gaa atc aat cgt gat gat cta 4627  
 Ile Ile Glu Ala Ala Ala Glu Cys Leu Glu Ile Asn Arg Asp Asp Leu  
 1495 1500 1505  
  
 aac ggc acc atg gcg aaa cac gac aac agg cca acg atg gtg ttg ttc 4675  
 Asn Gly Thr Met Ala Lys His Asp Asn Arg Pro Thr Met Val Leu Phe  
 1510 1515 1520 1525  
  
 gat act gtt cct ggt gga gct ggt att acc cga aaa gtt cga gaa aac 4723  
 Asp Thr Val Pro Gly Gly Ala Gly Ile Thr Arg Lys Val Arg Glu Asn  
 1530 1535 1540  
  
 ttc cct caa gta ctc gaa gcg gca att aga agg gtc gaa acc tgt tct 4771  
 Phe Pro Gln Val Leu Glu Ala Ala Ile Arg Arg Val Glu Thr Cys Ser  
 1545 1550 1555  
  
 tgt ggc atc gat act tcg tgt tat gcc tgt ttg cga tca ttt tct aac 4819  
 Cys Gly Ile Asp Thr Ser Cys Tyr Ala Cys Leu Arg Ser Phe Ser Asn  
 1560 1565 1570  
  
 cag cgt ttc cat ctc gat tta agg cgc gat att gca ttg gac ttg ctt 4867  
 Gln Arg Phe His Leu Asp Leu Arg Arg Asp Ile Ala Leu Asp Leu Leu  
 1575 1580 1585  
  
 cac cat atg gcg gtt gcg atg cca aaa tct gag tagataaacac cagctaccca 4920  
 His His Met Ala Val Ala Met Pro Lys Ser Glu  
 1590 1595 1600  
  
 cag 4923

&lt;210&gt; 36

&lt;211&gt; 1600

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 36

Met Ser Asn Ala Pro Lys Lys Ser Phe Ser Asp Phe Phe Ser Pro Leu  
 1 5 10 15

Ala Thr Glu Thr Glu Thr Thr Ile Thr Leu Ser Ala Ile Glu Val Glu  
 20 25 30

Lys Val Asn Ala Lys Thr Glu Val Thr Arg Asn Ile Asp Pro Val Glu

35	40	45
Ala Ala Glu Gln Ile Ser Arg Asp Tyr Arg Arg Tyr Leu Lys Thr Leu		
50	55	60
Ile Ser Pro Ser Asn Lys Thr Ile Ala Ala Glu Phe Asn Arg Glu Ile		
65	70	75 80
Asp Glu Ser Glu Asn Leu Val Tyr Gly Pro Ile Leu Gln Leu Thr Pro		
	85	90 95
Pro Tyr Ala Pro Gly Lys Ser Pro Ala Gln Leu Ile Asp Glu Gly Val		
	100	105 110
Leu Ser Pro Asn Phe Ser Arg Leu Asp Ala Ala Leu Pro Lys Asp Arg		
	115	120 125
Pro Leu Tyr Gln His Gln Glu Asp Ala Leu Arg Lys Ile Ala Ser Gly		
	130	135 140
Arg Asn Leu Ile Val Ser Thr Gly Thr Gly Ser Gly Lys Thr Glu Ser		
	145	150 155 160
Phe Leu Ile Pro Ile Phe Asp Gln Leu Leu Arg Gln Gln Gln Ala Gly		
	165	170 175
Glu Leu Asn Pro Gly Val Arg Ala Leu Leu Leu Tyr Pro Met Asn Ala		
	180	185 190
Leu Ala Asn Asp Gln Glu Lys Arg Leu Arg Glu Leu Leu Ala Asp Thr		
	195	200 205
Pro Glu Ile Thr Phe Gly Arg Tyr Thr Gly Asp Thr Lys Gln Thr Arg		
	210	215 220
Glu Glu Ala Glu Lys Tyr Phe Lys Leu Ile Asn Gly Arg Asn Ala Thr		
	225	230 235 240
Pro Leu Pro Asn Glu Leu Ile Ser Arg Asp Glu Met Gln Glu Asn Pro		
	245	250 255
Pro His Ile Leu Leu Thr Asn Tyr Ala Met Leu Glu Tyr Leu Leu Leu		
	260	265 270
Arg Pro Ala Asp Asn Ala Phe Phe Asp Asp Ala Tyr Ser Asn Asn Trp		
	275	280 285
Lys Phe Leu Val Leu Asp Glu Ala His Val Tyr Ala Gly Ala Gln Gly		
	290	295 300
Thr Glu Val Gly Met Leu Met Arg Arg Leu Lys Asp Arg Val Gln Arg		
	305	310 315 320
Gly Asn Pro Leu Gln Cys Ile Ala Thr Ser Ala Ser Leu Glu Gly Thr		
	325	330 335
Lys Glu Ala Ile Met Thr Phe Gly Gln Asp Leu Phe Gly Glu Pro Phe		
	340	345 350
Glu Phe Val Asn Glu Asp Pro Ser Arg Gln Asp Leu Val Ser Ala His		
	355	360 365

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Arg Arg Lys Leu Pro Lys Thr Phe Thr Trp Ser Leu Pro Asp Glu Leu  
 370 375 380  
 Phe Asp Gln Pro Leu Glu Ser Asp Gly Leu Phe Gln Ala Leu Gln Glu  
 385 390 395 400  
 Arg Gly Gly Asp Gln Tyr Glu Glu Leu Ser Lys Glu Glu His Ile Val  
 405 410 415  
 Lys Leu Arg Glu Leu Ser Gln Gln Ser Ser Thr Arg Val Glu Asp Ile  
 420 425 430  
 Gly Lys Gly Leu Trp Pro Asn Val Thr Asp Lys Ala Ser Met His Arg  
 435 440 445  
 Thr His Met Leu Val Asn Leu Gly Ser Gly Val Leu Ser His Asp Gly  
 450 455 460  
 Val Pro Ala Leu Ser Ala Arg Tyr His Met Phe Val Arg Ala Val Glu  
 465 470 475 480  
 Gly Ala Phe Leu Gly Tyr Thr Glu Gln Gly Lys Pro Ile Val Ser Leu  
 485 490 495  
 Asp Arg Gln Val Thr Leu Gly Asp Thr Ala Arg Pro Met Tyr Glu Met  
 500 505 510  
 Gly Ala Cys Ile Lys Cys Gly Thr Val His Ile Ser Ala His Asn Asp  
 515 520 525  
 Ser Gly Phe Leu Val Pro Pro Glu Asn Ser Ser Asn Phe Asp Glu Gln  
 530 535 540  
 Gln Leu Lys Trp Val Val Leu Thr Asp Asp Phe Glu Thr Ala Asp Ile  
 545 550 555 560  
 Asp Glu Asp Asp Leu Glu Thr Asp Ala Asp Glu Asn Val Lys Val Leu  
 565 570 575  
 Glu Leu Gln Lys Leu Cys Thr Ala Cys Gly Lys Leu Asn Gly Lys Asn  
 580 585 590  
 Ser Leu Leu Cys Ser Gly Cys Ser Ser His His Asp Gln Phe Ile Asp  
 595 600 605  
 Val Lys Ile Leu Glu Pro Arg Asn Gly Ser Gln Leu Thr Cys Thr Arg  
 610 615 620  
 Cys Gly Gly Arg Glu Lys Asn Leu Ile Arg Arg Leu Arg Thr Asp Ser  
 625 630 635 640  
 Asn Ala Ala Pro Ser Val Leu Thr Thr Ser Leu Phe Gln Leu Leu Pro  
 645 650 655  
 Glu Ser Ala Asp Gln Asp Thr Ser Arg Lys Ile Gly Ala Gly Arg Lys  
 660 665 670  
 Leu Leu Thr Phe Ser Asp Ser Arg Gln Ala Ala Ala Tyr Ala Ala Pro  
 675 680 685



Tyr Leu Gln Ala Ser Tyr Thr Arg Leu Leu Glu Arg Arg Ile Leu Ile  
 690 695 700  
 Glu Thr Leu Arg Asp Glu Glu Phe Thr Glu Gly Ala Ser Ile Glu Arg  
 705 710 715 720  
 Trp Ile Ser Arg Ala Ser Glu Val Ala Lys Asn Asn Arg Val Leu Ala  
 725 730 735  
 Asn Asn Leu Asn Pro Arg Glu Thr Leu Glu Gln Thr Gly Asn Trp Val  
 740 745 750  
 Phe Ala Asp Leu Ala Ser Thr Val Arg Ser Ser Ser Thr Glu Gly Leu  
 755 760 765  
 Gly Leu Ala Lys Ile Glu Leu Thr Pro Glu Ala Leu Ser Gln Leu Ser  
 770 775 780  
 Phe Arg Lys Pro Leu Gly Glu Met Phe Gly Asp Pro Asp Ala Ala Asp  
 785 790 795 800  
 Ala Phe Phe Asn Leu Phe Ala Gln Glu Phe Arg His Lys Gly Ala Ile  
 805 810 815  
 Asn Cys Pro Asp Tyr Val Asn Leu Glu Asp Glu Arg Phe Gly Pro Arg  
 820 825 830  
 Arg Gly Gln His Phe Phe Thr Lys Asp Gly Gly Arg Lys Ser Thr Arg  
 835 840 845  
 Arg Leu Tyr Ser Trp Ile Pro Gln Arg Gly Thr Asn Asn Arg Lys Asp  
 850 855 860  
 Phe Ile Thr Lys Val Leu Asn Arg Ile Gly Gln Ala Gly Asp Glu Gly  
 865 870 875 880  
 Glu Asn Ile Thr Thr Leu Leu His His Leu Trp Asn Asp Tyr Thr Asn  
 885 890 895  
 Ser Glu Ile Leu Lys Val Pro Gly Glu Lys Ala Glu Gly Tyr Thr Leu  
 900 905 910  
 Asn Tyr Asn Ser Leu Gln Val Ser Pro Gly Lys Gln His Ser Trp Tyr  
 915 920 925  
 Glu Cys Asp Thr Cys Arg Asn Thr Thr Pro Phe Asn Val Leu Gly Leu  
 930 935 940  
 Cys Pro His Gly Phe Cys Lys Gly Lys Leu Lys Glu Ile Asp Thr Phe  
 945 950 955 960  
 Leu Pro Glu Tyr Ala Thr Asn His Tyr Arg Lys Leu Ala Thr Ser Leu  
 965 970 975  
 Glu Ile Leu Pro Leu Ser Ala Lys Glu His Thr Ala Gln Trp Thr Pro  
 980 985 990  
 Thr Glu Ala Ala Glu Val Gln Lys Glu Phe Ile Glu Gly Lys Ile Asn  
 995 1000 1005  
 Val Leu Ser Cys Ser Thr Thr Phe Glu Leu Gly Val Asp Val Gly Asp

1010	1015	1020	
Leu Gln Ser Val Met Met Arg Asn Val Pro Pro Arg Thr Ala Asn Tyr			
1025	1030	1035	1040
Val Gln Arg Ala Gly Arg Ala Gly Arg Arg Ser Gly Ser Ala Ala Phe			
1045	1050		1055
Val Leu Thr Phe Ala Lys Arg Ser Ser His Asp Leu Ala Val Phe Lys			
1060	1065		1070
Asn Pro Thr Gln Met Ile Asp Gly Glu Met Thr Val Pro Phe Leu His			
1075	1080		1085
Ile Asn Asn Ala Arg Ile Ala Arg Arg His Thr Tyr Ser Ile Ala Leu			
1090	1095		1100
Ala Ala Phe Phe Arg Glu Gln Ala Ala Gln Asn Arg Phe Trp Lys Lys			
1105	1110	1115	1120
Ala Gly Glu Phe Phe Leu Gly Thr Asp Ala Ala Pro Tyr Leu Arg Pro			
1125	1130		1135
Ala Val Ala Glu Gln Glu Ala Thr Glu Ile Leu Glu Glu Phe Leu Ser			
1140	1145		1150
Pro Val Pro Asn Tyr Ile Thr Glu Ala Leu Arg Arg Val Phe Pro Glu			
1155	1160		1165
Ser Leu His Glu Asp Leu Asp Ile Glu Asn Gln Gly Trp Val Lys Gln			
1170	1175		1180
Phe Leu Glu Ile Phe Asp Thr Thr Arg Gln Glu Ile Ser Glu Asp Phe			
1185	1190	1195	1200
Gln Thr Leu Lys Lys Met Gln Gly Arg Ala Leu Gly Ser Glu Gln Gly			
1205	1210		1215
Lys Lys Ala Asp Ala Phe Lys Arg Thr Ile Thr Thr Leu Met Asp Gln			
1220	1225		1230
Asp Leu Leu Gly Tyr Leu Ala Lys Lys Asn Met Leu Pro Lys Tyr Ser			
1235	1240		1245
Phe Pro Val Asp Thr Val Asp Leu Gln Thr Asn Phe Ser Glu Ala Gly			
1250	1255		1260
Asn Lys Val Ser Leu Ser Arg Asp Leu Gln Leu Ala Ile Thr Asp Tyr			
1265	1270	1275	1280
Ala Pro Gly Ala Glu Leu Val Ala Gly Gly Lys Leu Trp Lys Ser Ala			
1285	1290		1295
Gly Ile Arg His Leu Ala Gly Lys Lys Val Glu Thr Phe Tyr Trp Thr			
1300	1305		1310
Thr Cys Thr Glu Cys Lys His Thr Glu Thr Ser Arg Phe Gly Phe Thr			
1315	1320		1325
Ser Glu Asp Val Cys Ser Gln Cys Ser Ala Pro Ile Ser Leu Gly Lys			
1330	1335		1340

Glu Asn Lys Phe Leu Ile Pro Arg Phe Gly Phe Val Ala Asp Pro Asn  
 1345 1350 1355 1360  
 Pro Thr Glu Val Gly Thr Ala Pro Pro Val Arg Ser Ser Asn Arg Leu  
 1365 1370 1375  
 Glu Phe Val Lys Gln Phe Gly Val Lys Asp Asp Ser Glu Glu Phe Ser  
 1380 1385 1390  
 Asn Ser Asp Gly Thr Ala Thr Ala Gln Val Leu Thr Ser Ser Trp Ser  
 1395 1400 1405  
 Arg Thr Glu Met Gly Ala Leu Glu Thr Gly Pro Asn Lys Asn Gly Phe  
 1410 1415 1420  
 Trp Tyr Cys Gln Thr Cys Gly Phe Gly Thr Pro Asn Gly Ala Glu Ile  
 1425 1430 1435 1440  
 Pro Lys Ser His Arg Asn Pro Arg Thr Lys Gln Gln Cys Gly Thr Tyr  
 1445 1450 1455  
 Tyr Leu Glu Pro His Ser Leu Gly His Thr Tyr Gln Thr Asp Ile Ala  
 1460 1465 1470  
 Thr Val Ala Val Pro Ser Tyr Thr Asn Leu Asp Phe Glu Gly Trp Arg  
 1475 1480 1485  
 Ser Gly Met Tyr Ala Ile Ile Glu Ala Ala Ala Glu Cys Leu Glu Ile  
 1490 1495 1500  
 Asn Arg Asp Asp Leu Asn Gly Thr Met Ala Lys His Asp Asn Arg Pro  
 1505 1510 1515 1520  
 Thr Met Val Leu Phe Asp Thr Val Pro Gly Gly Ala Gly Ile Thr Arg  
 1525 1530 1535  
 Lys Val Arg Glu Asn Phe Pro Gln Val Leu Glu Ala Ala Ile Arg Arg  
 1540 1545 1550  
 Val Glu Thr Cys Ser Cys Gly Ile Asp Thr Ser Cys Tyr Ala Cys Leu  
 1555 1560 1565  
 Arg Ser Phe Ser Asn Gln Arg Phe His Leu Asp Leu Arg Arg Asp Ile  
 1570 1575 1580  
 Ala Leu Asp Leu Leu His His Met Ala Val Ala Met Pro Lys Ser Glu  
 1585 1590 1595 1600

<210> 37  
 <211> 2799  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2776)

&lt;223&gt; RXN01606

&lt;400&gt; 37

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ctccaccctg gcgaatagaa caaacaaggt tcttcgcatg aaggactacc acccagaact 60

gaaggtctaa aagcttttcc cgcccgggtc aatagcgtta atg gca gaa tca aac 115
                                   Met Ala Glu Ser Asn
                                   1 5

gct atg gac cgg gca caa atc tct gca ctg cta gat aga gca cag cac 163
Ala Met Asp Arg Ala Gln Ile Ser Ala Leu Leu Asp Arg Ala Gln His
                                   10 15 20

aca atc aac ctt gcc gaa caa gca aac aac gtg ctc cga ctg ttg aaa 211
Thr Ile Asn Leu Ala Glu Gln Ala Asn Asn Val Leu Arg Leu Leu Lys
                                   25 30 35

aca ccc gga acg gcc aca gta ggg gac aac ggg aca ctc ggc acc gat 259
Thr Pro Gly Thr Ala Thr Val Gly Asp Asn Gly Thr Leu Gly Thr Asp
                                   40 45 50

acc tat ctg atc cca tcc cgc aac atc acc tgg cct gac aac ctg tat 307
Thr Tyr Leu Ile Pro Ser Arg Asn Ile Thr Trp Pro Asp Asn Leu Tyr
                                   55 60 65

gtc aac gtc ttt cta gac ggc atg aat gca gaa gcc acc ctt acc gat 355
Val Asn Val Phe Leu Asp Gly Met Asn Ala Glu Ala Thr Leu Thr Asp
                                   70 75 80 85

tac gtc gca tca gtc gct tcg atc cca cgc cta tgc cag atc atc aac 403
Tyr Val Ala Ser Val Ala Ser Ile Pro Arg Leu Cys Gln Ile Ile Asn
                                   90 95 100

gag ggc caa ggc ggc atg ttc cgc aga cta ttc aac ccc acc aag gtc 451
Glu Gly Gln Gly Gly Met Phe Arg Arg Leu Phe Asn Pro Thr Lys Val
                                   105 110 115

caa gcc ggc gac caa gct gtc ttc gac ctc atg gtc aaa ctc gac gag 499
Gln Ala Gly Asp Gln Ala Val Phe Asp Leu Met Val Lys Leu Asp Glu
                                   120 125 130

att tca tct acc acc cac gaa gtc tcc cgc atg ctc gag ggc gtc cac 547
Ile Ser Ser Thr Thr His Glu Val Ser Arg Met Leu Glu Gly Val His
                                   135 140 145

gct gcc cgc acc cgc caa caa caa ggc gtt gca ctt ttc cca ggt att 595
Ala Ala Arg Thr Arg Gln Gln Gln Gly Val Ala Leu Phe Pro Gly Ile
                                   150 155 160 165

cat gga gtg gga gag cgc tac atc gaa cgc gca caa cag gta ctc gcc 643
His Gly Val Gly Glu Arg Tyr Ile Glu Arg Ala Gln Gln Val Leu Ala
                                   170 175 180

tca gcc ctc ggt atc gct gga ttc ggt gcc gaa ccc tgg gac gga cat 691
Ser Ala Leu Gly Ile Ala Gly Phe Gly Ala Glu Pro Trp Asp Gly His
                                   185 190 195

acc ctt gcc caa gcg cgc cgg gta gtc caa cgc tac gcc caa gat cct 739
Thr Leu Ala Gln Ala Arg Arg Val Val Gln Arg Tyr Ala Gln Asp Pro
                                   200 205 210

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aac tcc gaa tac cgg ctg aaa agc gaa gcc gag aaa cac ctc aca tcc Asn Ser Glu Tyr Arg Leu Lys Ser Glu Ala Glu Lys His Leu Thr Ser 215 220 225	787
atc aac gag ctc cgc gta cag ata ctc ctc gaa caa ctc ccc gtt gat Ile Asn Glu Leu Arg Val Gln Ile Leu Leu Glu Gln Leu Pro Val Asp 230 235 240 245	835
gcc cta cgc atg gct acc gac cac cgc ctg cgc ttt gga tcc ctc gat Ala Leu Arg Met Ala Thr Asp His Arg Leu Arg Phe Gly Ser Leu Asp 250 255 260	883
tcc atc cac gtc gca acc gtc gcc gac gtc cta aaa aca cac acc tcc Ser Ile His Val Ala Thr Val Ala Asp Val Leu Lys Thr His Thr Ser 265 270 275	931
atc ctc acc acc gtg caa ggt atc ggc gcc caa acc gcg ggg cgg atg Ile Leu Thr Thr Val Gln Gly Ile Gly Ala Gln Thr Ala Gly Arg Met 280 285 290	979
aaa gcc gca gca gaa aca ctc aaa caa gaa gca cta cgc cgc caa aac Lys Ala Ala Ala Glu Thr Leu Lys Gln Glu Ala Leu Arg Arg Gln Asn 295 300 305	1027
acc tcc atc ggc gac gaa cct acc caa ccc gcc atg cgt cta atc aac Thr Ser Ile Gly Asp Glu Pro Thr Gln Pro Ala Met Arg Leu Ile Asn 310 315 320 325	1075
gtg ctg gcc cgc ttc gac caa acc gaa acc atc acg ccc gaa gaa cgc Val Leu Ala Arg Phe Asp Gln Thr Glu Thr Ile Thr Pro Glu Glu Arg 330 335 340	1123
gcc cgc cgc acc cgc gtc atc gac tac gta gaa cac ata ccc cca agc Ala Arg Arg Thr Arg Val Ile Asp Tyr Val Glu His Ile Pro Pro Ser 345 350 355	1171
ctc gac ccc tac atc gtc atc aac cca gca acg cct gag ttc aac aac Leu Asp Pro Tyr Ile Val Ile Asn Pro Ala Thr Pro Glu Phe Asn Asn 360 365 370	1219
ttc acc gac gac ctc cgc tgg atc gac gca aac ccc aac ctc ttc cac Phe Thr Asp Asp Leu Arg Trp Ile Asp Ala Asn Pro Asn Leu Phe His 375 380 385	1267
cca caa aca atc acc acc cca ccc gcc gac atc tgg gac gac tac atc Pro Gln Thr Ile Thr Thr Pro Pro Ala Asp Ile Trp Asp Asp Tyr Ile 390 395 400 405	1315
tcc cgt ccc gct cac tac caa ggc ctg cta gcc acg ctg ctc ggc cgc Ser Arg Pro Ala His Tyr Gln Gly Leu Leu Ala Thr Leu Leu Gly Arg 410 415 420	1363
gac atc gaa ggc gca gac gaa ctc ctc gac gcc acc acc ctc caa aaa Asp Ile Glu Gly Ala Asp Glu Leu Leu Asp Ala Thr Thr Leu Gln Lys 425 430 435	1411
atc aga gac ctc acc ctc gac aaa act cat ctc acc gac ctc cac ctc Ile Arg Asp Leu Thr Leu Asp Lys Thr His Leu Thr Asp Leu His Leu 440 445 450	1459
cgc gga tac caa tca ttc ggc gcc cgc ttc gcc atc atc caa aag aaa	1507

Arg Gly Tyr Gln Ser Phe Gly Ala Arg Phe Ala Ile Ile Gln Lys Lys	
455 460 465	
acc ctc ctc ggc gac gac atg gga ctc ggc aaa aca gtc caa gcc ctc	1555
Thr Leu Leu Gly Asp Asp Met Gly Leu Gly Lys Thr Val Gln Ala Leu	
470 475 480 485	
tcc gca gct gca cac ctt gcc gcc acc gaa aaa gac ttc cgc acc ctc	1603
Ser Ala Ala Ala His Leu Ala Ala Thr Glu Lys Asp Phe Arg Thr Leu	
490 495 500	
gtc gtc gta ccc gca tcc gtc att gtt aac tgg acc cgc gaa tgc aaa	1651
Val Val Val Pro Ala Ser Val Ile Val Asn Trp Thr Arg Glu Cys Lys	
505 510 515	
cgc ttc ctc aac ctc ccc gta ttc atc gcc cac gga gac aac aaa caa	1699
Arg Phe Leu Asn Leu Pro Val Phe Ile Ala His Gly Asp Asn Lys Gln	
520 525 530	
gac gcc atc aac gcc tgg tct aac acc aac gga atc gca atc tgc acc	1747
Asp Ala Ile Asn Ala Trp Ser Asn Thr Asn Gly Ile Ala Ile Cys Thr	
535 540 545	
tac gac ggc gtc cgc acc atg gac atc ccc gcg ccg ggt ctg gtc att	1795
Tyr Asp Gly Val Arg Thr Met Asp Ile Pro Ala Pro Gly Leu Val Ile	
550 555 560 565	
gcc gat gaa gcc cac ctg atc aaa aac ccc tcc acc aaa cgc acc caa	1843
Ala Asp Glu Ala His Leu Ile Lys Asn Pro Ser Thr Lys Arg Thr Gln	
570 575 580	
gca ctg cgc aaa ctt atc gac gcc gcc cca tac acc ctt ctg atg acc	1891
Ala Leu Arg Lys Leu Ile Asp Ala Ala Pro Tyr Thr Leu Leu Met Thr	
585 590 595	
ggc aca cca cta gaa aac aaa gtg gaa gag ttt gta aat ctc gtg cgc	1939
Gly Thr Pro Leu Glu Asn Lys Val Glu Glu Phe Val Asn Leu Val Arg	
600 605 610	
tac atc caa ccg gag ctg atc acc cgt ggc atg tcc aaa atg cag gcc	1987
Tyr Ile Gln Pro Glu Leu Ile Thr Arg Gly Met Ser Lys Met Gln Ala	
615 620 625	
gag aat ttc cgc gag cgc atc gca cca gcc tat ctg cgc aga aat caa	2035
Glu Asn Phe Arg Glu Arg Ile Ala Pro Ala Tyr Leu Arg Arg Asn Gln	
630 635 640 645	
gct gat gtg ctt gac gaa ctc cca gag cgc acc gac tcc atc gac tgg	2083
Ala Asp Val Leu Asp Glu Leu Pro Glu Arg Thr Asp Ser Ile Asp Trp	
650 655 660	
atc gac ctc acc cca gaa gac cgc agc gcc tac gac gac caa gtc cgc	2131
Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr Asp Asp Gln Val Arg	
665 670 675	
caa ggc agc tgg atg ggc atg cgc cgc tcc gcc atg ctc tca cca aca	2179
Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala Met Leu Ser Pro Thr	
680 685 690	
cca cgc cta act tcc gca aaa atg caa cgc atc cta gaa ctc ttc gaa	2227
Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile Leu Glu Leu Phe Glu	

695	700	705	
gaa gca gaa gaa cac ggc cgc aaa gcc ctc atc ttc acc tac ttc ctc			2275
Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile Phe Thr Tyr Phe Leu			
710	715	720	725
gac gtc ctc gac gaa ctg gaa aag cat cta ggc gag cgc gtc atc ggc			2323
Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly Glu Arg Val Ile Gly			
730	735		740
cgc att tcc ggc gac gtg cca gcc acc aag cgc caa ttg ctt gtc gac			2371
Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg Gln Leu Leu Val Asp			
745	750		755
gcc ctg tcc cac tcc aaa ccc gga tcc gcc ctc att gcc caa atc acc			2419
Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu Ile Ala Gln Ile Thr			
760	765		770
gcc ggg gga gta ggc cta aac atc caa tcc gcg agc cta tgc att att			2467
Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala Ser Leu Cys Ile Ile			
775	780		785
tgt gaa cct caa gta aag cca acc atc gaa cag cag gcc gtc gcc cga			2515
Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln Gln Ala Val Ala Arg			
790	795		800
gtc cac cgc atg ggc caa acc gcc acc gtc caa gtc cac cga ctc atc			2563
Val His Arg Met Gly Gln Thr Ala Thr Val Gln Val His Arg Leu Ile			
810		815	820
ggc gac gaa acc gca gac gaa cgc atg cta gaa atc ctg gca ggc aaa			2611
Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu Ile Leu Ala Gly Lys			
825		830	835
act cac gtc ttc gac gtc tac gcc cgg cta tct gaa acc gca gag att			2659
Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser Glu Thr Ala Glu Ile			
840		845	850
cca gat gct gtg gat atc act gaa tca cag ctg gca gca cgg gtt att			2707
Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu Ala Ala Arg Val Ile			
855	860		865
gat gag gag cgt gca cgg tta ggg ctt act gaa tcc act ggc cct aaa			2755
Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu Ser Thr Gly Pro Lys			
870	875	880	885
gat gaa gaa acg gcc tta agc tagttgccta aggccggaat taa			2799
Asp Glu Glu Thr Ala Leu Ser			
890			

&lt;210&gt; 38

&lt;211&gt; 892

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

Met	Ala	Glu	Ser	Asn	Ala	Met	Asp	Arg	Ala	Gln	Ile	Ser	Ala	Leu	Leu
1					5					10				15	

Asp Arg Ala Gln His Thr Ile Asn Leu Ala Glu Gln Ala Asn Asn Val

20	25	30
Leu Arg Leu Leu Lys Thr Pro Gly Thr Ala Thr Val Gly Asp Asn Gly		
35	40	45
Thr Leu Gly Thr Asp Thr Tyr Leu Ile Pro Ser Arg Asn Ile Thr Trp		
50	55	60
Pro Asp Asn Leu Tyr Val Asn Val Phe Leu Asp Gly Met Asn Ala Glu		
65	70	75
Ala Thr Leu Thr Asp Tyr Val Ala Ser Val Ala Ser Ile Pro Arg Leu		
85	90	95
Cys Gln Ile Ile Asn Glu Gly Gln Gly Gly Met Phe Arg Arg Leu Phe		
100	105	110
Asn Pro Thr Lys Val Gln Ala Gly Asp Gln Ala Val Phe Asp Leu Met		
115	120	125
Val Lys Leu Asp Glu Ile Ser Ser Thr Thr His Glu Val Ser Arg Met		
130	135	140
Leu Glu Gly Val His Ala Ala Arg Thr Arg Gln Gln Gln Gly Val Ala		
145	150	155
Leu Phe Pro Gly Ile His Gly Val Gly Glu Arg Tyr Ile Glu Arg Ala		
165	170	175
Gln Gln Val Leu Ala Ser Ala Leu Gly Ile Ala Gly Phe Gly Ala Glu		
180	185	190
Pro Trp Asp Gly His Thr Leu Ala Gln Ala Arg Arg Val Val Gln Arg		
195	200	205
Tyr Ala Gln Asp Pro Asn Ser Glu Tyr Arg Leu Lys Ser Glu Ala Glu		
210	215	220
Lys His Leu Thr Ser Ile Asn Glu Leu Arg Val Gln Ile Leu Leu Glu		
225	230	235
Gln Leu Pro Val Asp Ala Leu Arg Met Ala Thr Asp His Arg Leu Arg		
245	250	255
Phe Gly Ser Leu Asp Ser Ile His Val Ala Thr Val Ala Asp Val Leu		
260	265	270
Lys Thr His Thr Ser Ile Leu Thr Thr Val Gln Gly Ile Gly Ala Gln		
275	280	285
Thr Ala Gly Arg Met Lys Ala Ala Ala Glu Thr Leu Lys Gln Glu Ala		
290	295	300
Leu Arg Arg Gln Asn Thr Ser Ile Gly Asp Glu Pro Thr Gln Pro Ala		
305	310	315
Met Arg Leu Ile Asn Val Leu Ala Arg Phe Asp Gln Thr Glu Thr Ile		
325	330	335
Thr Pro Glu Glu Arg Ala Arg Arg Thr Arg Val Ile Asp Tyr Val Glu		
340	345	350



His Ile Pro Pro Ser Leu Asp Pro Tyr Ile Val Ile Asn Pro Ala Thr  
 355 360 365  
 Pro Glu Phe Asn Asn Phe Thr Asp Asp Leu Arg Trp Ile Asp Ala Asn  
 370 375 380  
 Pro Asn Leu Phe His Pro Gln Thr Ile Thr Thr Pro Pro Ala Asp Ile  
 385 390 395 400  
 Trp Asp Asp Tyr Ile Ser Arg Pro Ala His Tyr Gln Gly Leu Leu Ala  
 405 410 415  
 Thr Leu Leu Gly Arg Asp Ile Glu Gly Ala Asp Glu Leu Leu Asp Ala  
 420 425 430  
 Thr Thr Leu Gln Lys Ile Arg Asp Leu Thr Leu Asp Lys Thr His Leu  
 435 440 445  
 Thr Asp Leu His Leu Arg Gly Tyr Gln Ser Phe Gly Ala Arg Phe Ala  
 450 455 460  
 Ile Ile Gln Lys Lys Thr Leu Leu Gly Asp Asp Met Gly Leu Gly Lys  
 465 470 475 480  
 Thr Val Gln Ala Leu Ser Ala Ala Ala His Leu Ala Ala Thr Glu Lys  
 485 490 495  
 Asp Phe Arg Thr Leu Val Val Val Pro Ala Ser Val Ile Val Asn Trp  
 500 505 510  
 Thr Arg Glu Cys Lys Arg Phe Leu Asn Leu Pro Val Phe Ile Ala His  
 515 520 525  
 Gly Asp Asn Lys Gln Asp Ala Ile Asn Ala Trp Ser Asn Thr Asn Gly  
 530 535 540  
 Ile Ala Ile Cys Thr Tyr Asp Gly Val Arg Thr Met Asp Ile Pro Ala  
 545 550 555 560  
 Pro Gly Leu Val Ile Ala Asp Glu Ala His Leu Ile Lys Asn Pro Ser  
 565 570 575  
 Thr Lys Arg Thr Gln Ala Leu Arg Lys Leu Ile Asp Ala Ala Pro Tyr  
 580 585 590  
 Thr Leu Leu Met Thr Gly Thr Pro Leu Glu Asn Lys Val Glu Glu Phe  
 595 600 605  
 Val Asn Leu Val Arg Tyr Ile Gln Pro Glu Leu Ile Thr Arg Gly Met  
 610 615 620  
 Ser Lys Met Gln Ala Glu Asn Phe Arg Glu Arg Ile Ala Pro Ala Tyr  
 625 630 635 640  
 Leu Arg Arg Asn Gln Ala Asp Val Leu Asp Glu Leu Pro Glu Arg Thr  
 645 650 655  
 Asp Ser Ile Asp Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr  
 660 665 670

Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala  
 675 680 685  
 Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile  
 690 695 700  
 Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile  
 705 710 715 720  
 Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly  
 725 730 735  
 Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg  
 740 745 750  
 Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu  
 755 760 765  
 Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala  
 770 775 780  
 Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln  
 785 790 795 800  
 Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln  
 805 810 815  
 Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu  
 820 825 830  
 Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser  
 835 840 845  
 Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu  
 850 855 860  
 Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu  
 865 870 875 880  
 Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser  
 885 890

&lt;210&gt; 39

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(708)

&lt;223&gt; FRXA01797

&lt;400&gt; 39

ggg tct ata gcg tgg att gac ctc acc cca gaa gac cgc agc gcc tac 48  
 Gly Ser Ile Ala Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr  
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gac gac caa gtc cgc caa gcc agc tgg atg gcc atg cgc cgc tcc gcc 96  
 Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala  
 20 25 30

atg ctc tca cca aca cca cgc cta act tcc gca aaa atg caa cgc atc 144  
 Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile  
 35 40 45

cta gaa ctc ttc gaa gaa gca gaa gaa cac ggc cgc aaa gcc ctc atc 192  
 Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile  
 50 55 60

ttc acc tac ttc ctc gac gtc ctc gac gaa ctg gaa aag cat cta ggc 240  
 Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly  
 65 70 75 80

gag cgc gtc atc ggc cgc att tcc ggc gac gtg cca gcc acc aag cgc 288  
 Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg  
 85 90 95

caa ttg ctt gtc gac gcc ctg tcc cac tcc aaa ccc gga tcc gcc ctc 336  
 Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu  
 100 105 110

att gcc caa atc acc gcc ggg gga gta ggc cta aac atc caa tcc gcg 384  
 Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala  
 115 120 125

agc cta tgc att att tgt gaa cct caa gta aag cca acc atc gaa cag 432  
 Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln  
 130 135 140

cag gcc gtc gcc cga gtc cac cgc atg ggc caa acc gcc acc gtc caa 480  
 Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln  
 145 150 155 160

gtc cac cga ctc atc ggc gac gaa acc gca gac gaa cgc atg cta gaa 528  
 Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu  
 165 170 175

atc ctg gca ggc aaa act cac gtc ttc gac gtc tac gcc cgg cta tct 576  
 Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser  
 180 185 190

gaa acc gca gag att cca gat gct gtg gat atc act gaa tca cag ctg 624  
 Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu  
 195 200 205

gca gca cgg gtt att gat gag gag cgt gca cgg tta ggg ctt act gaa 672  
 Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu  
 210 215 220

tcc act ggc cct aaa gat gaa gaa acg gcc tta agc tagttgccta 718  
 Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser  
 225 230 235

aggccggaat taa 731

&lt;210&gt; 40

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 40

Gly Ser Ile Ala Trp Ile Asp Leu Thr Pro Glu Asp Arg Ser Ala Tyr  
 1 5 10 15

Asp Asp Gln Val Arg Gln Gly Ser Trp Met Gly Met Arg Arg Ser Ala  
 20 25 30

Met Leu Ser Pro Thr Pro Arg Leu Thr Ser Ala Lys Met Gln Arg Ile  
 35 40 45

Leu Glu Leu Phe Glu Glu Ala Glu Glu His Gly Arg Lys Ala Leu Ile  
 50 55 60

Phe Thr Tyr Phe Leu Asp Val Leu Asp Glu Leu Glu Lys His Leu Gly  
 65 70 75 80

Glu Arg Val Ile Gly Arg Ile Ser Gly Asp Val Pro Ala Thr Lys Arg  
 85 90 95

Gln Leu Leu Val Asp Ala Leu Ser His Ser Lys Pro Gly Ser Ala Leu  
 100 105 110

Ile Ala Gln Ile Thr Ala Gly Gly Val Gly Leu Asn Ile Gln Ser Ala  
 115 120 125

Ser Leu Cys Ile Ile Cys Glu Pro Gln Val Lys Pro Thr Ile Glu Gln  
 130 135 140

Gln Ala Val Ala Arg Val His Arg Met Gly Gln Thr Ala Thr Val Gln  
 145 150 155 160

Val His Arg Leu Ile Gly Asp Glu Thr Ala Asp Glu Arg Met Leu Glu  
 165 170 175

Ile Leu Ala Gly Lys Thr His Val Phe Asp Val Tyr Ala Arg Leu Ser  
 180 185 190

Glu Thr Ala Glu Ile Pro Asp Ala Val Asp Ile Thr Glu Ser Gln Leu  
 195 200 205

Ala Ala Arg Val Ile Asp Glu Glu Arg Ala Arg Leu Gly Leu Thr Glu  
 210 215 220

Ser Thr Gly Pro Lys Asp Glu Glu Thr Ala Leu Ser  
 225 230 235

&lt;210&gt; 41

&lt;211&gt; 1299

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1276)

&lt;223&gt; RXN01030

&lt;400&gt; 41

cctccccggc cacacgcccc agaggggttc tttttcatcc tttttaaaat atacttatat 60

gtattaatcc cctctttgtg cagcatagga gactactgct atg acc tca aca acc 115

	Met	Thr	Ser	Thr	Thr	
	1				5	
caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc						163
Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp Thr His Ser Glu Pro						
	10				20	
tgg gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt						211
Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro Phe Gln Lys Val Val						
	25			30	35	
cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg						259
Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly Ile Phe Leu Thr Met						
	40		45		50	
ggg ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag						307
Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala Leu Thr Tyr Ile Gln						
	55		60		65	
cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc						355
Pro Pro Gly His Ile Leu Val Val Ala Pro Leu Asn Ile Ser Arg Leu						
	70		75		80	85
acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc						403
Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile Pro Val Asn Ala Ile						
		90		95		100
tcg ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc						451
Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu Thr Arg Ala Lys Arg						
	105		110		115	
ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac						499
Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro Pro Thr Leu Tyr Tyr						
	120		125		130	
atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg						547
Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn Tyr Phe Gly Asp Arg						
	135		140		145	
tgg ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat						595
Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser Gln Thr Ile Ser Asp						
	150		155		160	165
ata tcc tcc aag cgc act aga gcg ctc ttt tct gtg cga ccc tat atc						643
Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser Val Arg Pro Tyr Ile						
	170		175		180	
ggc aga cta att ctg ctc acc gga acc ccc agc gcc aac aag ttc gac						691
Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser Ala Asn Lys Phe Asp						
	185		190		195	
tcc att tac gcc caa gtc gca gtg cta gat tat ggt gcc agc ctg ggt						739
Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr Gly Ala Ser Leu Gly						
	200		205		210	
gac aac atc gac gta ttc cga gcc aga tgg tgt gcg ccc gac att att						787
Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys Ala Pro Asp Ile Ile						
	215		220		225	
acc gat aaa caa gtg cgt cgc tgg aag ccg gct aac aag cag gct gaa						835
Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala Asn Lys Gln Ala Glu						

230 235 240 245

gca gag gtg tac cgc act att agc cac ctg gtc atg tct gcc gtc aac 883  
Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val Met Ser Ala Val Asn  
250 255 260

acg gat att aag ctg cca ccg ctg cat ttt gtt gat cac gag gta cac 931  
Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val Asp His Glu Val His  
265 270 275

atg agc gac gat gag cac cgc gac tac gag ctc ttc aaa aag gac gcg 979  
Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu Phe Lys Lys Asp Ala  
280 285 290

gtg ctt gct gca ttg ctc gat atg gct gaa gag aat gag ggt ggc gaa 1027  
Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu Asn Glu Gly Gly Glu  
295 300 305

ggc gct gat gac act gac gct gct gat tca gcg aca acg acc cca cct 1075  
Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala Thr Thr Thr Pro Pro  
310 315 320 325

gcg tca tca cag cca aca aac cct gcc atc ccc gct gga ctg ctt cag 1123  
Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro Ala Gly Leu Leu Gln  
330 335 340

gca ata caa caa acc cag gac acc aat ggt cgc gcc atc gcg cct gtg 1171  
Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg Ala Ile Ala Pro Val  
345 350 355

acc aca gct gaa ctt gat cat ttt gat gat ctg cca gta cag cgc caa 1219  
Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu Pro Val Gln Arg Gln  
360 365 370

gaa gat ctt ggc acc tta gtt gtt atc tct gct gtt cac gca agc gac 1267  
Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala Val His Ala Ser Asp  
375 380 385

tct gcg gca tgaaactgct gcaatcgca ggt 1299  
Ser Ala Ala  
390

&lt;210&gt; 42

&lt;211&gt; 392

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 42

Met Thr Ser Thr Thr Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp  
1 5 10 15

Thr His Ser Glu Pro Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro  
20 25 30

Phe Gln Lys Val Val Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly  
35 40 45

Ile Phe Leu Thr Met Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala  
50 55 60

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu  
 65 70 75 80  
 Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile  
 85 90 95  
 Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu  
 100 105 110  
 Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro  
 115 120 125  
 Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn  
 130 135 140  
 Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser  
 145 150 155 160  
 Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser  
 165 170 175  
 Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser  
 180 185 190  
 Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr  
 195 200 205  
 Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys  
 210 215 220  
 Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala  
 225 230 235 240  
 Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val  
 245 250 255  
 Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val  
 260 265 270  
 Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu  
 275 280 285  
 Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu  
 290 295 300  
 Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala  
 305 310 315 320  
 Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro  
 325 330 335  
 Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg  
 340 345 350  
 Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu  
 355 360 365  
 Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala  
 370 375 380  
 Val His Ala Ser Asp Ser Ala Ala

390

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<220>
<221> CDS
<222> (101)..(1276)
<223> FRXA01030
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<400> 43																	
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gtattaatcc cctctttgtg cagcatagga gactactgct atg acc tca aca acc																	115
Met Thr Ser Thr Thr																	
1 5																	
caa cct ggc aca aca cct gag ctc agc gca gac act cat tct gag ccc																	163
Gln	Pro	Gly	Thr	Thr	Pro	Glu	Leu	Ser	Ala	Asp	Thr	His	Ser	Glu	Pro		
10 15 20																	
tgg gat gtc gtc atc gaa aac acc ctt gaa cct ttt caa aaa gtc gtt																	211
Trp	Asp	Val	Val	Ile	Glu	Asn	Thr	Leu	Glu	Pro	Phe	Gln	Lys	Val	Val		
25 30 35																	
cgt caa ttt att att gac cgc ccc tat tcc ggc att ttc ctc acc atg																	259
Arg	Gln	Phe	Ile	Ile	Asp	Arg	Pro	Tyr	Ser	Gly	Ile	Phe	Leu	Thr	Met		
40 45 50																	
ggc ggc ggc aaa aca ctc act acc ctc tcc gca ttg acc tat atc cag																	307
Gly	Gly	Gly	Lys	Thr	Leu	Thr	Leu	Ser	Ala	Leu	Thr	Tyr	Ile	Gln			
55 60 65																	
cca cct gga cac att ctg gtt gtc gcg cct cta aat atc tct cga ctc																	355
Pro	Pro	Gly	His	Ile	Leu	Val	Val	Ala	Pro	Leu	Asn	Ile	Ser	Arg	Leu		
70 75 80 85																	
acc tgg ccc gaa gag gtt cgc aag tgg aat atc cct gtt aac gca atc																	403
Thr	Trp	Pro	Glu	Glu	Val	Arg	Lys	Trp	Asn	Ile	Pro	Val	Asn	Ala	Ile		
90 95 100																	
tcg ctg atc acc aat gag cgc ggc acc aaa ctc acc cgc gcc aaa cgc																	451
Ser	Leu	Ile	Thr	Asn	Glu	Arg	Gly	Thr	Lys	Leu	Thr	Arg	Ala	Lys	Arg		
105 110 115																	
ctc aaa ctc tat gag gaa aca gcg acc aca cca cca acg ctg tat tac																	499
Leu	Lys	Leu	Tyr	Glu	Glu	Thr	Ala	Thr	Thr	Pro	Pro	Thr	Leu	Tyr	Tyr		
120 125 130																	
atc acc att aat ctg ctc gaa gat att gtc aat tac ttt ggt gat agg																	547
Ile	Thr	Ile	Asn	Leu	Leu	Glu	Asp	Ile	Val	Asn	Tyr	Phe	Gly	Asp	Arg		
135 140 145																	
tgg ccg ttt tgg aca gtc att att gat gag tca cag aca atc tct gat																	595
Trp	Pro	Phe	Trp	Thr	Val	Ile	Ile	Asp	Glu	Ser	Gln	Thr	Ile	Ser	Asp		
150 155 160 165																	
ata tcc tcc aag cgc act aga gcg ctc ttt tct gtg cga ccc tat atc																	643



Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser Val Arg Pro Tyr Ile  
 170 175 180

ggc aga cta att ctg ctc acc gga acc ccc agc gcc aac aag ttc gac 691  
 Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser Ala Asn Lys Phe Asp  
 185 190 195

tcc att tac gcc caa gtc gca gtg cta gat tat ggt gcc agc ctg ggt 739  
 Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr Gly Ala Ser Leu Gly  
 200 205 210

gac aac atc gac gta ttc cga gcc aga tgg tgt gcg ccc gac att att 787  
 Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys Ala Pro Asp Ile Ile  
 215 220 225

acc gat aaa caa gtg cgt cgc tgg aag ccg gct aac aag cag gct gaa 835  
 Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala Asn Lys Gln Ala Glu  
 230 235 240 245

gca gag gtg tac cgc act att agc cac ctg gtc atg tct gcc gtc aac 883  
 Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val Met Ser Ala Val Asn  
 250 255 260

acg gat att aag ctg cca ccg ctg cat ttt gtt gat cac gag gta cac 931  
 Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val Asp His Glu Val His  
 265 270 275

atg agc gac gat gag cac cgc gac tac gag ctc ttc aaa aag gac gcg 979  
 Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu Phe Lys Lys Asp Ala  
 280 285 290

gtg ctt gct gca ttg ctc gat atg gct gaa gag aat gag ggt ggc gaa 1027  
 Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu Asn Glu Gly Gly Glu  
 295 300 305

ggc gct gat gac act gac gct gct gat tca gcg aca acg acc cca cct 1075  
 Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala Thr Thr Thr Pro Pro  
 310 315 320 325

gcg tca tca cag cca aca aac cct gcc atc ccc gct gga ctg ctt cag 1123  
 Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro Ala Gly Leu Leu Gln  
 330 335 340

gca ata caa caa acc cag gac acc aat ggt cgc gcc atc gcg cct gtg 1171  
 Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg Ala Ile Ala Pro Val  
 345 350 355

acc aca gct gaa ctt gat cat ttt gat gat ctg cca gta cag cgc caa 1219  
 Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu Pro Val Gln Arg Gln  
 360 365 370

gaa gat ctt ggc acc tta gtt gtt atc tct gct gtt cac gca agc gac 1267  
 Glu Asp Leu Gly Thr Leu Val Ile Ser Ala Val His Ala Ser Asp  
 375 380 385

tct gcg gca tgaaactgct gcaatacgca ggt 1299  
 Ser Ala Ala  
 390

&lt;210&gt; 44

&lt;211&gt; 392

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 44

Met Thr Ser Thr Thr Gln Pro Gly Thr Thr Pro Glu Leu Ser Ala Asp  
 1 5 10 15

Thr His Ser Glu Pro Trp Asp Val Val Ile Glu Asn Thr Leu Glu Pro  
 20 25 30

Phe Gln Lys Val Val Arg Gln Phe Ile Ile Asp Arg Pro Tyr Ser Gly  
 35 40 45

Ile Phe Leu Thr Met Gly Gly Gly Lys Thr Leu Thr Thr Leu Ser Ala  
 50 55 60

Leu Thr Tyr Ile Gln Pro Pro Gly His Ile Leu Val Val Ala Pro Leu  
 65 70 75 80

Asn Ile Ser Arg Leu Thr Trp Pro Glu Glu Val Arg Lys Trp Asn Ile  
 85 90 95

Pro Val Asn Ala Ile Ser Leu Ile Thr Asn Glu Arg Gly Thr Lys Leu  
 100 105 110

Thr Arg Ala Lys Arg Leu Lys Leu Tyr Glu Glu Thr Ala Thr Thr Pro  
 115 120 125

Pro Thr Leu Tyr Tyr Ile Thr Ile Asn Leu Leu Glu Asp Ile Val Asn  
 130 135 140

Tyr Phe Gly Asp Arg Trp Pro Phe Trp Thr Val Ile Ile Asp Glu Ser  
 145 150 155 160

Gln Thr Ile Ser Asp Ile Ser Ser Lys Arg Thr Arg Ala Leu Phe Ser  
 165 170 175

Val Arg Pro Tyr Ile Gly Arg Leu Ile Leu Leu Thr Gly Thr Pro Ser  
 180 185 190

Ala Asn Lys Phe Asp Ser Ile Tyr Ala Gln Val Ala Val Leu Asp Tyr  
 195 200 205

Gly Ala Ser Leu Gly Asp Asn Ile Asp Val Phe Arg Ala Arg Trp Cys  
 210 215 220

Ala Pro Asp Ile Ile Thr Asp Lys Gln Val Arg Arg Trp Lys Pro Ala  
 225 230 235 240

Asn Lys Gln Ala Glu Ala Glu Val Tyr Arg Thr Ile Ser His Leu Val  
 245 250 255

Met Ser Ala Val Asn Thr Asp Ile Lys Leu Pro Pro Leu His Phe Val  
 260 265 270

Asp His Glu Val His Met Ser Asp Asp Glu His Arg Asp Tyr Glu Leu  
 275 280 285

Phe Lys Lys Asp Ala Val Leu Ala Ala Leu Leu Asp Met Ala Glu Glu  
 290 295 300

Asn Glu Gly Gly Glu Gly Ala Asp Asp Thr Asp Ala Ala Asp Ser Ala  
305 310 315 320

Thr Thr Thr Pro Pro Ala Ser Ser Gln Pro Thr Asn Pro Ala Ile Pro  
325 330 335

Ala Gly Leu Leu Gln Ala Ile Gln Gln Thr Gln Asp Thr Asn Gly Arg  
340 345 350

Ala Ile Ala Pro Val Thr Thr Ala Glu Leu Asp His Phe Asp Asp Leu  
355 360 365

Pro Val Gln Arg Gln Glu Asp Leu Gly Thr Leu Val Val Ile Ser Ala  
370 375 380

Val His Ala Ser Asp Ser Ala Ala  
385 390

<210> 45

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(697)

<223> RXA01739

<400> 45

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cctgggcgcg agataaacia aactaaggga gctttttaca gtg atc aat ttg cag 115  
Val Ile Asn Leu Gln  
1 5

gac ctc gac gag gat caa cgc atc gct gct tct gcg cct cgc gga cca 163  
Asp Leu Asp Glu Asp Gln Arg Ile Ala Ala Ser Ala Pro Arg Gly Pro  
10 15 20

gtg tgc att ctc gcc gga gcc gcc acg ggt aaa act cga acg att act 211  
Val Cys Ile Leu Ala Gly Ala Gly Thr Gly Lys Thr Arg Thr Ile Thr  
25 30 35

tat cgc atc gcg cat ctg att gat cag ggt ttt gtg agc ccg aat cgt 259  
Tyr Arg Ile Ala His Leu Ile Asp Gln Gly Phe Val Ser Pro Asn Arg  
40 45 50

gtt ctt gct gtg acg ttt aca tcc cgc gcg gca ggg gag atg cgt cat 307  
Val Leu Ala Val Thr Phe Thr Ser Arg Ala Ala Gly Glu Met Arg His  
55 60 65

cgc ttg aat ctc atg ggg atc ggt gcc gtg cag gca agg aca ttc cac 355  
Arg Leu Asn Leu Met Gly Ile Gly Gly Val Gln Ala Arg Thr Phe His  
70 75 80 85

gca gca gcg agg aag cag ttg ttg tat ttc tgg cct cag gtg gcg ggt 403  
Ala Ala Ala Arg Lys Gln Leu Leu Tyr Phe Trp Pro Gln Val Ala Gly  
90 95 100

aat ctg ccg tgg cgc ctg ttg gat aat aag ttt caa ctt gtg ggt cgt 451  
 Asn Leu Pro Trp Arg Leu Leu Asp Asn Lys Phe Gln Leu Val Gly Arg  
 105 110 115  
 gcg gtt cgt ggt gcg cgg ttg gaa tcg cag act gaa aaa gtt cgc gat 499  
 Ala Val Arg Gly Ala Arg Leu Glu Ser Gln Thr Glu Lys Val Arg Asp  
 120 125 130  
 att ttg ggt gaa att gag tgg gcg aag gcg tcg ttg att aca cct gag 547  
 Ile Leu Gly Glu Ile Glu Trp Ala Lys Ala Ser Leu Ile Thr Pro Glu  
 135 140 145  
 cag tat ccg gat cgt ttg ggt acg agg acc cct ccg gcg ccc gcg gag 595  
 Gln Tyr Pro Asp Arg Leu Gly Thr Arg Thr Pro Pro Ala Pro Ala Glu  
 150 155 160 165  
 aaa atc gct gag gtg tat cag cga tac gaa aac atg aag gca acc cct 643  
 Lys Ile Ala Glu Val Tyr Gln Arg Tyr Glu Asn Met Lys Ala Thr Pro  
 170 175 180  
 gag ggg atg ttg ctt gat ttc gac gat ctg ttg ctt cac acc gcc ggg 691  
 Glu Gly Met Leu Leu Asp Phe Asp Asp Leu Leu Leu His Thr Ala Gly  
 185 190 195  
 gcg ttg tagaattccc cggcgggtggc gga 720  
 Ala Leu

<210> 46  
 <211> 199  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 46  
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 20 25 30  
 Thr Arg Thr Ile Thr Tyr Arg Ile Ala His Leu Ile Asp Gln Gly Phe  
 35 40 45  
 Val Ser Pro Asn Arg Val Leu Ala Val Thr Phe Thr Ser Arg Ala Ala  
 50 55 60  
 Gly Glu Met Arg His Arg Leu Asn Leu Met Gly Ile Gly Gly Val Gln  
 65 70 75 80  
 Ala Arg Thr Phe His Ala Ala Ala Arg Lys Gln Leu Leu Tyr Phe Trp  
 85 90 95  
 Pro Gln Val Ala Gly Asn Leu Pro Trp Arg Leu Leu Asp Asn Lys Phe  
 100 105 110  
 Gln Leu Val Gly Arg Ala Val Arg Gly Ala Arg Leu Glu Ser Gln Thr  
 115 120 125  
 Glu Lys Val Arg Asp Ile Leu Gly Glu Ile Glu Trp Ala Lys Ala Ser  
 130 135 140

Leu Ile Thr Pro Glu Gln Tyr Pro Asp Arg Leu Gly Thr Arg Thr Pro  
 145 150 155 160

Pro Ala Pro Ala Glu Lys Ile Ala Glu Val Tyr Gln Arg Tyr Glu Asn  
 165 170 175

Met Lys Ala Thr Pro Glu Gly Met Leu Leu Asp Phe Asp Asp Leu Leu  
 180 185 190

Leu His Thr Ala Gly Ala Leu  
 195

<210> 47  
 <211> 1992  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1969)  
 <223> RXA02359

<400> 47  
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 Val Glu Leu Pro Ser  
 1 5

cct ggt gag gcg ctc gca cat gca ggg cac acc cca gaa gtc ctg gaa 163  
 Pro Gly Glu Ala Leu Ala His Ala Gly His Thr Pro Glu Val Leu Glu  
 10 15 20

gcc gag ctc ggc att gac ccg gct gcc acc cgt att gtg ttg gaa ctt 211  
 Ala Glu Leu Gly Ile Asp Pro Ala Ala Thr Arg Ile Val Leu Glu Leu  
 25 30 35

gcc tca gag gat gac atc gca gca gcg ctt cct agc agc ccg acg tgg 259  
 Ala Ser Glu Asp Asp Ile Ala Ala Leu Pro Ser Ser Pro Thr Trp  
 40 45 50

gaa aaa gac gca ctt atc ggc ctt gtc gcc ggt ttg agc att gaa gat 307  
 Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly Leu Ser Ile Glu Asp  
 55 60 65

atc cgc gaa tcg ctc gct atc ccc gca cct tcc aca gag ccg gat acc 355  
 Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser Thr Glu Pro Asp Thr  
 70 75 80 85

cgc agc gaa gat acc agg ctc att gct ggg ctt aaa acc cca gca gcg 403  
 Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu Lys Thr Pro Ala Ala  
 90 95 100

caa atg gac ttt gcc tat ttg gat acc cca aat agc aat gac ctg cgc 451  
 Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn Ser Asn Asp Leu Arg  
 105 110 115

cgc gtt att gaa act gaa ggt ttt gat agc tgg cgc gtg tat atc gac 499  
 Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp Arg Val Tyr Ile Asp

120	125	130	
ccc agc cag cgc tcc tta gtc acc cgc aac ttc agc gga tgc ggt cgc			547
Pro Ser Gln Arg Ser Leu Val Thr Arg Asn Phe Ser Gly Ser Gly Arg			
135	140	145	
gtt ttt ggt gga gct ggc acc ggc aaa acc gtg gtg gta gtc cac cgt			595
Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val Val Val Val His Arg			
150	155	160	165
gcc aac cgc ctg gtc act tct gat gga cac ctt gag acc gac gat aag			643
Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu Glu Thr Asp Asp Lys			
	170	175	180
acg cct cga gtc ctg ctc acc acc tat acc cgc ggt ttg gcc gat gcg			691
Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg Gly Leu Ala Asp Ala			
	185	190	195
ttg aaa tcc tcc atg aac gcg ctt aat ccc act ttc ccc gag gca gaa			739
Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr Phe Pro Glu Ala Glu			
	200	205	210
aaa ccc ggt agt cct ggc ttg tgg atc agc gga att gat gcc ttg gca			787
Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly Ile Asp Ala Leu Ala			
	215	220	225
aat aag gtg gtt gcg cta gca aac acc gcc gaa cgt gag gca gca acc			835
Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu Arg Glu Ala Ala Thr			
230	235	240	245
act gct atc ttg ggg cgt gca gcc ggc aga atc acc cca ttc atc gcg			883
Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile Thr Pro Phe Ile Gly			
	250	255	260
aac ggc gaa caa gaa ttt tgg atc gac gcg atc att tcc gca gat ccc			931
Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile Ile Ser Ala Asp Pro			
	265	270	275
ggc gat cta tca gaa gaa atc agc aat act gaa ttc ctc gcc caa gag			979
Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu Phe Leu Ala Gln Glu			
	280	285	290
ttt gaa acc gta atc cta gcc cgc gga atc acc caa gaa aag gac tat			1027
Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr Gln Glu Lys Asp Tyr			
	295	300	305
ctg cgt gca cct cgt ccc ggc cgt ggt acc cca cta aac cgc gta caa			1075
Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro Leu Asn Arg Val Gln			
310	315	320	325
cgc aaa aaa gtg tgg gcg att att cag caa ttc atg act tcc tgt gcg			1123
Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe Met Thr Ser Cys Ala			
	330	335	340
cgc gaa gga aag atg tcc tgg cca gcg ctt tcc tcc atc gcc gca aac			1171
Arg Glu Gly Lys Met Ser Trp Pro Ala Leu Ser Ser Ile Ala Ala Asn			
	345	350	355
atc ctg gag cag cgc gcc gcc gcc ggc cag ggc cgg cta ttt gac cat			1219
Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly Arg Leu Phe Asp His			
	360	365	370

gtg ctt atc gac gag gcc cag gac ttc cac gcc gga cat tgg ctc tta	1267
Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala Gly His Trp Leu Leu	
375 380 385	
ctc agg gct gcg gta gcc gaa ggt ccc aat gac atc ttc ttg gct gag	1315
Leu Arg Ala Ala Val Glu Gly Pro Asn Asp Ile Phe Leu Ala Glu	
390 395 400 405	
gat tca cac cag cgc atc tac ggc caa cat cat gtg cta agc cgt ttt	1363
Asp Ser His Gln Arg Ile Tyr Gly Gln His His Val Leu Ser Arg Phe	
410 415 420	
ggg att tcc acc cgc ggt cgg gcg tct aag cga ctc acc ctt aac tac	1411
Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg Leu Thr Leu Asn Tyr	
425 430 435	
cgc acc acc gcc gaa aac ctc agt tac gca ctt ggc atg ctc acc ggt	1459
Arg Thr Thr Ala Glu Asn Leu Ser Tyr Ala Leu Gly Met Leu Thr Gly	
440 445 450	
gaa tgg acc gac gcc gaa ggc gaa acg gac aca att gag cac tat cgc	1507
Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr Ile Glu His Tyr Arg	
455 460 465	
tca gcg cgt aag ggc ccc aag cca cac ctc tac caa ttt gaa tct gag	1555
Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr Gln Phe Glu Ser Glu	
470 475 480 485	
acc gac gag ttc gaa gca atc gct gag ctc atc aag gtg tgg cag gac	1603
Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile Lys Val Trp Gln Asp	
490 495 500	
agg acc acc gat gta cgc atc ggc att ttg gca cgc acc cgt cct ttg	1651
Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala Arg Thr Arg Pro Leu	
505 510 515	
atc aac cgc gtg gtt aat gcg ctc tct gag cag ggc atc gat gcc gtc	1699
Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln Gly Ile Asp Ala Val	
520 525 530	
aag acg caa aat gcc gaa ctt gca gcc cac gaa act gtc agt gta atg	1747
Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu Thr Val Ser Val Met	
535 540 545	
aca atg cac gga gct aaa ggc atg gag ttt acc cat gtc atc ttg atc	1795
Thr Met His Gly Ala Lys Gly Met Glu Phe Thr His Val Ile Leu Ile	
550 555 560 565	
gga atg ggc cgt gac ctc att cct ttg caa tac acc atg caa ggt tta	1843
Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr Thr Met Gln Gly Leu	
570 575 580	
ggc gag gcc gag cgt aac gac gcc caa cag cgc gaa cgc tcc ttg ctc	1891
Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg Glu Arg Ser Leu Leu	
585 590 595	
tac gtt gca gct tct cgt gca cgt gat gcc ctt gtt ctc acc acg cat	1939
Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu Val Leu Thr Thr His	
600 605 610	

act gag cct tgc gag ttg ctg ccg cgg gtt tagagcacca agtaactaaa 1989  
 Thr Glu Pro Ser Glu Leu Leu Pro Arg Val  
 615 620

ggt

1992

&lt;210&gt; 48

&lt;211&gt; 623

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 48

Val Glu Leu Pro Ser Pro Gly Glu Ala Leu Ala His Ala Gly His Thr  
 1 5 10 15

Pro Glu Val Leu Glu Ala Glu Leu Gly Ile Asp Pro Ala Ala Thr Arg  
 20 25 30

Ile Val Leu Glu Leu Ala Ser Glu Asp Asp Ile Ala Ala Ala Leu Pro  
 35 40 45

Ser Ser Pro Thr Trp Glu Lys Asp Ala Leu Ile Gly Leu Val Ala Gly  
 50 55 60

Leu Ser Ile Glu Asp Ile Arg Glu Ser Leu Ala Ile Pro Ala Pro Ser  
 65 70 75 80

Thr Glu Pro Asp Thr Arg Ser Glu Asp Thr Arg Leu Ile Ala Gly Leu  
 85 90 95

Lys Thr Pro Ala Ala Gln Met Asp Phe Ala Tyr Leu Asp Thr Pro Asn  
 100 105 110

Ser Asn Asp Leu Arg Arg Val Ile Glu Thr Glu Gly Phe Asp Ser Trp  
 115 120 125

Arg Val Tyr Ile Asp Pro Ser Gln Arg Ser Leu Val Thr Arg Asn Phe  
 130 135 140

Ser Gly Ser Gly Arg Val Phe Gly Gly Ala Gly Thr Gly Lys Thr Val  
 145 150 155 160

Val Val Val His Arg Ala Asn Arg Leu Val Thr Ser Asp Gly His Leu  
 165 170 175

Glu Thr Asp Asp Lys Thr Pro Arg Val Leu Leu Thr Thr Tyr Thr Arg  
 180 185 190

Gly Leu Ala Asp Ala Leu Lys Ser Ser Met Asn Ala Leu Asn Pro Thr  
 195 200 205

Phe Pro Glu Ala Glu Lys Pro Gly Ser Pro Gly Leu Trp Ile Ser Gly  
 210 215 220

Ile Asp Ala Leu Ala Asn Lys Val Val Ala Leu Ala Asn Thr Ala Glu  
 225 230 235 240

Arg Glu Ala Ala Thr Thr Ala Ile Leu Gly Arg Ala Ala Gly Arg Ile  
 245 250 255



Thr Pro Phe Ile Gly Asn Gly Glu Gln Glu Phe Trp Ile Asp Ala Ile  
 260 265 270  
 Ile Ser Ala Asp Pro Gly Asp Leu Ser Glu Glu Ile Ser Asn Thr Glu  
 275 280 285  
 Phe Leu Ala Gln Glu Phe Glu Thr Val Ile Leu Ala Arg Gly Ile Thr  
 290 295 300  
 Gln Glu Lys Asp Tyr Leu Arg Ala Pro Arg Pro Gly Arg Gly Thr Pro  
 305 310 315 320  
 Leu Asn Arg Val Gln Arg Lys Lys Val Trp Ala Ile Ile Gln Gln Phe  
 325 330 335  
 Met Thr Ser Cys Ala Arg Glu Gly Lys Met Ser Trp Pro Ala Leu Ser  
 340 345 350  
 Ser Ile Ala Ala Asn Ile Leu Glu Gln Arg Ala Ala Ala Gly Gln Gly  
 355 360 365  
 Arg Leu Phe Asp His Val Leu Ile Asp Glu Ala Gln Asp Phe His Ala  
 370 375 380  
 Gly His Trp Leu Leu Leu Arg Ala Ala Val Ala Glu Gly Pro Asn Asp  
 385 390 395 400  
 Ile Phe Leu Ala Glu Asp Ser His Gln Arg Ile Tyr Gly Gln His His  
 405 410 415  
 Val Leu Ser Arg Phe Gly Ile Ser Thr Arg Gly Arg Ala Ser Lys Arg  
 420 425 430  
 Leu Thr Leu Asn Tyr Arg Thr Thr Ala Glu Asn Leu Ser Tyr Ala Leu  
 435 440 445  
 Gly Met Leu Thr Gly Glu Trp Thr Asp Ala Glu Gly Glu Thr Asp Thr  
 450 455 460  
 Ile Glu His Tyr Arg Ser Ala Arg Lys Gly Pro Lys Pro His Leu Tyr  
 465 470 475 480  
 Gln Phe Glu Ser Glu Thr Asp Glu Phe Glu Ala Ile Ala Glu Leu Ile  
 485 490 495  
 Lys Val Trp Gln Asp Arg Thr Thr Asp Val Arg Ile Gly Ile Leu Ala  
 500 505 510  
 Arg Thr Arg Pro Leu Ile Asn Arg Val Val Asn Ala Leu Ser Glu Gln  
 515 520 525  
 Gly Ile Asp Ala Val Lys Thr Gln Asn Ala Glu Leu Ala Ala His Glu  
 530 535 540  
 Thr Val Ser Val Met Thr Met His Gly Ala Lys Gly Met Glu Phe Thr  
 545 550 555 560  
 His Val Ile Leu Ile Gly Met Gly Arg Asp Leu Ile Pro Leu Gln Tyr  
 565 570 575  
 Thr Met Gln Gly Leu Gly Glu Ala Glu Arg Asn Asp Ala Gln Gln Arg

580

585

590

Glu Arg Ser Leu Leu Tyr Val Ala Ala Ser Arg Ala Arg Asp Ala Leu  
 595 600 605

Val Leu Thr Thr His Thr Glu Pro Ser Glu Leu Leu Pro Arg Val  
 610 615 620

&lt;210&gt; 49

&lt;211&gt; 2884

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2884)

&lt;223&gt; RXN02764

&lt;400&gt; 49

cttgcaggag ttctctgaga acaacgatcc gaatgttatt tcgaacctaa acaggggtgga 60

atcgacactc gtgtcgtatg ttctctgacaa gatttgaggt atg tcg gaa tac aaa 115  
 Met Ser Glu Tyr Lys  
 1 5

cca ccc att cca tcg gat cca caa gtt cgg ctg att aag cca aca tcc 163  
 Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu Ile Lys Pro Thr Ser  
 10 15 20

aag ctt cgt cct cgt tcg tgg gag ggc gaa gtt tcg cat tta gtt aaa 211  
 Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val Ser His Leu Val Lys  
 25 30 35

caa ggc acc ggt ttg tgg cgg gtg act ggt gag gcg ggc tcg ggg gtg 259  
 Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu Ala Gly Ser Gly Val  
 40 45 50

agc tcc gct gtt gtc gat act gtc ctt gaa cgc att cgc caa ggg tgg 307  
 Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg Ile Arg Gln Gly Trp  
 55 60 65

gag ccg tca tcg atg ttg gtt gtc gcc acg tcg aaa gag gcg gcg agt 355  
 Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser Lys Glu Ala Ala Ser  
 70 75 80 85

cgc ttg agg caa gag atc tcg gaa tcc gta gcc cag atg gat tat gtg 403  
 Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala Gln Met Asp Tyr Val  
 90 95 100

tcg gag ggg ccg ttg gtg cga tcg gtg cac tcg gtg gct ttc gcg ctg 451  
 Ser Glu Gly Pro Leu Val Arg Ser Val His Ser Val Ala Phe Ala Leu  
 105 110 115

att cgt gat gcg tcg gat gat gat gtg cgg ttg att acg ggc gct gag 499  
 Ile Arg Asp Ala Ser Asp Asp Asp Val Arg Leu Ile Thr Gly Ala Glu  
 120 125 130

caa gat gcg gtg att cgg gag ttg ctg cgt ggt cat gct gat gat ggt 547  
 Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly His Ala Asp Asp Gly  
 135 140 145

cgt ggg ggg tgg ccg cag gag cag cgt gag ggt ttg cgg atg gtg ggg 595  
 Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly Leu Arg Met Val Gly  
 150 155 160 165

ttc gct agg cag ttg cgt gac ttt ttg ctt cgt gcg gtg gag cgt ggt 643  
 Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg Ala Val Glu Arg Gly  
 170 175 180

gtg ggc cct gat gag ttg gtg gaa ttg ggg gag cga ttt gag cgc gcc 691  
 Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu Arg Phe Glu Arg Ala  
 185 190 195

aat tgg gtt gct gcg ggt gag ttc ctt cgt gag tac aag cag gtg atg 739  
 Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu Tyr Lys Gln Val Met  
 200 205 210

aag ctg tcg ggg gcg cat agt ttt tct gcg tct gag ttg gtg act gaa 787  
 Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser Glu Leu Val Thr Glu  
 215 220 225

gcg ctg cgt ggt cct gag ccg tcg gtg aag tat cgc ggt gtg ttt att 835  
 Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr Arg Gly Val Phe Ile  
 230 235 240 245

gat gat gcg cag cat ttg gat ccg aag tcg gcg gaa ctt gtg tcg cgg 883  
 Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala Glu Leu Val Ser Arg  
 250 255 260

ttt ttc cct gag gcg gag ttg gct gtg gtg gcg ggt gat ccg cag cag 931  
 Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala Gly Asp Pro Gln Gln  
 265 270 275

tcg gtg ttt agg ttc cgt ggt gcg aat ccg gat ttt ctc acc aag ttg 979  
 Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp Phe Leu Thr Lys Leu  
 280 285 290

agt gtg gat cac gag gtg gtg ttg aag ggg agg agg aaa gcg tcg aca 1027  
 Ser Val Asp His Glu Val Val Leu Lys Gly Arg Arg Lys Ala Ser Thr  
 295 300 305

agc att gtc gtg gca gag acc gag tcg gcg cat gcg gac ctg ctt gct 1075  
 Ser Ile Val Val Ala Glu Thr Glu Ser Ala His Ala Asp Leu Leu Ala  
 310 315 320 325

gac acg gtg cgg cgc gcg cat ctc att gat ggg cgc agc tgg tcg gag 1123  
 Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly Arg Ser Trp Ser Glu  
 330 335 340

atc gct gtt atc gtg cgc tcg gcc ggc atg att gcg ccg att tgg cgc 1171  
 Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile Ala Pro Ile Trp Arg  
 345 350 355

acc ctg ctg gcc gcc gcc gtg ccc gtg cac atc agc ccg act gat gtg 1219  
 Thr Leu Leu Ala Ala Gly Val Pro Val His Ile Ser Pro Thr Asp Val  
 360 365 370

gtg ctc gcc gaa caa cgt atc gtt gcc gca atg att ctc ggg ctg cgc 1267  
 Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met Ile Leu Gly Leu Arg  
 375 380 385

gcg ctg acg gaa tcg ctc aac gcc atc gag ttg gag gat ctt ctc cta 1315  
 Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu Glu Asp Leu Leu Leu  
 390 395 400 405

gga ccg atc ggt ggc gcc gat ccg gtg act ctg cgt cgt ttg ctg cgc 1363  
 Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu Arg Arg Leu Leu Arg  
 410 415 420

ggg ttg cgg cag gcg gag atg aag atg ggt ggg cag agg cga gcg atc 1411  
 Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly Gln Arg Arg Ala Ile  
 425 430 435

gag gtg ctc aga agc ctg ctc gca gag tcg gat gcg gag atg ttg ggc 1459  
 Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp Ala Glu Met Leu Gly  
 440 445 450

ttt ttg acc gat cgt gag ctg aat ttg ctc gag cgg gtg cga tct gtg 1507  
 Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu Arg Val Arg Ser Val  
 455 460 465

ttg gaa gcg ggt cgt gaa gcg ctc gcg gaa cac ggc agt atc gaa gag 1555  
 Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His Gly Ser Ile Glu Glu  
 470 475 480 485

gtg ttg tgg gcg ctg tgg tcg gcg acc gat ctg tcg aac tcg ttg tcc 1603  
 Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu Ser Asn Ser Leu Ser  
 490 495 500

gcg atc agc ctt cga ggc ggc gca tcg ggg tcc cag gcc gat cgc gat 1651  
 Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser Gln Ala Asp Arg Asp  
 505 510 515

ttg gat gcg atg atg gcg ctt ttc gac gcc gcc ggc gac tac gtg gag 1699  
 Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala Gly Asp Tyr Val Glu  
 520 525 530

cgc tac ccg tca gcg ggc gtg cgg agt ttc att ctg cat att tct gag 1747  
 Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile Leu His Ile Ser Glu  
 535 540 545

cag gaa ctt ccg acc ggc atg cgt gag cga cgc ggc gcg atc ccg gag 1795  
 Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg Gly Ala Ile Pro Glu  
 550 555 560 565

gcc gtc gag gtg ctg acg gcg cac gcg acg acg ggt cgt gag tgg aag 1843  
 Ala Val Glu Val Leu Thr Ala His Ala Thr Thr Gly Arg Glu Trp Lys  
 570 575 580

cgc gtg atc gtt gct gag gtg cag gag ggc agt tgg ccg tcg ctc ggt 1891  
 Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser Trp Pro Ser Leu Gly  
 585 590 595

gaa act ggc acg ctg ctt ggt cag gaa gag ttc gtc gat ttg gtg gat 1939  
 Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe Val Asp Leu Val Asp  
 600 605 610

gag ggt att gat ccc gat atc atc att tcc cga tcc gcc gaa cga ctg 1987  
 Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg Ser Ala Glu Arg Leu  
 615 620 625

gcg gag gaa cgc cga ctg ttc tac ctc gcc acc acc aga tcc acc gaa 2035

Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr Thr Arg Ser Thr Glu	630	635	640	645	
tcg ctc ctg gtt acc gct gtg aat tcc ccc gac tcc gac gaa gtc cgc					2083
Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp Ser Asp Glu Val Arg	650		655	660	
gaa ccc tcc cgg ttt ttg gaa ttg ctg agt caa ccg atc gtt gtt ctc					2131
Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln Pro Ile Val Val Leu	665		670	675	
gag ggg gag gaa gct tcg gcg atc gcg gaa ccg gag gag att ggg cat					2179
Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro Glu Glu Ile Gly His	680		685	690	
cgg ttg ttg tcg att cct gcg atg gtt gct gag ttg cgt cgt gtg gtg					2227
Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu Leu Arg Arg Val Val	695		700	705	
aat gat ccg cgg gat ccg cgt cgg aag cag gct gcg agg cag ttg tcg					2275
Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala Ala Arg Gln Leu Ser	710		715	720	725
agg ctt gcg gag gcg ggg att ccg ggt gcg aat cct gcc gag tgg acg					2323
Arg Leu Ala Glu Ala Gly Ile Pro Gly Ala Asn Pro Ala Glu Trp Thr	730		735	740	
aat ctg cgc act ccg tcg act gat gag gag ttg atc aag ggg gcg gtg					2371
Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu Ile Lys Gly Ala Val	745		750	755	
tcg ttg tcg ccg tcg cgg att gag cag ttg ttg aat tgt ccg ctg cgc					2419
Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu Asn Cys Pro Leu Arg	760		765	770	
gct gtg ttg gat cgt ttg gac agt gag gag gaa acg ccg atc gcg atg					2467
Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu Thr Pro Ile Ala Met	775		780	785	
ctc aag ggc acc ttg gtg cac gcg ttt gcg gag gcg gtc gcc ggt ggc					2515
Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu Ala Val Ala Gly Gly	790		795	800	805
gtc gat gcg gcg ctc gcc gaa gag aag gtg acc agc gcc tac atg cag					2563
Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr Ser Ala Tyr Met Gln	810		815	820	
ctg gcg aac gtg ccg agc tgg tcg cgc gaa agc acc gaa att gct ttt					2611
Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser Thr Glu Ile Ala Phe	825		830	835	
cga cgc atc ctc tca cgt acc gat acc tgg ctg aag act tct cgc gcc					2659
Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu Lys Thr Ser Arg Ala	840		845	850	
gat ttt acg gaa gtg gga acg gag atg gac gta tcg gtg acc atc gat					2707
Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val Ser Val Thr Ile Asp	855		860	865	
gac tcc gta tcg atc cgt ggt cgc atg gac cgt ttg gag cga aac aaa					2755
Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg Leu Glu Arg Asn Lys					

870	875	880	885	
tcc ggc gag ttg gtg gtt gtt gat ttc aaa acg ggc aaa act caa atc				2803
Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr Gly Lys Thr Gln Ile				
890	895	900		
gct gca aaa gac atg ggc gat cac cca cag ttg ttt gcg tat caa ttg				2851
Ala Ala Lys Asp Met Gly Asp His Pro Gln Leu Phe Ala Tyr Gln Leu				
905	910	915		
gcg ttg tcg aaa ggc gtg ctg cat ggt gac aaa				2884
Ala Leu Ser Lys Gly Val Leu His Gly Asp Lys				
920	925			

<210> 50  
 <211> 928  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 50  
 Met Ser Glu Tyr Lys Pro Pro Ile Pro Ser Asp Pro Gln Val Arg Leu  
 1 5 10 15  
 Ile Lys Pro Thr Ser Lys Leu Arg Pro Arg Ser Trp Glu Gly Glu Val  
 20 25 30  
 Ser His Leu Val Lys Gln Gly Thr Gly Leu Trp Arg Val Thr Gly Glu  
 35 40 45  
 Ala Gly Ser Gly Val Ser Ser Ala Val Val Asp Thr Val Leu Glu Arg  
 50 55 60  
 Ile Arg Gln Gly Trp Glu Pro Ser Ser Met Leu Val Val Ala Thr Ser  
 65 70 75 80  
 Lys Glu Ala Ala Ser Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala  
 85 90 95  
 Gln Met Asp Tyr Val Ser Glu Gly Pro Leu Val Arg Ser Val His Ser  
 100 105 110  
 Val Ala Phe Ala Leu Ile Arg Asp Ala Ser Asp Asp Val Arg Leu  
 115 120 125  
 Ile Thr Gly Ala Glu Gln Asp Ala Val Ile Arg Glu Leu Leu Arg Gly  
 130 135 140  
 His Ala Asp Asp Gly Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly  
 145 150 155 160  
 Leu Arg Met Val Gly Phe Ala Arg Gln Leu Arg Asp Phe Leu Leu Arg  
 165 170 175  
 Ala Val Glu Arg Gly Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu  
 180 185 190  
 Arg Phe Glu Arg Ala Asn Trp Val Ala Ala Gly Glu Phe Leu Arg Glu  
 195 200 205  
 Tyr Lys Gln Val Met Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser

210	215	220
Glu Leu Val Thr Glu Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr		
225	230	235 240
Arg Gly Val Phe Ile Asp Asp Ala Gln His Leu Asp Pro Lys Ser Ala		
	245	250 255
Glu Leu Val Ser Arg Phe Phe Pro Glu Ala Glu Leu Ala Val Val Ala		
	260	265 270
Gly Asp Pro Gln Gln Ser Val Phe Arg Phe Arg Gly Ala Asn Pro Asp		
	275	280 285
Phe Leu Thr Lys Leu Ser Val Asp His Glu Val Val Leu Lys Gly Arg		
	290	295 300
Arg Lys Ala Ser Thr Ser Ile Val Val Ala Glu Thr Glu Ser Ala His		
305	310	315 320
Ala Asp Leu Leu Ala Asp Thr Val Arg Arg Ala His Leu Ile Asp Gly		
	325	330 335
Arg Ser Trp Ser Glu Ile Ala Val Ile Val Arg Ser Ala Gly Met Ile		
	340	345 350
Ala Pro Ile Trp Arg Thr Leu Leu Ala Ala Gly Val Pro Val His Ile		
	355	360 365
Ser Pro Thr Asp Val Val Leu Ala Glu Gln Arg Ile Val Ala Ala Met		
	370	375 380
Ile Leu Gly Leu Arg Ala Leu Thr Glu Ser Leu Asn Ala Ile Glu Leu		
385	390	395 400
Glu Asp Leu Leu Leu Gly Pro Ile Gly Gly Ala Asp Pro Val Thr Leu		
	405	410 415
Arg Arg Leu Leu Arg Gly Leu Arg Gln Ala Glu Met Lys Met Gly Gly		
	420	425 430
Gln Arg Arg Ala Ile Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp		
	435	440 445
Ala Glu Met Leu Gly Phe Leu Thr Asp Arg Glu Leu Asn Leu Leu Glu		
	450	455 460
Arg Val Arg Ser Val Leu Glu Ala Gly Arg Glu Ala Leu Ala Glu His		
465	470	475 480
Gly Ser Ile Glu Glu Val Leu Trp Ala Leu Trp Ser Ala Thr Asp Leu		
	485	490 495
Ser Asn Ser Leu Ser Ala Ile Ser Leu Arg Gly Gly Ala Ser Gly Ser		
	500	505 510
Gln Ala Asp Arg Asp Leu Asp Ala Met Met Ala Leu Phe Asp Ala Ala		
	515	520 525
Gly Asp Tyr Val Glu Arg Tyr Pro Ser Ala Gly Val Arg Ser Phe Ile		
	530	535 540

Leu His Ile Ser Glu Gln Glu Leu Pro Thr Gly Met Arg Glu Arg Arg  
 545 550 555 560  
 Gly Ala Ile Pro Glu Ala Val Glu Val Leu Thr Ala His Ala Thr Thr  
 565 570 575  
 Gly Arg Glu Trp Lys Arg Val Ile Val Ala Glu Val Gln Glu Gly Ser  
 580 585 590  
 Trp Pro Ser Leu Gly Glu Thr Gly Thr Leu Leu Gly Gln Glu Glu Phe  
 595 600 605  
 Val Asp Leu Val Asp Glu Gly Ile Asp Pro Asp Ile Ile Ile Ser Arg  
 610 615 620  
 Ser Ala Glu Arg Leu Ala Glu Glu Arg Arg Leu Phe Tyr Leu Ala Thr  
 625 630 635 640  
 Thr Arg Ser Thr Glu Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp  
 645 650 655  
 Ser Asp Glu Val Arg Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln  
 660 665 670  
 Pro Ile Val Val Leu Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro  
 675 680 685  
 Glu Glu Ile Gly His Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu  
 690 695 700  
 Leu Arg Arg Val Val Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala  
 705 710 715 720  
 Ala Arg Gln Leu Ser Arg Leu Ala Glu Ala Gly Ile Pro Gly Ala Asn  
 725 730 735  
 Pro Ala Glu Trp Thr Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu  
 740 745 750  
 Ile Lys Gly Ala Val Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu  
 755 760 765  
 Asn Cys Pro Leu Arg Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu  
 770 775 780  
 Thr Pro Ile Ala Met Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu  
 785 790 795 800  
 Ala Val Ala Gly Gly Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr  
 805 810 815  
 Ser Ala Tyr Met Gln Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser  
 820 825 830  
 Thr Glu Ile Ala Phe Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu  
 835 840 845  
 Lys Thr Ser Arg Ala Asp Phe Thr Glu Val Gly Thr Glu Met Asp Val  
 850 855 860



Ser Val Thr Ile Asp Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg  
 865 870 875 880

Leu Glu Arg Asn Lys Ser Gly Glu Leu Val Val Val Asp Phe Lys Thr  
 885 890 895

Gly Lys Thr Gln Ile Ala Ala Lys Asp Met Gly Asp His Pro Gln Leu  
 900 905 910

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 Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu Arg Phe Glu Arg Ala  
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 Lys Leu Ser Gly Ala His Ser Phe Ser Ala Ser Glu Leu Val Thr Glu  
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 Ala Leu Arg Gly Pro Glu Pro Ser Val Lys Tyr Arg Gly Val Phe Ile  
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gat gat gcg cag cat ttg gat ccg aag tcg gcg gaa ctt gtg tcg cgg 883  
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atc gct gtt atc gtg cgc tcg gcc ggc atg att gcg ccg att tgg cgc 1171  
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Val	Leu	Ala	Glu	Gln	Arg	Ile	Val	Ala	Ala	Met	Ile	Leu	Gly	Leu	Arg	
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Ala	Leu	Thr	Glu	Ser	Leu	Asn	Ala	Ile	Glu	Leu	Glu	Asp	Leu	Leu	Leu	
390						395						400			405	
gga	ccg	atc	ggg	ggc	gcc	gat	ccg	gtg	act	ctg	cgt	cgt	ttg	ctg	cgc	1363
Gly	Pro	Ile	Gly	Gly	Ala	Asp	Pro	Val	Thr	Leu	Arg	Arg	Leu	Leu	Arg	
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Gly	Leu	Arg	Gln	Ala	Glu	Met	Lys	Met	Gly	Gly	Gln	Arg	Arg	Ala	Ile	
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Glu	Val	Leu	Arg	Ser	Leu	Leu	Ala	Glu	Ser	Asp	Ala	Glu	Met	Leu	Gly	
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Phe	Leu	Thr	Asp	Arg	Glu	Leu	Asn	Leu	Leu	Glu	Arg	Val	Arg	Ser	Val	
455						460						465				
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Leu	Glu	Ala	Gly	Arg	Glu	Ala	Leu	Ala	Glu	His	Gly	Ser	Ile	Glu	Glu	
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Val	Leu	Trp	Ala	Leu	Trp	Ser	Ala	Thr	Asp	Leu	Ser	Asn	Ser	Leu	Ser	
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gcg	atc	agc	ctt	cga	ggc	ggc	gca	tcg	ggg	tcc	cag	gcc	gat	cgc	gat	1651
Ala	Ile	Ser	Leu	Arg	Gly	Gly	Ala	Ser	Gly	Ser	Gln	Ala	Asp	Arg	Asp	
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Leu	Asp	Ala	Met	Met	Ala	Leu	Phe	Asp	Ala	Ala	Gly	Asp	Tyr	Val	Glu	
520						525						530				
cgc	tac	ccg	tca	gcg	ggc	gtg	cgg	agt	ttc	att	ctg	cat	att	tct	gag	1747
Arg	Tyr	Pro	Ser	Ala	Gly	Val	Arg	Ser	Phe	Ile	Leu	His	Ile	Ser	Glu	
535						540						545				
cag	gaa	ctt	ccg	acc	ggc	atg	cgt	gag	cga	cgc	ggc	gcg	atc	ccg	gag	1795
Gln	Glu	Leu	Pro	Thr	Gly	Met	Arg	Glu	Arg	Arg	Gly	Ala	Ile	Pro	Glu	
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Ala	Val	Glu	Val	Leu	Thr	Ala	His	Ala	Thr	Thr	Gly	Arg	Glu	Trp	Lys	
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cgc	gtg	atc	gtt	gct	gag	gtg	cag	gag	ggc	agt	tgg	ccg	tcg	ctc	ggt	1891
Arg	Val	Ile	Val	Ala	Glu	Val	Gln	Glu	Gly	Ser	Trp	Pro	Ser	Leu	Gly</	

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tcg ctc ctg gtt acc gct gtg aat tcc ccc gac tcc gac gaa gtc cgc Ser Leu Leu Val Thr Ala Val Asn Ser Pro Asp Ser Asp Glu Val Arg 650 655 660			2083
gaa ccc tcc cgg ttt ttg gaa ttg ctg agt caa ccg atc gtt gtt ctc Glu Pro Ser Arg Phe Leu Glu Leu Leu Ser Gln Pro Ile Val Val Leu 665 670 675			2131
gag ggg gag gaa gct tcg gcg atc gcg gaa ccg gag gag att ggg cat Glu Gly Glu Glu Ala Ser Ala Ile Ala Glu Pro Glu Glu Ile Gly His 680 685 690			2179
cgg ttg ttg tcg att cct gcg atg gtt gct gag ttg cgt cgt gtg gtg Arg Leu Leu Ser Ile Pro Ala Met Val Ala Glu Leu Arg Arg Val Val 695 700 705			2227
aat gat ccg cgg gat ccg cgt cgg aag cag gct gcg agg cag ttg tcg Asn Asp Pro Arg Asp Pro Arg Arg Lys Gln Ala Ala Arg Gln Leu Ser 710 715 720 725			2275
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aat ctg cgc act ccg tcg act gat gag gag ttg atc aag ggg gcg gtg Asn Leu Arg Thr Pro Ser Thr Asp Glu Glu Leu Ile Lys Gly Ala Val 745 750 755			2371
tcg ttg tcg ccg tcg cgg att gag cag ttg ttg aat tgt ccg ctg cgc Ser Leu Ser Pro Ser Arg Ile Glu Gln Leu Leu Asn Cys Pro Leu Arg 760 765 770			2419
gct gtg ttg gat cgt ttg gac agt gag gag gaa acg ccg atc gcg atg Ala Val Leu Asp Arg Leu Asp Ser Glu Glu Glu Thr Pro Ile Ala Met 775 780 785			2467
ctc aag ggc acc ttg gtg cac gcg ttt gcg gag gcg gtc gcc ggt ggc Leu Lys Gly Thr Leu Val His Ala Phe Ala Glu Ala Val Ala Gly Gly 790 795 800 805			2515
gtc gat gcg gcg ctc gcc gaa gag aag gtg acc agc gcc tac atg cag Val Asp Ala Ala Leu Ala Glu Glu Lys Val Thr Ser Ala Tyr Met Gln 810 815 820			2563
ctg gcg aac gtg ccg agc tgg tcg cgc gaa agc acc gaa att gct ttt Leu Ala Asn Val Pro Ser Trp Ser Arg Glu Ser Thr Glu Ile Ala Phe 825 830 835			2611
cga cgc atc ctc tca cgt acc gat acc tgg ctg aag act tct cgc gcc Arg Arg Ile Leu Ser Arg Thr Asp Thr Trp Leu Lys Thr Ser Arg Ala 840 845 850			2659

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gct gca aaa gac atg ggc gat cac cca cag ttg ttt gcg tat caa ttg 2851  
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Lys Glu Ala Ala Ser Arg Leu Arg Gln Glu Ile Ser Glu Ser Val Ala  
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Gln Met Asp Tyr Val Ser Glu Gly Pro Leu Val Arg Ser Val His Ser  
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Val Ala Phe Ala Leu Ile Arg Asp Ala Ser Asp Asp Asp Val Arg Leu  
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His Ala Asp Asp Gly Arg Gly Gly Trp Pro Gln Glu Gln Arg Glu Gly  
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Ala Val Glu Arg Gly Val Gly Pro Asp Glu Leu Val Glu Leu Gly Glu  
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 Gln Arg Arg Ala Ile Glu Val Leu Arg Ser Leu Leu Ala Glu Ser Asp  
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Ser	Ala	Tyr	Met	Gln	Leu	Ala	Asn	Val	Pro	Ser	Trp	Ser	Arg	Glu	Ser
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 Ser Val Thr Ile Asp Asp Ser Val Ser Ile Arg Gly Arg Met Asp Arg  
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 ctc acc gcc acc caa acg ccg gcc act gtc acg gaa tac ctc ctc aag 192  
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 Leu Val Ser Glu Met Asp Asn His Met Val Thr Ala Glu Asp Ile Arg  
 65 70 75 80  
 gag gag tcc gat ccg ttc att aag ctt ttc gac gaa ctc ccc aag ggc 288  
 Glu Glu Ser Asp Pro Phe Ile Lys Leu Phe Asp Glu Leu Pro Lys Gly  
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 aag ggt cag cgc gac aac ctc aac gcc gaa atg acg aag tgg cgg gat 336  
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Thr Gln Val Ala Arg Leu Gln Tyr Leu Pro Leu Val Lys Ala Leu Lys	
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Glu Glu Leu His Asn Gln Ala Val Val Thr Phe Gly Glu Gln Met Ser	
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Lys Ala Ala His Leu Ala Ser Thr His Pro Gln Val Gly Tyr Ser Gln	
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Arg Arg Arg Phe Arg Val Val Met Leu Asp Glu Tyr Gln Asp Thr Ser	
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His Ser Gln Arg Val Leu Leu Ser Ser Leu Phe Gly Gly Thr Asp Pro	
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Gly Leu Thr Val Asn Ala Val Gly Asp Pro Met Gln Ala Ile Tyr Gly	
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Trp Arg Gly Ala Thr Ala Ala Asn Leu Glu Asn Phe Val Asp Asp Phe	
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Pro Val Ile His Leu Asp Gly Lys Thr Arg Ala Pro Lys Asn Glu Leu	
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Thr Thr Ser Trp Arg Asn Pro Pro Glu Val Leu Thr Leu Ala Asn Ala	
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Gln Pro Leu Gln Pro Arg Glu Gly Ala Pro Thr Gly Glu Val Ser Leu	
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Gly Trp Phe Gly Thr Ala Ala Gln Glu Arg Glu Phe Val Ala Asp Glu	
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Met Val Lys His Trp Asn Ala Arg Glu Glu Lys Gly Thr Phe Thr Ala	
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Leu Thr Lys Arg Gly Ile Pro Val Glu Ile Val Gly Leu Ser Gly Leu	
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Leu Asp Ile Pro Glu Ile Ala Asp Leu Ile Ser Leu Ala Thr Met Leu	
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Val Arg Pro His Asp Asn Arg Ala Ala Leu Arg Ile Leu Ala Gly Pro	
370 375 380	
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cgc aat att gcg ggt cgt gtg tct cgt gag cgt cga gag aag aac cca	1248
Arg Asn Ile Ala Gly Arg Val Ser Arg Glu Arg Arg Glu Lys Asn Pro	
405 410 415	
gat cca tta gcg gag ctt gat gcg att att gag gaa gcg act gcg att	1296
Asp Pro Leu Ala Glu Leu Asp Ala Ile Ile Glu Glu Ala Thr Ala Ile	
420 425 430	
gaa ccg gaa gct gtg gtt ggt cta gct gat gcg gtt gcc gat ttg ggt	1344
Glu Pro Glu Ala Val Val Gly Leu Ala Asp Ala Val Ala Asp Leu Gly	
435 440 445	
gag ggc gat cgt ttc agc gag gag ggg ttg agt cgt ttg aag cga ctg	1392
Glu Gly Asp Arg Phe Ser Glu Glu Gly Leu Ser Arg Leu Lys Arg Leu	
450 455 460	
gcc act cag ttg cga tat ttg cgt aag tac agc ttg ggt cgt tcg gtg	1440
Ala Thr Gln Leu Arg Tyr Leu Arg Lys Tyr Ser Leu Gly Arg Ser Val	
465 470 475 480	
gcg gac att ttt gct gat att gaa act gtg ttc aat att cgc acg gag	1488
Ala Asp Ile Phe Ala Asp Ile Glu Thr Val Phe Asn Ile Arg Thr Glu	
485 490 495	
gtg ttg tcg agg cag gat cct cac gcc gat ggt gct gct gga acg gtg	1536
Val Leu Ser Arg Gln Asp Pro His Ala Asp Gly Ala Ala Gly Thr Val	
500 505 510	
cat ttg gat aag ttc gca gaa gag gtc gca agt cac ggt ggc att ggg	1584
His Leu Asp Lys Phe Ala Glu Glu Val Ala Ser His Gly Gly Ile Gly	
515 520 525	
ctg cct gag ctg ttg gac tat ttt gag ctc gcg aag gat cag gaa gag	1632
Leu Pro Glu Leu Leu Asp Tyr Phe Glu Leu Ala Lys Asp Gln Glu Glu	
530 535 540	
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Gly Leu Glu Pro Gly Glu Val Thr Val Arg Ser Asp Arg Val Gln Ile	
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Leu Thr Val His Lys Ala Lys Gly Leu Glu Trp Asp Ile Val Ser Val	
565 570 575	
ttg cat gcc gat gcg tcg acc tat gat gcg aag gct tcg acg tgg ttg	1776
Leu His Ala Asp Ala Ser Thr Tyr Asp Ala Lys Ala Ser Thr Trp Leu	
580 585 590	
aaa aat gtc acg atg atc ccg tcg tcg ctt cgt ggc gat gcc ggg acc	1824

Lys	Asn	Val	Thr	Met	Ile	Pro	Ser	Ser	Leu	Arg	Gly	Asp	Ala	Gly	Thr		
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ggc	gcc	cca	gag	atg	gat	acc	tct	gag	gcg	gac	gat	cgc	aaa	gct	ctg	1872	
Gly	Ala	Pro	Glu	Met	Asp	Thr	Ser	Glu	Ala	Asp	Asp	Arg	Lys	Ala	Leu		
	610					615					620						
gaa	gat	tcc	ggc	aag	gag	tac	acc	agt	gaa	gtg	cgt	gag	ggg	tta	cgg	1920	
Glu	Asp	Ser	Gly	Lys	Glu	Tyr	Thr	Ser	Glu	Val	Arg	Glu	Gly	Leu	Arg		
	625				630					635					640		
gag	gaa	aat	tcg	cga	ctg	ttt	tat	gtc	ggt	atc	acg	cgc	agc	gaa	cgg	1968	
Glu	Glu	Asn	Ser	Arg	Leu	Phe	Tyr	Val	Gly	Ile	Thr	Arg	Ser	Glu	Arg		
				645					650					655			
gtg	ttg	ctc	gtg	acg	ggc	tcg	gcg	ctt	gat	gaa	agt	ggc	aca	aag	gcg	2016	
Val	Leu	Leu	Val	Thr	Gly	Ser	Ala	Leu	Asp	Glu	Ser	Gly	Thr	Lys	Ala		
			660					665					670				
aaa	gtt	ccc	tac	ggc	cac	ttg	gag	atc	ctt	cgg	gat	aaa	gcg	ccg	gag	2064	
Lys	Val	Pro	Tyr	Gly	His	Leu	Glu	Ile	Leu	Arg	Asp	Lys	Ala	Pro	Glu		
		675					680					685					
tgc	gtg	gtg	tcg	tgg	tgg	gaa	ggg	gaa	gag	ggg	gac	gtc	gaa	aag	caa	2112	
Cys	Val	Val	Ser	Trp	Trp	Glu	Gly	Glu	Glu	Gly	Asp	Val	Glu	Lys	Gln		
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aaa	cct	gcg	gaa	ggc	gtc	ttc	ccg	caa	ctg	ctc	gcc	gct	gac	tcc	tcc	2160	
Lys	Pro	Ala	Glu	Gly	Val	Phe	Pro	Gln	Leu	Leu	Ala	Ala	Asp	Ser	Ser		
	705				710					715					720		
ggc	gcg	gat	ttg	gtg	cgc	ggc	ccg	cgc	gcc	gag	cca	aac	aac	gag	ggc	2208	
Gly	Ala	Asp	Leu	Val	Arg	Gly	Pro	Arg	Ala	Glu	Pro	Asn	Asn	Glu	Gly		
				725					730					735			
ggg	ctg	gaa	agc	ttg	tgg	gaa	aaa	gag	gta	agc	gcg	ctt	atc	gac	gaa	2256	
Gly	Leu	Glu	Ser	Leu	Trp	Glu	Lys	Glu	Val	Ser	Ala	Leu	Ile	Asp	Glu		
			740				745						750				
cac	cgc	cgc	ctt	tcc	aac	ccc	atc	gtc	gaa	gtc	gaa	acg	ccc	cgc	gaa	2304	
His	Arg	Arg	Leu	Ser	Asn	Pro	Ile	Val	Glu	Val	Glu	Thr	Pro	Arg	Glu		
			755				760					765					
ctc	acg	gcc	acc	gac	ctc	gtc	tct	atg	aaa	aac	aat	ccc	gaa	cag	ttc	2352	
Leu	Thr	Ala	Thr	Asp	Leu	Val	Ser	Met	Lys	Asn	Asn	Pro	Glu	Gln	Phe		
	770					775					780						
gcc	cga	cga	atg	cgt	cgc	cct	gtc	ccg	ttc	aaa	cca	aac	acc	tac	gca	2400	
Ala	Arg	Arg	Met	Arg	Arg	Pro	Val	Pro	Phe	Lys	Pro	Asn	Thr	Tyr	Ala		
	785				790					795					800		
aaa	cgc	ggc	aca	ctg	ttc	cac	caa	tgg	ctc	gaa	gat	cgg	ttt	ggc	agc	2448	
Lys	Arg	Gly	Thr	Leu	Phe	His	Gln	Trp	Leu	Glu	Asp	Arg	Phe	Gly	Ser		
				805				810					815				
acc	gcg	ctt	ctc	gac	gaa	acc	gag	ctc	ccc	ggc	atc	gac	gag	gac	tac	2496	
Thr	Ala	Leu	Leu	Asp	Glu	Thr	Glu	Leu	Pro	Gly	Ile	Asp	Glu	Asp	Tyr		
			820					825					830				
tcg	gat	gac	gca	ttc	atc	gaa	ctc	cgc	gac	gcg	ttc	cta	gga	tct	act	2544	
Ser	Asp	Asp	Ala	Phe	Ile	Glu	Leu	Arg	Asp	Ala	Phe	Leu	Gly	Ser	Thr		

835	840	845	
tgg gaa aac cgc aca ccg gaa ttc gtc gaa cat ccc ttc gaa gta acg			2592
Trp Glu Asn Arg Thr Pro Glu Phe Val Glu His Pro Phe Glu Val Thr			
850	855	860	
atc ggc gaa cac gtc atc cgc ggc cgc atg gac gcc gtc ttc cac acc			2640
Ile Gly Glu His Val Ile Arg Gly Arg Met Asp Ala Val Phe His Thr			
865	870	875	880
gat ggc acc tgg atg gtg gtc gac tgg aaa acc gga cgc acc cca acc			2688
Asp Gly Thr Trp Met Val Val Asp Trp Lys Thr Gly Arg Thr Pro Thr			
885	890	895	
ggc ccc gaa atg gac gca gcg atc atc cag ctc gct gtc tat aga ctc			2736
Gly Pro Glu Met Asp Ala Ala Ile Ile Gln Leu Ala Val Tyr Arg Leu			
900	905	910	
gcc tgg gca cga ctc aaa ggc ctc gaa cct gaa gaa gtc cgc gca gca			2784
Ala Trp Ala Arg Leu Lys Gly Leu Glu Pro Glu Glu Val Arg Ala Ala			
915	920	925	
ttc cat tac gtc gcc cac gat cac acc ttt gag ccg aac gat ctg ccg			2832
Phe His Tyr Val Ala His Asp His Thr Phe Glu Pro Asn Asp Leu Pro			
930	935	940	
act caa gaa gaa cta gcc cgg ctg ctc agt cag gaa tgatgcgccct			2878
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Glu Leu Tyr His Ile Ala Arg Asn Val Val Asn Asn Tyr Asp Gly Glu			
35	40	45	
Leu Thr Ala Thr Gln Thr Pro Ala Thr Val Thr Glu Tyr Leu Leu Lys			
50	55	60	
Leu Val Ser Glu Met Asp Asn His Met Val Thr Ala Glu Asp Ile Arg			
65	70	75	80
Glu Glu Ser Asp Pro Phe Ile Lys Leu Phe Asp Glu Leu Pro Lys Gly			
85	90	95	
Lys Gly Gln Arg Asp Asn Leu Asn Ala Glu Met Thr Lys Trp Arg Asp			
100	105	110	
Thr Gln Val Ala Arg Leu Gln Tyr Leu Pro Leu Val Lys Ala Leu Lys			

115	120	125
Glu Glu Leu His Asn Gln Ala Val Val Thr Phe Gly Glu Gln Met Ser 130	135	140
Lys Ala Ala His Leu Ala Ser Thr His Pro Gln Val Gly Tyr Ser Gln 145	150	155 160
Arg Arg Arg Phe Arg Val Val Met Leu Asp Glu Tyr Gln Asp Thr Ser 165	170	175
His Ser Gln Arg Val Leu Leu Ser Ser Leu Phe Gly Gly Thr Asp Pro 180	185	190
Gly Leu Thr Val Asn Ala Val Gly Asp Pro Met Gln Ala Ile Tyr Gly 195	200	205
Trp Arg Gly Ala Thr Ala Ala Asn Leu Glu Asn Phe Val Asp Asp Phe 210	215	220
Pro Val Ile His Leu Asp Gly Lys Thr Arg Ala Pro Lys Asn Glu Leu 225	230	235 240
Thr Thr Ser Trp Arg Asn Pro Pro Glu Val Leu Thr Leu Ala Asn Ala 245	250	255
Val Ser Arg Glu Val Leu Gly Ser Pro Asp Ala Pro Thr Arg Thr Val 260	265	270
Gln Pro Leu Gln Pro Arg Glu Gly Ala Pro Thr Gly Glu Val Ser Leu 275	280	285
Gly Trp Phe Gly Thr Ala Ala Gln Glu Arg Glu Phe Val Ala Asp Glu 290	295	300
Met Val Lys His Trp Asn Ala Arg Glu Glu Lys Gly Thr Phe Thr Ala 305	310	315 320
Ala Val Leu Val Arg Lys Lys Arg His Ser Ala Pro Met Ala Glu Glu 325	330	335
Leu Thr Lys Arg Gly Ile Pro Val Glu Ile Val Gly Leu Ser Gly Leu 340	345	350
Leu Asp Ile Pro Glu Ile Ala Asp Leu Ile Ser Leu Ala Thr Met Leu 355	360	365
Val Arg Pro His Asp Asn Arg Ala Ala Leu Arg Ile Leu Ala Gly Pro 370	375	380
His Val Gly Leu Gly Val Ala Asp Leu Gln Arg Leu Gln Gly Arg Ala 385	390	395 400
Arg Asn Ile Ala Gly Arg Val Ser Arg Glu Arg Arg Glu Lys Asn Pro 405	410	415
Asp Pro Leu Ala Glu Leu Asp Ala Ile Ile Glu Glu Ala Thr Ala Ile 420	425	430
Glu Pro Glu Ala Val Val Gly Leu Ala Asp Ala Val Ala Asp Leu Gly 435	440	445

Glu Gly Asp Arg Phe Ser Glu Gly Leu Ser Arg Leu Lys Arg Leu  
 450 455 460  
 Ala Thr Gln Leu Arg Tyr Leu Arg Lys Tyr Ser Leu Gly Arg Ser Val  
 465 470 475 480  
 Ala Asp Ile Phe Ala Asp Ile Glu Thr Val Phe Asn Ile Arg Thr Glu  
 485 490 495  
 Val Leu Ser Arg Gln Asp Pro His Ala Asp Gly Ala Ala Gly Thr Val  
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 His Leu Asp Lys Phe Ala Glu Glu Val Ala Ser His Gly Gly Ile Gly  
 515 520 525  
 Leu Pro Glu Leu Leu Asp Tyr Phe Glu Leu Ala Lys Asp Gln Glu Glu  
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 Gly Leu Glu Pro Gly Glu Val Thr Val Arg Ser Asp Arg Val Gln Ile  
 545 550 555 560  
 Leu Thr Val His Lys Ala Lys Gly Leu Glu Trp Asp Ile Val Ser Val  
 565 570 575  
 Leu His Ala Asp Ala Ser Thr Tyr Asp Ala Lys Ala Ser Thr Trp Leu  
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 Lys Asn Val Thr Met Ile Pro Ser Ser Leu Arg Gly Asp Ala Gly Thr  
 595 600 605  
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 Glu Asp Ser Gly Lys Glu Tyr Thr Ser Glu Val Arg Glu Gly Leu Arg  
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 Glu Glu Asn Ser Arg Leu Phe Tyr Val Gly Ile Thr Arg Ser Glu Arg  
 645 650 655  
 Val Leu Leu Val Thr Gly Ser Ala Leu Asp Glu Ser Gly Thr Lys Ala  
 660 665 670  
 Lys Val Pro Tyr Gly His Leu Glu Ile Leu Arg Asp Lys Ala Pro Glu  
 675 680 685  
 Cys Val Val Ser Trp Trp Glu Gly Glu Glu Gly Asp Val Glu Lys Gln  
 690 695 700  
 Lys Pro Ala Glu Gly Val Phe Pro Gln Leu Leu Ala Ala Asp Ser Ser  
 705 710 715 720  
 Gly Ala Asp Leu Val Arg Gly Pro Arg Ala Glu Pro Asn Asn Glu Gly  
 725 730 735  
 Gly Leu Glu Ser Leu Trp Glu Lys Glu Val Ser Ala Leu Ile Asp Glu  
 740 745 750  
 His Arg Arg Leu Ser Asn Pro Ile Val Glu Val Glu Thr Pro Arg Glu  
 755 760 765

Leu Thr Ala Thr Asp Leu Val Ser Met Lys Asn Asn Pro Glu Gln Phe  
 770 775 780  
 Ala Arg Arg Met Arg Arg Pro Val Pro Phe Lys Pro Asn Thr Tyr Ala  
 785 790 795 800  
 Lys Arg Gly Thr Leu Phe His Gln Trp Leu Glu Asp Arg Phe Gly Ser  
 805 810 815  
 Thr Ala Leu Leu Asp Glu Thr Glu Leu Pro Gly Ile Asp Glu Asp Tyr  
 820 825 830  
 Ser Asp Asp Ala Phe Ile Glu Leu Arg Asp Ala Phe Leu Gly Ser Thr  
 835 840 845  
 Trp Glu Asn Arg Thr Pro Glu Phe Val Glu His Pro Phe Glu Val Thr  
 850 855 860  
 Ile Gly Glu His Val Ile Arg Gly Arg Met Asp Ala Val Phe His Thr  
 865 870 875 880  
 Asp Gly Thr Trp Met Val Val Asp Trp Lys Thr Gly Arg Thr Pro Thr  
 885 890 895  
 Gly Pro Glu Met Asp Ala Ala Ile Ile Gln Leu Ala Val Tyr Arg Leu  
 900 905 910  
 Ala Trp Ala Arg Leu Lys Gly Leu Glu Pro Glu Glu Val Arg Ala Ala  
 915 920 925  
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 945 950 955

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 Met Asn Thr Ser Pro  
 1 5  
 ttt acc cca ggt tcc ccc gat ctc atc gat ggc ttg aat gag caa cag 163  
 Phe Thr Pro Gly Ser Pro Asp Leu Ile Asp Gly Leu Asn Glu Gln Gln  
 10 15 20  
 cgt gct gct gtg gag cat atc ggt tct ccg ctg ctg att gtc gct ggt 211  
 Arg Ala Ala Val Glu His Ile Gly Ser Pro Leu Leu Ile Val Ala Gly  
 25 30 35

gct ggt tca ggc aag act gct gtg ttg acc agg cgt att gct tat tta 259  
 Ala Gly Ser Gly Lys Thr Ala Val Leu Thr Arg Arg Ile Ala Tyr Leu  
 40 45 50

atg cgt tac cgt ggt gtg cat ccg cag caa att ttg gcc att acc ttt 307  
 Met Arg Tyr Arg Gly Val His Pro Gln Gln Ile Leu Ala Ile Thr Phe  
 55 60 65

acc aat aag gct gcc gct gag atg cgt gag cgt gtc agt cag ctg gtg 355  
 Thr Asn Lys Ala Ala Ala Glu Met Arg Glu Arg Val Ser Gln Leu Val  
 70 75 80 85

ggc ccg gtt gcg gag cgc atg tgg gtg gct acg ttc cac tcg gtg tgt 403  
 Gly Pro Val Ala Glu Arg Met Trp Val Ala Thr Phe His Ser Val Cys  
 90 95 100

gtg cgt att ttg cgt cag cag gcg cag ttg gtg gag ggg ctg aac act 451  
 Val Arg Ile Leu Arg Gln Gln Ala Gln Leu Val Glu Gly Leu Asn Thr  
 105 110 115

aac ttc act att tat gat tcg gat gat tcg agg cgt ttg ctc acg atg 499  
 Asn Phe Thr Ile Tyr Asp Ser Asp Asp Ser Arg Arg Leu Leu Thr Met  
 120 125 130

atc gcc aag gat ctg gag ttg gat att aag aag ttc tcg gcg cgt acg 547  
 Ile Ala Lys Asp Leu Glu Leu Asp Ile Lys Lys Phe Ser Ala Arg Thr  
 135 140 145

ttg ctg ggt gct att tct aat ttg aaa aat gag ttg gtt act ccg cag 595  
 Leu Leu Gly Ala Ile Ser Asn Leu Lys Asn Glu Leu Val Thr Pro Gln  
 150 155 160 165

gag gct ctt gcg gat gct gaa cgc acg cac aat cct tat gaa aca gtc 643  
 Glu Ala Leu Ala Asp Ala Glu Arg Thr His Asn Pro Tyr Glu Thr Val  
 170 175 180

gtg gcc agg gcg ttt tcg gag tat cag agc agg ctt cgc cgt gcc aac 691  
 Val Ala Arg Ala Phe Ser Glu Tyr Gln Ser Arg Leu Arg Arg Ala Asn  
 185 190 195

gct gtg gat ttt gat gat ttg att ggg gag act gtt cgg att ttc cgg 739  
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 200 205 210

gag cat cca cct gtt gcg gag tat tac cgc aga cgt ttc cgc cac gtg 787  
 Glu His Pro Pro Val Ala Glu Tyr Tyr Arg Arg Arg Phe Arg His Val  
 215 220 225

ctg atc gat gag tat cag gac acc aac cac gct cag tat gag ctg att 835  
 Leu Ile Asp Glu Tyr Gln Asp Thr Asn His Ala Gln Tyr Glu Leu Ile  
 230 235 240 245

tct acg ctc gtc ggc aag cct gac cag gat ccg tct gag ctg tgt gtt 883  
 Ser Thr Leu Val Gly Lys Pro Asp Gln Asp Pro Ser Glu Leu Cys Val  
 250 255 260

gtg ggt gat tcg gat cag tct att tat gct ttc cgt ggc gcc acg atc 931  
 Val Gly Asp Ser Asp Gln Ser Ile Tyr Ala Phe Arg Gly Ala Thr Ile  
 265 270 275



cgc aac att gaa gag ttt gag cgc gat ttc tcc aac gcc cgc acc att 979  
 Arg Asn Ile Glu Glu Phe Glu Arg Asp Phe Ser Asn Ala Arg Thr Ile  
 280 285 290

ttg ctg gag cag aat tac cgt tcc acc cag acg att ctt tct gct gcc 1027  
 Leu Leu Glu Gln Asn Tyr Arg Ser Thr Gln Thr Ile Leu Ser Ala Ala  
 295 300 305

aac gcg gtg att tct caa aat gag aac cgt cga cct aaa aac ctg tgg 1075  
 Asn Ala Val Ile Ser Gln Asn Glu Asn Arg Arg Pro Lys Asn Leu Trp  
 310 315 320 325

act gcg ctg ggg gag ggc gag cag atc att ggt tat gtt gcc gac aat 1123  
 Thr Ala Leu Gly Glu Gly Glu Gln Ile Ile Gly Tyr Val Ala Asp Asn  
 330 335 340

gag cac gat gaa gcc cgt ttt att gct agt gag atc gac aat tta gtt 1171  
 Glu His Asp Glu Ala Arg Phe Ile Ala Ser Glu Ile Asp Asn Leu Val  
 345 350 355

gac cac ggc atg agc tat tcc gac atc gcg atc atg tac cgc acg aac 1219  
 Asp His Gly Met Ser Tyr Ser Asp Ile Ala Ile Met Tyr Arg Thr Asn  
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aat tcc tgc cgc gca cta gag gat gtc ttc atg cgc acc ggc gtc ccc 1267  
 Asn Ser Ser Arg Ala Leu Glu Asp Val Phe Met Arg Thr Gly Val Pro  
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 Tyr Lys Val Val Gly Gly Thr Lys Phe Tyr Glu Arg Lys Glu Ile Arg  
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 Asp Ile Ile Ala Tyr Leu Arg Val Leu Glu Asn Pro Asp Asp Thr Val  
 410 415 420

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 Asn Leu Arg Arg Ile Ile Asn Thr Pro Lys Arg Gly Ile Gly Asp Arg  
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 455 460 465

gcg cgc ggc aag aat gcg gcg att aag ttc aat gag ctt ttc gac gcc 1555  
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 470 475 480 485

ctc cgc tcc gaa ctc ccc acc atg gtc aat gag gtc acc ggc ctg cca 1603  
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gac atc ggc caa gtc atc agt cgc atc ctc gac atc act ggc tac aag 1651  
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 505 510 515

gca gaa ctt gag gca tcc aac gac cct caa gat ggc gca cgc cta gac 1699

Ala Glu Leu Glu Ala Ser Asn Asp Pro Gln Asp Gly Ala Arg Leu Asp	
520 525 530	
aac ctg aac gag ctt gtc tcc gtg gcc cgc gag ttc tcc tcc gac gcc	1747
Asn Leu Asn Glu Leu Val Ser Val Ala Arg Glu Phe Ser Ser Asp Ala	
535 540 545	
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Ala Asn Arg Met Val Asn Glu Val Pro Glu Gly Glu Ala Gln Pro Gly	
550 555 560 565	
agc tta cag gca ttc ttg gag cga gtc tcc ctg gtt gcc gac gcc gac	1843
Ser Leu Gln Ala Phe Leu Glu Arg Val Ser Leu Val Ala Asp Ala Asp	
570 575 580	
caa atc ccc gat tcc gac aac ggc gta gtc acc ctc atg acc ctg cat	1891
Gln Ile Pro Asp Ser Asp Asn Gly Val Val Thr Leu Met Thr Leu His	
585 590 595	
acc gcc aag ggc ctt gaa ttc ccc atc gtg ttc ctc aca ggc tgg gaa	1939
Thr Ala Lys Gly Leu Glu Phe Pro Ile Val Phe Leu Thr Gly Trp Glu	
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gac gga cag ttc cca cac ctg cgt tcc ctt ggt gat gcc aaa gaa ctt	1987
Asp Gly Gln Phe Pro His Leu Arg Ser Leu Gly Asp Ala Lys Glu Leu	
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Ala Glu Glu Arg Arg Leu Ala Tyr Val Gly Ile Thr Arg Ala Arg Lys	
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cgc ctc tac atg acc aga gcc atg ctg cgt agc tcc tgg ggc aac ccg	2083
Arg Leu Tyr Met Thr Arg Ala Met Leu Arg Ser Ser Trp Gly Asn Pro	
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Val Thr Asn Pro Pro Ser Arg Phe Leu Gln Glu Val Pro Ala Glu Leu	
665 670 675	
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Ile Asp Trp Arg Arg Glu Glu Pro Gln Met Ser Ser Ala Trp Ala Pro	
680 685 690	
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Arg Pro Thr Arg Ser Ile Pro Thr Lys Thr Arg Thr Asn Asn Lys Gln	
695 700 705	
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Leu Asp Leu Ser Val Gly Asp Arg Val Asn His Asp Lys Tyr Gly Leu	
710 715 720 725	
gga acc gtg ctc tct tca gat ggc agc ggc ccc cga gcc acc gtc acc	2323
Gly Thr Val Leu Ser Ser Asp Gly Ser Gly Pro Arg Ala Thr Val Thr	
730 735 740	
atc gat ttc ggt tcc tcc ggc aag gtt aga ttg atg ctt ctt ggt ggc	2371
Ile Asp Phe Gly Ser Ser Gly Lys Val Arg Leu Met Leu Leu Gly Gly	
745 750 755	
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Val Pro Met Glu Lys Leu	

760

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&lt;211&gt; 763

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&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 56

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Leu Ile Val Ala Gly Ala Gly Ser Gly Lys Thr Ala Val Leu Thr Arg  
 35 40 45

Arg Ile Ala Tyr Leu Met Arg Tyr Arg Gly Val His Pro Gln Gln Ile  
 50 55 60

Leu Ala Ile Thr Phe Thr Asn Lys Ala Ala Ala Glu Met Arg Glu Arg  
 65 70 75 80

Val Ser Gln Leu Val Gly Pro Val Ala Glu Arg Met Trp Val Ala Thr  
 85 90 95

Phe His Ser Val Cys Val Arg Ile Leu Arg Gln Gln Ala Gln Leu Val  
 100 105 110

Glu Gly Leu Asn Thr Asn Phe Thr Ile Tyr Asp Ser Asp Asp Ser Arg  
 115 120 125

Arg Leu Leu Thr Met Ile Ala Lys Asp Leu Glu Leu Asp Ile Lys Lys  
 130 135 140

Phe Ser Ala Arg Thr Leu Leu Gly Ala Ile Ser Asn Leu Lys Asn Glu  
 145 150 155 160

Leu Val Thr Pro Gln Glu Ala Leu Ala Asp Ala Glu Arg Thr His Asn  
 165 170 175

Pro Tyr Glu Thr Val Val Ala Arg Ala Phe Ser Glu Tyr Gln Ser Arg  
 180 185 190

Leu Arg Arg Ala Asn Ala Val Asp Phe Asp Asp Leu Ile Gly Glu Thr  
 195 200 205

Val Arg Ile Phe Arg Glu His Pro Pro Val Ala Glu Tyr Tyr Arg Arg  
 210 215 220

Arg Phe Arg His Val Leu Ile Asp Glu Tyr Gln Asp Thr Asn His Ala  
 225 230 235 240

Gln Tyr Glu Leu Ile Ser Thr Leu Val Gly Lys Pro Asp Gln Asp Pro  
 245 250 255

Ser Glu Leu Cys Val Val Gly Asp Ser Asp Gln Ser Ile Tyr Ala Phe  
 260 265 270

Arg Gly Ala Thr Ile Arg Asn Ile Glu Glu Phe Glu Arg Asp Phe Ser

275	280	285
Asn Ala Arg Thr Ile Leu Leu Glu Gln Asn Tyr Arg Ser Thr Gln Thr 290	295	300
Ile Leu Ser Ala Ala Asn Ala Val Ile Ser Gln Asn Glu Asn Arg Arg 305	310	315 320
Pro Lys Asn Leu Trp Thr Ala Leu Gly Glu Gly Glu Gln Ile Ile Gly 325	330	335
Tyr Val Ala Asp Asn Glu His Asp Glu Ala Arg Phe Ile Ala Ser Glu 340	345	350
Ile Asp Asn Leu Val Asp His Gly Met Ser Tyr Ser Asp Ile Ala Ile 355	360	365
Met Tyr Arg Thr Asn Asn Ser Ser Arg Ala Leu Glu Asp Val Phe Met 370	375	380
Arg Thr Gly Val Pro Tyr Lys Val Val Gly Gly Thr Lys Phe Tyr Glu 385	390	395 400
Arg Lys Glu Ile Arg Asp Ile Ile Ala Tyr Leu Arg Val Leu Glu Asn 405	410	415
Pro Asp Asp Thr Val Asn Leu Arg Arg Ile Ile Asn Thr Pro Lys Arg 420	425	430
Gly Ile Gly Asp Arg Ala Gln Ala Phe Ile Ala Leu His Ser Glu Asn 435	440	445
Asn Gln Ile Ser Phe Gly Gln Ala Leu Leu Asp Ala Ala Leu Gly Lys 450	455	460
Val Asp Leu Leu Gly Ala Arg Gly Lys Asn Ala Ala Ile Lys Phe Asn 465	470	475 480
Glu Leu Phe Asp Ala Leu Arg Ser Glu Leu Pro Thr Met Val Asn Glu 485	490	495
Val Thr Gly Leu Pro Asp Ile Gly Gln Val Ile Ser Arg Ile Leu Asp 500	505	510
Ile Thr Gly Tyr Lys Ala Glu Leu Glu Ala Ser Asn Asp Pro Gln Asp 515	520	525
Gly Ala Arg Leu Asp Asn Leu Asn Glu Leu Val Ser Val Ala Arg Glu 530	535	540
Phe Ser Ser Asp Ala Ala Asn Arg Met Val Asn Glu Val Pro Glu Gly 545	550	555 560
Glu Ala Gln Pro Gly Ser Leu Gln Ala Phe Leu Glu Arg Val Ser Leu 565	570	575
Val Ala Asp Ala Asp Gln Ile Pro Asp Ser Asp Asn Gly Val Val Thr 580	585	590
Leu Met Thr Leu His Thr Ala Lys Gly Leu Glu Phe Pro Ile Val Phe 595	600	605

Leu Thr Gly Trp Glu Asp Gly Gln Phe Pro His Leu Arg Ser Leu Gly  
610 615 620

Asp Ala Lys Glu Leu Ala Glu Glu Arg Arg Leu Ala Tyr Val Gly Ile  
625 630 635 640

Thr Arg Ala Arg Lys Arg Leu Tyr Met Thr Arg Ala Met Leu Arg Ser  
645 650 655

Ser Trp Gly Asn Pro Val Thr Asn Pro Pro Ser Arg Phe Leu Gln Glu  
660 665 670

Val Pro Ala Glu Leu Ile Asp Trp Arg Arg Glu Glu Pro Gln Met Ser  
675 680 685

Ser Ala Trp Ala Pro Arg Pro Thr Arg Ser Ile Pro Thr Lys Thr Arg  
690 695 700

Thr Asn Asn Lys Gln Leu Asp Leu Ser Val Gly Asp Arg Val Asn His  
705 710 715 720

Asp Lys Tyr Gly Leu Gly Thr Val Leu Ser Ser Asp Gly Ser Gly Pro  
725 730 735

Arg Ala Thr Val Thr Ile Asp Phe Gly Ser Ser Gly Lys Val Arg Leu  
740 745 750

Met Leu Leu Gly Gly Val Pro Met Glu Lys Leu  
755 760

<210> 57

<211> 1070

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1047)

<223> RXN02819

<400> 57

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gtt ctc gca gta gtg atg acg cct gct aat cag agc aga gat ccc cgc 96  
Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg  
20 25 30

cca tgg gtg acc acc gaa tct ggt tgg tca ggt cgt gtg gat gcg gaa 144  
Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu  
35 40 45

tcc ttt act aat ccg ccg atc acc att ggg cat atg cgt ctg cct cgc 192  
Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg  
50 55 60

caa gct att gaa gag cct cgc cgc aat gcc cgg cgc gtc cag gaa ctg 240  
Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu

65	70	75	80	
ttt agg cgt gag cac ttc aag cga ccc aac aag atg cgg gag ttt gct				288
Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala				
	85	90	95	
cgg gtt cgt ccc aat gag gca gtg acc aaa ctg cgt aat gct att cgg				336
Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg				
	100	105	110	
gat cat gag gcg cat cat tgg cct gat cgg gag cac ttg gct cgc acc				384
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr				
	115	120	125	
gcg gag cgt atg atc cgt aaa gaa cgt gat ctg gct aag ttg acc ggc				432
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly				
	130	135	140	
aat gtg gat aaa gcc agg gaa acc ctc ggt agg acg ttt gag cgc att				480
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile				
	145	150	155	160
ttg tcg ctg ctc agt gaa atg gac tat gtg gat tac tct aat cca gat				528
Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp				
	165	170	175	
aat cca gtg atc act gat gaa ggt gag cgt ttg gcg aaa atc cac agt				576
Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser				
	180	185	190	
gag gca gac ctg ttg gtt gct cag tgc ctc aag cgt ggc att tgg gac				624
Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg Gly Ile Trp Asp				
	195	200	205	
aac ctt gat ccc gca gag ctc gcc ggt gtg gtg agt atg tgc acg ttt				672
Asn Leu Asp Pro Ala Glu Leu Ala Gly Val Val Ser Met Cys Thr Phe				
	210	215	220	
gaa aat cgt cgc gaa acc ggt ggt gag gct caa gct gtc aca gag gcc				720
Glu Asn Arg Arg Glu Thr Gly Gly Glu Ala Gln Ala Val Thr Glu Ala				
	225	230	235	240
atg gct gat tcc atg aat agc gtg gaa cgt att tgg ggt gag ctg gtt				768
Met Ala Asp Ser Met Asn Ser Val Glu Arg Ile Trp Gly Glu Leu Val				
	245	250	255	
gaa gat gag cgc cgt cac cgt ctg cca att act cgc cag ccg gaa gca				816
Glu Asp Glu Arg Arg His Arg Leu Pro Ile Thr Arg Gln Pro Glu Ala				
	260	265	270	
ggt ttt gcc acc gcg atc cac cag tgg gct tca ggt gct ccg ctg gga				864
Gly Phe Ala Thr Ala Ile His Gln Trp Ala Ser Gly Ala Pro Leu Gly				
	275	280	285	
tat tgc atg gct gcg gca gcg gaa aac ggc gcg gag ttg acc cct ggt				912
Tyr Cys Met Ala Ala Ala Ala Glu Asn Gly Ala Glu Leu Thr Pro Gly				
	290	295	300	
gac ttc gtg cgc tgg tgc cgt caa gtc atc gat ctt cta gag cag gtt				960
Asp Phe Val Arg Trp Cys Arg Gln Val Ile Asp Leu Leu Glu Gln Val				
	305	310	315	320

gct aag act gcc tac ttt gat gag acc aca cgg aat gct cgt cag gct 1008  
 Ala Lys Thr Ala Tyr Phe Asp Glu Thr Thr Arg Asn Ala Arg Gln Ala  
                   325                                  330                                  335

att gat gcg att agg cgt gga gtt gtg gcg atc ggt tcc tagcgagcta 1057  
 Ile Asp Ala Ile Arg Arg Gly Val Val Ala Ile Gly Ser  
                   340                                  345

gctatgttcg agc 1070

<210> 58  
 <211> 349  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 58  
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Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg  
                   20                                  25                                  30

Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu  
                   35                                  40                                  45

Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg  
                   50                                  55                                  60

Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu  
   65                                  70                                  75                                  80

Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala  
                                   85                                  90                                  95

Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg  
                   100                                  105                                  110

Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr  
                   115                                  120                                  125

Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly  
                   130                                  135                                  140

Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile  
   145                                  150                                  155                                  160

Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp  
                                   165                                  170                                  175

Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser  
                   180                                  185                                  190

Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg Gly Ile Trp Asp  
                   195                                  200                                  205

Asn Leu Asp Pro Ala Glu Leu Ala Gly Val Val Ser Met Cys Thr Phe  
   210                                  215                                  220

Glu Asn Arg Arg Glu Thr Gly Gly Glu Ala Gln Ala Val Thr Glu Ala

225                      230                      235                      240  
 Met Ala Asp Ser Met Asn Ser Val Glu Arg Ile Trp Gly Glu Leu Val  
                          245                      250                      255  
 Glu Asp Glu Arg Arg His Arg Leu Pro Ile Thr Arg Gln Pro Glu Ala  
                          260                      265                      270  
 Gly Phe Ala Thr Ala Ile His Gln Trp Ala Ser Gly Ala Pro Leu Gly  
                          275                      280                      285  
 Tyr Cys Met Ala Ala Ala Ala Glu Asn Gly Ala Glu Leu Thr Pro Gly  
                          290                      295                      300  
 Asp Phe Val Arg Trp Cys Arg Gln Val Ile Asp Leu Leu Glu Gln Val  
 305                      310                      315                      320  
 Ala Lys Thr Ala Tyr Phe Asp Glu Thr Thr Arg Asn Ala Arg Gln Ala  
                          325                      330                      335  
 Ile Asp Ala Ile Arg Arg Gly Val Val Ala Ile Gly Ser  
                          340                      345

<210> 59  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(612)  
 <223> FRXA02819

<400> 59  
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 Lys Leu Gln Ile Gly Asp Val Ile Ala Met Pro Gly Arg Lys Arg Pro  
   1                      5                      10                      15  
 gtt ctc gca gta gtg atg acg cct gct aat cag agc aga gat ccc cgc    96  
 Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg  
                          20                      25                      30  
 cca tgg gtg acc acc gaa tct ggt tgg tca ggt cgt gtg gat gcg gaa    144  
 Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu  
                          35                      40                      45  
 tcc ttt act aat ccg ccg atc acc att ggg cat atg cgt ctg cct cgc    192  
 Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg  
                          50                      55                      60  
 caa gct att gaa gag cct cgc cgc aat gcc cgg cgc gtc cag gaa ctg    240  
 Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu  
                          65                      70                      75                      80  
 ttt agg cgt gag cac ttc aag cga ccc aac aag atg cgg gag ttt gct    288  
 Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala  
                          85                      90                      95  
 cgg gtt cgt ccc aat gag gca gtg acc aaa ctg cgt aat gct att cgg    336  
 Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg



100	105	110	
gat cat gag gcg cat cat tgg cct gat cgg gag cac ttg gct cgc acc			384
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr			
115	120	125	
gcg gag cgt atg atc cgt aaa gaa cgt gat ctg gct aag ttg acc ggc			432
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly			
130	135	140	
aat gtg gat aaa gcc agg gaa acc ctc ggt agg acg ttt gag cgc att			480
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile			
145	150	155	160
ttg tcg ctg ctc agt gaa atg gac tat gtg gat tac tct aat cca gat			528
Leu Ser Leu Leu Ser Glu Met Asp Tyr Val Asp Tyr Ser Asn Pro Asp			
165	170	175	
aat cca gtg atc act gat gaa ggt gag cgt ttg gcg aaa atc cac agt			576
Asn Pro Val Ile Thr Asp Glu Gly Glu Arg Leu Ala Lys Ile His Ser			
180	185	190	
gag gca gac ctg ttg gtt gct cag tgc ctc aag cgt			612
Glu Ala Asp Leu Leu Val Ala Gln Cys Leu Lys Arg			
195	200		
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<212> PRT			
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<400> 60			
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Val Leu Ala Val Val Met Thr Pro Ala Asn Gln Ser Arg Asp Pro Arg			
20	25	30	
Pro Trp Val Thr Thr Glu Ser Gly Trp Ser Gly Arg Val Asp Ala Glu			
35	40	45	
Ser Phe Thr Asn Pro Pro Ile Thr Ile Gly His Met Arg Leu Pro Arg			
50	55	60	
Gln Ala Ile Glu Glu Pro Arg Arg Asn Ala Arg Arg Val Gln Glu Leu			
65	70	75	80
Phe Arg Arg Glu His Phe Lys Arg Pro Asn Lys Met Arg Glu Phe Ala			
85	90	95	
Arg Val Arg Pro Asn Glu Ala Val Thr Lys Leu Arg Asn Ala Ile Arg			
100	105	110	
Asp His Glu Ala His His Trp Pro Asp Arg Glu His Leu Ala Arg Thr			
115	120	125	
Ala Glu Arg Met Ile Arg Lys Glu Arg Asp Leu Ala Lys Leu Thr Gly			
130	135	140	
Asn Val Asp Lys Ala Arg Glu Thr Leu Gly Arg Thr Phe Glu Arg Ile			

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<210> 61
<211> 1705
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1705)
<223> RXA01157
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ggtgacgtgc	tctagggcct	agccaggtac	ccttagaggc	atg	agt	ttt	tct	gcc											115	
				Met	Ser	Phe	Ser	Ala												
				1				5												
gaa aag ggc acc cac ctt tca gag ttc ata gca gac ctg ggc ttt gat																			163	
Glu Lys Gly Thr His Leu Ser Glu Phe Ile Ala Asp Leu Gly Phe Asp																				
			10					15						20						
ctg gac gag ttc caa atc aaa ggc tgc cac gct gtg gaa gaa gac cac																			211	
Leu Asp Glu Phe Gln Ile Lys Gly Cys His Ala Val Glu Glu Asp His																				
			25					30						35						
ggt gtt tta gta tgt gcg ccc acc ggc gcg ggc aaa aca att gtt ggt																			259	
Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly Lys Thr Ile Val Gly																				
			40				45						50							
gaa ttc gca gtg tcc ctc gca tta tcg cgg ggg aca aag tgt ttc tac																			307	
Glu Phe Ala Val Ser Leu Ala Leu Ser Arg Gly Thr Lys Cys Phe Tyr																				
			55			60					65									
acc acc ccc atc aaa gcg ctg agc aac cag aag tac cac gat ttg gtg																			355	
Thr Thr Pro Ile Lys Ala Leu Ser Asn Gln Lys Tyr His Asp Leu Val																				
			70			75				80				85						
gct aaa cac ggc tcc gat gcc gtt ggt ctg ctc acc ggt gat gtt tcc																			403	
Ala Lys His Gly Ser Asp Ala Val Gly Leu Leu Thr Gly Asp Val Ser																				
				90				95						100						
att aac cat gat gct gac atc gtg gtc atg acc acc gaa gtg ctg cgc																			451	
Ile Asn His Asp Ala Asp Ile Val Val Met Thr Thr Glu Val Leu Arg																				
			105				110						115							
aac atg att tac gcg ggc tct ttt gcg ctt gag cgc tta agc cac gtg																			499	
Asn Met Ile Tyr Ala Gly Ser Phe Ala Leu Glu Arg Leu Ser His Val																				
			120			125					130									

gtc atg gat gag atc cac ttc ctt gct gat gcc tcc cgt ggc gcg gtg	547
Val Met Asp Glu Ile His Phe Leu Ala Asp Ala Ser Arg Gly Ala Val	
135 140 145	
tgg gaa gaa gtg atc ctc aac ttg gat gat tcc gtc aac atc atc ggt	595
Trp Glu Glu Val Ile Leu Asn Leu Asp Asp Ser Val Asn Ile Ile Gly	
150 155 160 165	
cta tct gcc acg gtg tcc aac tca gag gag ttt ggt gag tgg ctg acc	643
Leu Ser Ala Thr Val Ser Asn Ser Glu Glu Phe Gly Glu Trp Leu Thr	
170 175 180	
act gtt cgc ggc gat acc cgt gtg att gtt act gat cac cgc ccc gtt	691
Thr Val Arg Gly Asp Thr Arg Val Ile Val Thr Asp His Arg Pro Val	
185 190 195	
ccg ctt gat cag tac atg atg gtg cag cgc aaa gtg atg cca ctg ttt	739
Pro Leu Asp Gln Tyr Met Met Val Gln Arg Lys Val Met Pro Leu Phe	
200 205 210	
gag cct ggc acc gat gga cgc gtg aac aag gag tta gag gca acg att	787
Glu Pro Gly Thr Asp Gly Arg Val Asn Lys Glu Leu Glu Ala Thr Ile	
215 220 225	
gat cgc ctc aac agc aag caa agc gaa caa ggc cgt gcg gca tac cgc	835
Asp Arg Leu Asn Ser Lys Gln Ser Glu Gln Gly Arg Ala Ala Tyr Arg	
230 235 240 245	
tct ggt gaa ggc ttc cgt gca cgc agc aaa ggc gat aag cag gat tct	883
Ser Gly Glu Gly Phe Arg Ala Arg Ser Lys Gly Asp Lys Gln Asp Ser	
250 255 260	
cgc act ggt aag cca cgg gaa caa gac cgc cac agg cca ctg ggt cgg	931
Arg Thr Gly Lys Pro Arg Glu Gln Asp Arg His Arg Pro Leu Gly Arg	
265 270 275	
cct gaa gtg ctc agc atc ctc aag ggc atc aac atg ctg cca gcg att	979
Pro Glu Val Leu Ser Ile Leu Lys Gly Ile Asn Met Leu Pro Ala Ile	
280 285 290	
acg ttt atc ttc tcc cgc gcg ggc tgt gat ggt gcg ctg tac caa tgc	1027
Thr Phe Ile Phe Ser Arg Ala Gly Cys Asp Gly Ala Leu Tyr Gln Cys	
295 300 305	
ttg cgt tct aag ttg gtc ttg acg gat caa gca gaa tca gaa gag att	1075
Leu Arg Ser Lys Leu Val Leu Thr Asp Gln Ala Glu Ser Glu Glu Ile	
310 315 320 325	
gca cgc att gtc gac gcc ggc gtg gtg ggg atc ccc gag gaa gac ctt	1123
Ala Arg Ile Val Asp Ala Gly Val Val Gly Ile Pro Glu Glu Asp Leu	
330 335 340	
caa gta ctg aac ttt aag cag tgg cgt gct gca ctg atg cgc ggt ttc	1171
Gln Val Leu Asn Phe Lys Gln Trp Arg Ala Ala Leu Met Arg Gly Phe	
345 350 355	
gca gcc cac cac gcg ggt atg ctt cca gcg ttt agg cac atc gtg gaa	1219
Ala Ala His His Ala Gly Met Leu Pro Ala Phe Arg His Ile Val Glu	
360 365 370	
gag ctc ttt gtt aaa ggt ctt gtc cgc gcg gtg ttt gcc acg gaa acc	1267

Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val Phe Ala Thr Glu Thr  
 375 380 385  
 ctg gca ttg gga atc aac atg cca gcg cgc acc gtg gtg ttg gaa aag 1315  
 Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr Val Val Leu Glu Lys  
 390 395 400 405  
 atg gtc aaa ttt gac ggc gaa ggc cac gtt gat ctc acc cct ggc caa 1363  
 Met Val Lys Phe Asp Gly Glu Gly His Val Asp Leu Thr Pro Gly Gln  
 410 415 420  
 tac acg cag ctg acc ggt cgt gct ggt cga cgt ggc atc gat gtg ttg 1411  
 Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg Gly Ile Asp Val Leu  
 425 430 435  
 ggt aat gct gtg gtg cag tgg tca cca gca ctt gat cca cga tgg gtg 1459  
 Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu Asp Pro Arg Trp Val  
 440 445 450  
 gca ggt ctt gcc tct acg cgt acc tac ccg ctg atc tct acg ttc cag 1507  
 Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu Ile Ser Thr Phe Gln  
 455 460 465  
 ccg ggc tac aac atg tcg gtt aac ctg ctg aaa acc att ggt tat gag 1555  
 Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys Thr Ile Gly Tyr Glu  
 470 475 480 485  
 cct tcg ctg cgc ctt ttg gaa aaa tct ttt gca cag ttc caa gcc gat 1603  
 Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala Gln Phe Gln Ala Asp  
 490 495 500  
 ggt tcc gtc gtg ggc gat gtg cgt gaa att gaa cgt gca gaa gcc aag 1651  
 Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu Arg Ala Glu Ala Lys  
 505 510 515  
 gtg gca gaa ttg cgt gcc cag ctg aac aaa gag att gct gcc acc aac 1699  
 Val Ala Glu Leu Arg Ala Gln Leu Asn Lys Glu Ile Ala Ala Thr Asn  
 520 525 530  
 cct gcg 1705  
 Pro Ala  
 535

&lt;210&gt; 62

&lt;211&gt; 535

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 62

Met Ser Phe Ser Ala Glu Lys Gly Thr His Leu Ser Glu Phe Ile Ala  
 1 5 10 15

Asp Leu Gly Phe Asp Leu Asp Glu Phe Gln Ile Lys Gly Cys His Ala  
 20 25 30

Val Glu Glu Asp His Gly Val Leu Val Cys Ala Pro Thr Gly Ala Gly  
 35 40 45

Lys Thr Ile Val Gly Glu Phe Ala Val Ser Leu Ala Leu Ser Arg Gly  
 50 55 60

Thr Lys Cys Phe Tyr Thr Thr Pro Ile Lys Ala Leu Ser Asn Gln Lys  
 65 70 75 80  
 Tyr His Asp Leu Val Ala Lys His Gly Ser Asp Ala Val Gly Leu Leu  
 85 90 95  
 Thr Gly Asp Val Ser Ile Asn His Asp Ala Asp Ile Val Val Met Thr  
 100 105 110  
 Thr Glu Val Leu Arg Asn Met Ile Tyr Ala Gly Ser Phe Ala Leu Glu  
 115 120 125  
 Arg Leu Ser His Val Val Met Asp Glu Ile His Phe Leu Ala Asp Ala  
 130 135 140  
 Ser Arg Gly Ala Val Trp Glu Glu Val Ile Leu Asn Leu Asp Asp Ser  
 145 150 155 160  
 Val Asn Ile Ile Gly Leu Ser Ala Thr Val Ser Asn Ser Glu Glu Phe  
 165 170 175  
 Gly Glu Trp Leu Thr Thr Val Arg Gly Asp Thr Arg Val Ile Val Thr  
 180 185 190  
 Asp His Arg Pro Val Pro Leu Asp Gln Tyr Met Met Val Gln Arg Lys  
 195 200 205  
 Val Met Pro Leu Phe Glu Pro Gly Thr Asp Gly Arg Val Asn Lys Glu  
 210 215 220  
 Leu Glu Ala Thr Ile Asp Arg Leu Asn Ser Lys Gln Ser Glu Gln Gly  
 225 230 235 240  
 Arg Ala Ala Tyr Arg Ser Gly Glu Gly Phe Arg Ala Arg Ser Lys Gly  
 245 250 255  
 Asp Lys Gln Asp Ser Arg Thr Gly Lys Pro Arg Glu Gln Asp Arg His  
 260 265 270  
 Arg Pro Leu Gly Arg Pro Glu Val Leu Ser Ile Leu Lys Gly Ile Asn  
 275 280 285  
 Met Leu Pro Ala Ile Thr Phe Ile Phe Ser Arg Ala Gly Cys Asp Gly  
 290 295 300  
 Ala Leu Tyr Gln Cys Leu Arg Ser Lys Leu Val Leu Thr Asp Gln Ala  
 305 310 315 320  
 Glu Ser Glu Glu Ile Ala Arg Ile Val Asp Ala Gly Val Val Gly Ile  
 325 330 335  
 Pro Glu Glu Asp Leu Gln Val Leu Asn Phe Lys Gln Trp Arg Ala Ala  
 340 345 350  
 Leu Met Arg Gly Phe Ala Ala His His Ala Gly Met Leu Pro Ala Phe  
 355 360 365  
 Arg His Ile Val Glu Glu Leu Phe Val Lys Gly Leu Val Arg Ala Val  
 370 375 380

Phe Ala Thr Glu Thr Leu Ala Leu Gly Ile Asn Met Pro Ala Arg Thr  
 385 390 395 400  
 Val Val Leu Glu Lys Met Val Lys Phe Asp Gly Glu Gly His Val Asp  
 405 410 415  
 Leu Thr Pro Gly Gln Tyr Thr Gln Leu Thr Gly Arg Ala Gly Arg Arg  
 420 425 430  
 Gly Ile Asp Val Leu Gly Asn Ala Val Val Gln Trp Ser Pro Ala Leu  
 435 440 445  
 Asp Pro Arg Trp Val Ala Gly Leu Ala Ser Thr Arg Thr Tyr Pro Leu  
 450 455 460  
 Ile Ser Thr Phe Gln Pro Gly Tyr Asn Met Ser Val Asn Leu Leu Lys  
 465 470 475 480  
 Thr Ile Gly Tyr Glu Pro Ser Leu Arg Leu Leu Glu Lys Ser Phe Ala  
 485 490 495  
 Gln Phe Gln Ala Asp Gly Ser Val Val Gly Asp Val Arg Glu Ile Glu  
 500 505 510  
 Arg Ala Glu Ala Lys Val Ala Glu Leu Arg Ala Gln Leu Asn Lys Glu  
 515 520 525  
 Ile Ala Ala Thr Asn Pro Ala  
 530 535

<210> 63  
 <211> 1974  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1951)  
 <223> RXN01876

<400> 63  
 tccggggcca cccgtatttg gatcgctcgtt atatcggtcg catgggtctt gatgtgcgtg 60  
 aagataatcc cgcacgttgc tgttggattg gcgctcccc atg gcg cgc ccg ttt 115  
 Met Ala Arg Pro Phe  
 1 5  
 tat ctg gcc acc acc gtt tca ccg gag ggc gtg cat atc cgc cgg cac 163  
 Tyr Leu Ala Thr Thr Val Ser Pro Glu Gly Val His Ile Arg Arg His  
 10 15 20  
 att cgc acc cgt ggg cgc gtt gtc acg ggt gtt gat gat gag gta ttg 211  
 Ile Arg Thr Arg Gly Arg Val Val Thr Gly Val Asp Asp Glu Val Leu  
 25 30 35  
 acc ggt gag atg gcc gat gtt atc gag cag ggt ggt gtc ggc tct gaa 259  
 Thr Gly Glu Met Ala Asp Val Ile Glu Gln Gly Gly Val Gly Ser Glu  
 40 45 50  
 tct gtg ctg cac cag gcg ttg gaa cag gcc cgc agc ggc cac atg cgc 307

Ser	Val	Leu	His	Gln	Ala	Leu	Glu	Gln	Ala	Arg	Ser	Gly	His	Met	Arg		
55						60					65						
aac	atc	gtt	gaa	aca	att	cag	cgc	gag	cag	gat	gag	atc	atc	cgc	gat	355	
Asn	Ile	Val	Glu	Thr	Ile	Gln	Arg	Glu	Gln	Asp	Glu	Ile	Ile	Arg	Asp		
70					75					80					85		
acc	acc	cgc	ggt	gtc	atg	gtt	gtt	caa	ggt	ggc	cct	gga	aca	ggt	aaa	403	
Thr	Thr	Arg	Gly	Val	Met	Val	Val	Gln	Gly	Gly	Pro	Gly	Thr	Gly	Lys		
				90					95					100			
act	gcg	gtc	gcg	ttg	cac	cgt	gtg	gct	tat	ctg	ctt	tat	acc	tgg	cgc	451	
Thr	Ala	Val	Ala	Leu	His	Arg	Val	Ala	Tyr	Leu	Leu	Tyr	Thr	Trp	Arg		
			105					110					115				
gat	cag	ctg	gct	aag	tct	ggc	gtg	ttg	atc	att	ggc	ccg	aac	aag	aca	499	
Asp	Gln	Leu	Ala	Lys	Ser	Gly	Val	Leu	Ile	Ile	Gly	Pro	Asn	Lys	Thr		
		120					125					130					
ttt	ttg	gag	tat	att	tct	cac	gtt	ttg	cct	gaa	ctc	ggc	gag	act	ggc	547	
Phe	Leu	Glu	Tyr	Ile	Ser	His	Val	Leu	Pro	Glu	Leu	Gly	Glu	Thr	Gly		
	135					140					145						
gtg	gtg	ttg	tcc	acc	gtc	ggt	gag	ctg	ttc	ccc	ggt	atc	gtc	cca	acg	595	
Val	Val	Leu	Ser	Thr	Val	Gly	Glu	Leu	Phe	Pro	Gly	Ile	Val	Pro	Thr		
	150				155					160					165		
ggt	tcc	gag	gac	act	ttg	acc	agg	gaa	att	aag	ggc	agc	gag	gaa	atg	643	
Gly	Ser	Glu	Asp	Thr	Leu	Thr	Arg	Glu	Ile	Lys	Gly	Ser	Glu	Glu	Met		
				170					175					180			
gcc	agc	att	ttg	gcc	gag	gca	gtc	aag	gcg	tat	caa	gtg	ctg	cca	gag	691	
Ala	Ser	Ile	Leu	Ala	Glu	Ala	Val	Lys	Ala	Tyr	Gln	Val	Leu	Pro	Glu		
			185					190					195				
aag	acc	atc	gtg	gtc	tct	gtt	gat	ggc	atc	gag	att	tcc	att	gat	gag	739	
Lys	Thr	Ile	Val	Val	Ser	Val	Asp	Gly	Ile	Glu	Ile	Ser	Ile	Asp	Glu		
		200					205					210					
aaa	acg	gtg	gca	aaa	tcc	cgc	acc	cga	gct	cgt	cgt	gcc	agg	cag	tcg	787	
Lys	Thr	Val	Ala	Lys	Ser	Arg	Thr	Arg	Ala	Arg	Arg	Ala	Arg	Gln	Ser		
	215					220					225						
cac	aat	tcc	gca	cgc	cca	att	ttc	cgc	gag	cat	tta	gtc	gaa	caa	ctc	835	
His	Asn	Ser	Ala	Arg	Pro	Ile	Phe	Arg	Glu	His	Leu	Val	Glu	Gln	Leu		
	230				235					240					245		
gcg	cac	caa	atg	gct	caa	acg	atc	ggc	gcg	gat	ccg	ctg	ggc	ggc	aaa	883	
Ala	His	Gln	Met	Ala	Gln	Thr	Ile	Gly	Ala	Asp	Pro	Leu	Gly	Gly	Lys		
			250					255						260			
aac	ctg	ctg	tca	gcc	gcc	gac	atc	gat	cag	ctg	cac	gat	gat	ttg	ctt	931	
Asn	Leu	Leu	Ser	Ala	Ala	Asp	Ile	Asp	Gln	Leu	His	Asp	Asp	Leu	Leu		
			265					270					275				
gac	gac	gcg	gcc	ctc	cag	tcc	gtc	atc	gac	gat	ttc	tgg	ccg	gag	ctc	979	
Asp	Asp	Ala	Ala	Leu	Gln	Ser	Val	Ile	Asp	Asp	Phe	Trp	Pro	Glu	Leu		
		280					285					290					
cgg	cct	cag	gac	gtc	ctg	cat	gat	ctg	ttg	att	tcc	gaa	gag	cgc	att	1027	
Arg	Pro	Gln	Asp	Val	Leu	His	Asp	Leu	Leu	Ile	Ser	Glu	Glu	Arg	Ile		

295	300	305	
aat gtt gct gcc gcg ggg tat gac gag gaa act aag tct gct ttg ctg			1075
Asn Val Ala Ala Ala Gly Tyr Asp Glu Glu Thr Lys Ser Ala Leu Leu			
310	315	320	325
cgt ggt gaa ctc gat ccg tgg gca cca tcg gac gct gca ttg ctt gat			1123
Arg Gly Glu Leu Asp Pro Trp Ala Pro Ser Asp Ala Ala Leu Leu Asp			
	330	335	340
gag tta gcc ctg ctc atc ggt ctt ccc gat cca gag gag gca cgg gag			1171
Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro Glu Glu Ala Arg Glu			
	345	350	355
aag gct gag gcc aaa tgg cgc gag cag atc gat gac gct cag gaa gtc			1219
Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp Asp Ala Gln Glu Val			
	360	365	370
ctg gac gtt ctt agt tca tca cag tca tcg gat att gat gat gtc acg			1267
Leu Asp Val Leu Ser Ser Ser Gln Ser Ser Asp Ile Asp Asp Val Thr			
	375	380	385
gaa gct gaa gtt ctc tcc gct ttc gac gtc atc gat gcg gaa act ttg			1315
Glu Ala Glu Val Leu Ser Ala Phe Asp Val Ile Asp Ala Glu Thr Leu			
	390	395	400
gca caa cgc caa act gtc acg gat aat cgc acc act gcg gaa cgt gca			1363
Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr Thr Ala Glu Arg Ala			
	410	415	420
cag gcg gat cat aag tgg gca tat ggt cac gtg att gta gat gaa gct			1411
Gln Ala Asp His Lys Trp Ala Tyr Gly His Val Ile Val Asp Glu Ala			
	425	430	435
cag gag ctc agt ccg atg gaa tgg cgc atg gtg ttt cgc cgt agc cct			1459
Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val Phe Arg Arg Ser Pro			
	440	445	450
tcg cga tgg atg acc ctt gtg ggc gat att gca caa act ggt tgg cct			1507
Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala Gln Thr Gly Trp Pro			
	455	460	465
gcc gcc gtt gac gat tgg gca gaa tca ctg tgg ccc ttc gtc gaa aag			1555
Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp Pro Phe Val Glu Lys			
	470	475	480
cgt ttc agg cac cac gag ctc acc gtt aac tac cgc acc ccg gcc gag			1603
Arg Phe Arg His His Glu Leu Thr Val Asn Tyr Arg Thr Pro Ala Glu			
	490	495	500
atc atg tcg gtg gcc aat gag ctt ttg acg cag atc aat cct gat att			1651
Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln Ile Asn Pro Asp Ile			
	505	510	515
gcg ccg gca atg gcg atc cgc gaa tct ggt cga gag gta gtg aac ttg			1699
Ala Pro Ala Met Ala Ile Arg Glu Ser Gly Arg Glu Val Val Asn Leu			
	520	525	530
ccg ctt gat gcc gat ttg tcg gca gtg atg gat agt ttg cgt gag gag			1747
Pro Leu Asp Ala Asp Leu Ser Ala Val Met Asp Ser Leu Arg Glu Glu			
	535	540	545



gat tca cag cgc acc atc gcg gtg att tct tcg cgc cgc cac cac gaa 1795  
 Asp Ser Gln Arg Thr Ile Ala Val Ile Ser Ser Arg Arg His His Glu  
 550 555 560 565  
 agc gat ttc tac ctg gtc gat gac atc aag ggc tta gag ttt gac cac 1843  
 Ser Asp Phe Tyr Leu Val Asp Asp Ile Lys Gly Leu Glu Phe Asp His  
 570 575 580  
 gtc atc gtg gtg gat cct gcg gga atc gtt gaa gaa tcc ccc cag gga 1891  
 Val Ile Val Val Asp Pro Ala Gly Ile Val Glu Glu Ser Pro Gln Gly  
 585 590 595  
 ttg caa gac ctc tac gtt gcg gtc act cgt gca acg cag agc ctc acc 1939  
 Leu Gln Asp Leu Tyr Val Ala Val Thr Arg Ala Thr Gln Ser Leu Thr  
 600 605 610  
 att tta ggt gag tagcaggtaa tgagctcagg gcc 1974  
 Ile Leu Gly Glu  
 615

<210> 64  
 <211> 617  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 64  
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 His Ile Arg Arg His Ile Arg Thr Arg Gly Arg Val Val Thr Gly Val  
 20 25 30  
 Asp Asp Glu Val Leu Thr Gly Glu Met Ala Asp Val Ile Glu Gln Gly  
 35 40 45  
 Gly Val Gly Ser Glu Ser Val Leu His Gln Ala Leu Glu Gln Ala Arg  
 50 55 60  
 Ser Gly His Met Arg Asn Ile Val Glu Thr Ile Gln Arg Glu Gln Asp  
 65 70 75 80  
 Glu Ile Ile Arg Asp Thr Thr Arg Gly Val Met Val Val Gln Gly Gly  
 85 90 95  
 Pro Gly Thr Gly Lys Thr Ala Val Ala Leu His Arg Val Ala Tyr Leu  
 100 105 110  
 Leu Tyr Thr Trp Arg Asp Gln Leu Ala Lys Ser Gly Val Leu Ile Ile  
 115 120 125  
 Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu Pro Glu  
 130 135 140  
 Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu Phe Pro  
 145 150 155 160  
 Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu Ile Lys  
 165 170 175

Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys Ala Tyr  
 180 185 190  
 Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly Ile Glu  
 195 200 205  
 Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg Ala Arg  
 210 215 220  
 Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg Glu His  
 225 230 235 240  
 Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly Ala Asp  
 245 250 255  
 Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp Gln Leu  
 260 265 270  
 His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile Asp Asp  
 275 280 285  
 Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu Leu Ile  
 290 295 300  
 Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu Glu Thr  
 305 310 315 320  
 Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro Ser Asp  
 325 330 335  
 Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro Asp Pro  
 340 345 350  
 Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln Ile Asp  
 355 360 365  
 Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser Ser Asp  
 370 375 380  
 Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp Val Ile  
 385 390 395 400  
 Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn Arg Thr  
 405 410 415  
 Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly His Val  
 420 425 430  
 Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg Met Val  
 435 440 445  
 Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp Ile Ala  
 450 455 460  
 Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser Leu Trp  
 465 470 475 480  
 Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val Asn Tyr  
 485 490 495  
 Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu Thr Gln

500	505	510
Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser Gly Arg 515	520	525
Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val Met Asp 530	535	540
Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile Ser Ser 545	550	555 560
Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile Lys Gly 565	570	575
Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile Val Glu 580	585	590
Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr Arg Ala 595	600	605
Thr Gln Ser Leu Thr Ile Leu Gly Glu 610	615	

<210> 65  
 <211> 1496  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1473)  
 <223> FRXA01876

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atc att ggc ccg aac aag aca ttt ttg gag tat att tct cac gtt ttg	48
Ile Ile Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu	
1 5 10 15	
cct gaa ctc ggc gag act ggc gtg gtg ttg tcc acc gtc ggt gag ctg	96
Pro Glu Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu	
20 25 30	
ttc ccc ggt atc gtc cca acg ggt tcc gag gac act ttg acc agg gaa	144
Phe Pro Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu	
35 40 45	
att aag ggc agc gag gaa atg gcc agc att ttg gcc gag gca gtc aag	192
Ile Lys Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys	
50 55 60	
gcg tat caa gtg ctg cca gag aag acc atc gtg gtc tct gtt gat ggc	240
Ala Tyr Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly	
65 70 75 80	
atc gag att tcc att gat gag aaa acg gtg gca aaa tcc cgc acc cga	288
Ile Glu Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg	
85 90 95	
gct cgt cgt gcc agg cag tcg cac aat tcc gca cgc cca att ttc cgc	336
Ala Arg Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg	

100	105	110	
gag cat tta gtc gaa caa ctc gcg cac caa atg gct caa acg atc ggc			384
Glu His Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly			
115	120	125	
gcg gat ccg ctg ggc ggc aaa aac ctg ctg tca gcc gcc gac atc gat			432
Ala Asp Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp			
130	135	140	
cag ctg cac gat gat ttg ctt gac gac gcg gcc ctc cag tcc gtc atc			480
Gln Leu His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile			
145	150	155	160
gac gat ttc tgg ccg gag ctc cgg cct cag gac gtc ctg cat gat ctg			528
Asp Asp Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu			
165	170	175	
ttg att tcc gaa gag cgc att aat gtt gct gcc gcg ggg tat gac gag			576
Leu Ile Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu			
180	185	190	
gaa act aag tct gct ttg ctg cgt ggt gaa ctc gat ccg tgg gca cca			624
Glu Thr Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro			
195	200	205	
tcg gac gct gca ttg ctt gat gag tta gcc ctg ctc atc ggt ctt ccc			672
Ser Asp Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro			
210	215	220	
gat cca gag gag gca cgg gag aag gct gag gcc aaa tgg cgc gag cag			720
Asp Pro Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln			
225	230	235	240
atc gat gac gct cag gaa gtc ctg gac gtt ctt agt tca tca cag tca			768
Ile Asp Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser			
245	250	255	
tcg gat att gat gat gtc acg gaa gct gaa gtt ctc tcc gct ttc gac			816
Ser Asp Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp			
260	265	270	
gtc atc gat gcg gaa act ttg gca caa cgc caa act gtc acg gat aat			864
Val Ile Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn			
275	280	285	
cgc acc act gcg gaa cgt gca cag gcg gat cat aag tgg gca tat ggt			912
Arg Thr Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly			
290	295	300	
cac gtg att gta gat gaa gct cag gag ctc agt ccg atg gaa tgg cgc			960
His Val Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg			
305	310	315	320
atg gtg ttt cgc cgt agc cct tcg cga tgg atg acc ctt gtg ggc gat			1008
Met Val Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp			
325	330	335	
att gca caa act ggt tgg cct gcc ggc gtt gac gat tgg gca gaa tca			1056
Ile Ala Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser			
340	345	350	

ctg tgg ccc ttc gtc gaa aag cgt ttc agg cac cac gag ctc acc gtt 1104  
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val  
 355 360 365  
  
 aac tac cgc acc ccg gcc gag atc atg tcg gtg gcc aat gag ctt ttg 1152  
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu  
 370 375 380  
  
 acg cag atc aat cct gat att gcg ccg gca atg gcg atc cgc gaa tct 1200  
 Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser  
 385 390 395 400  
  
 ggt cga gag gta gtg aac ttg ccg ctt gat gcc gat ttg tcg gca gtg 1248  
 Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val  
 405 410 415  
  
 atg gat agt ttg cgt gag gag gat tca cag cgc acc atc gcg gtg att 1296  
 Met Asp Ser Leu Arg Glu Glu Asp Ser Gln Arg Thr Ile Ala Val Ile  
 420 425 430  
  
 tct tcg cgc cgc cac cac gaa agc gat ttc tac ctg gtc gat gac atc 1344  
 Ser Ser Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile  
 435 440 445  
  
 aag ggc tta gag ttt gac cac gtc atc gtg gtg gat cct gcg gga atc 1392  
 Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile  
 450 455 460  
  
 gtt gaa gaa tcc ccc cag gga ttg caa gac ctc tac gtt gcg gtc act 1440  
 Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr  
 465 470 475 480  
  
 cgt gca acg cag agc ctc acc att tta ggt gag tagcagggtta tgagctcagg 1493  
 Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu  
 485 490  
  
 gcc 1496

&lt;210&gt; 66

&lt;211&gt; 491

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 66

Ile Ile Gly Pro Asn Lys Thr Phe Leu Glu Tyr Ile Ser His Val Leu  
 1 5 10 15

Pro Glu Leu Gly Glu Thr Gly Val Val Leu Ser Thr Val Gly Glu Leu  
 20 25 30

Phe Pro Gly Ile Val Pro Thr Gly Ser Glu Asp Thr Leu Thr Arg Glu  
 35 40 45

Ile Lys Gly Ser Glu Glu Met Ala Ser Ile Leu Ala Glu Ala Val Lys  
 50 55 60

Ala Tyr Gln Val Leu Pro Glu Lys Thr Ile Val Val Ser Val Asp Gly  
 65 70 75 80

Ile Glu Ile Ser Ile Asp Glu Lys Thr Val Ala Lys Ser Arg Thr Arg  
                     85                    90                    95  
 Ala Arg Arg Ala Arg Gln Ser His Asn Ser Ala Arg Pro Ile Phe Arg  
                     100                    105                    110  
 Glu His Leu Val Glu Gln Leu Ala His Gln Met Ala Gln Thr Ile Gly  
                     115                    120                    125  
 Ala Asp Pro Leu Gly Gly Lys Asn Leu Leu Ser Ala Ala Asp Ile Asp  
                     130                    135                    140  
 Gln Leu His Asp Asp Leu Leu Asp Asp Ala Ala Leu Gln Ser Val Ile  
                     145                    150                    155                    160  
 Asp Asp Phe Trp Pro Glu Leu Arg Pro Gln Asp Val Leu His Asp Leu  
                     165                    170                    175  
 Leu Ile Ser Glu Glu Arg Ile Asn Val Ala Ala Ala Gly Tyr Asp Glu  
                     180                    185                    190  
 Glu Thr Lys Ser Ala Leu Leu Arg Gly Glu Leu Asp Pro Trp Ala Pro  
                     195                    200                    205  
 Ser Asp Ala Ala Leu Leu Asp Glu Leu Ala Leu Leu Ile Gly Leu Pro  
                     210                    215                    220  
 Asp Pro Glu Glu Ala Arg Glu Lys Ala Glu Ala Lys Trp Arg Glu Gln  
                     225                    230                    235                    240  
 Ile Asp Asp Ala Gln Glu Val Leu Asp Val Leu Ser Ser Ser Gln Ser  
                     245                    250                    255  
 Ser Asp Ile Asp Asp Val Thr Glu Ala Glu Val Leu Ser Ala Phe Asp  
                     260                    265                    270  
 Val Ile Asp Ala Glu Thr Leu Ala Gln Arg Gln Thr Val Thr Asp Asn  
                     275                    280                    285  
 Arg Thr Thr Ala Glu Arg Ala Gln Ala Asp His Lys Trp Ala Tyr Gly  
                     290                    295                    300  
 His Val Ile Val Asp Glu Ala Gln Glu Leu Ser Pro Met Glu Trp Arg  
                     305                    310                    315                    320  
 Met Val Phe Arg Arg Ser Pro Ser Arg Trp Met Thr Leu Val Gly Asp  
                     325                    330                    335  
 Ile Ala Gln Thr Gly Trp Pro Ala Gly Val Asp Asp Trp Ala Glu Ser  
                     340                    345                    350  
 Leu Trp Pro Phe Val Glu Lys Arg Phe Arg His His Glu Leu Thr Val  
                     355                    360                    365  
 Asn Tyr Arg Thr Pro Ala Glu Ile Met Ser Val Ala Asn Glu Leu Leu  
                     370                    375                    380  
 Thr Gln Ile Asn Pro Asp Ile Ala Pro Ala Met Ala Ile Arg Glu Ser  
                     385                    390                    395                    400  
 Gly Arg Glu Val Val Asn Leu Pro Leu Asp Ala Asp Leu Ser Ala Val

405	410	415
Met Asp Ser Leu Arg Glu Glu Asp	Ser Gln Arg Thr Ile Ala Val Ile	
420	425	430
Ser Ser Arg Arg His His Glu Ser Asp Phe Tyr Leu Val Asp Asp Ile		
435	440	445
Lys Gly Leu Glu Phe Asp His Val Ile Val Val Asp Pro Ala Gly Ile		
450	455	460
Val Glu Glu Ser Pro Gln Gly Leu Gln Asp Leu Tyr Val Ala Val Thr		
465	470	475
Arg Ala Thr Gln Ser Leu Thr Ile Leu Gly Glu		
485	490	

<210> 67  
 <211> 1653  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1630)  
 <223> RXA00544

<400> 67  
 agttggaaat cacaaagcct cgggggtgggg gctttcgtgc cttctggaaa ggcctatgca 60  
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 Met Ala Thr Asp Thr  
 1 5  
 cac gcc gca agt ttt gat gat gac tac gta cct cca cag gag cca agc 163  
 His Ala Ala Ser Phe Asp Asp Asp Tyr Val Pro Pro Gln Glu Pro Ser  
 10 15 20  
 gat tcc ttc gcg gat gac gca cac gta gat gtc cct gct ccg gcg ttt 211  
 Asp Ser Phe Ala Asp Asp Ala His Val Asp Val Pro Ala Pro Ala Phe  
 25 30 35  
 gaa gat ttc tcc ccg gcc cag gcc ttt ggt cag gga act agg gga gga 259  
 Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln Gly Thr Arg Gly Gly  
 40 45 50  
 gac tct cag gcc ttc aag aag agg ggt cgc aag gac gag tcc cgt gaa 307  
 Asp Ser Gln Gly Phe Lys Lys Arg Gly Arg Lys Asp Glu Ser Arg Glu  
 55 60 65  
 tac cga gac ttc cgc caa cct ccc tat gac aat gac gct gag atg ggc 355  
 Tyr Arg Asp Phe Arg Gln Pro Pro Tyr Asp Asn Asp Ala Glu Met Gly  
 70 75 80 85  
 gtg ctg ggc gcg atg ctg ctc agt ccg acc acg gtc atc gac att ctg 403  
 Val Leu Gly Ala Met Leu Leu Ser Pro Thr Thr Val Ile Asp Ile Leu  
 90 95 100  
 gat atc ctc acc cca gaa gac ttc tac agg ccg tcc cac cag ctg att 451  
 Asp Ile Leu Thr Pro Glu Asp Phe Tyr Arg Pro Ser His Gln Leu Ile

105	110	115	
ttc cag gcg atc att gac ctg ttc agt gac aac cgt gat att gac ccc			499
Phe Gln Ala Ile Ile Asp Leu Phe Ser Asp Asn Arg Asp Ile Asp Pro			
120	125	130	
gtg att gtc tcc ggt cgc ctc gat cga acc aac gat ctg gac cgc gtc			547
Val Ile Val Ser Gly Arg Leu Asp Arg Thr Asn Asp Leu Asp Arg Val			
135	140	145	
ggc ggt ggc gcg tac ctc cac gac ctc atc cag tcc gtt ccc acc gca			595
Gly Gly Gly Ala Tyr Leu His Asp Leu Ile Gln Ser Val Pro Thr Ala			
150	155	160	165
gcc aac gcg cgc tac tat gcg gaa atc gtt tcg gaa aag gca gtg ctt			643
Ala Asn Ala Arg Tyr Tyr Ala Glu Ile Val Ser Glu Lys Ala Val Leu			
170	175	180	
cgc agg ctt gtc gac gcc ggc acc cgc gtc gtc cag ctc ggc tac gag			691
Arg Arg Leu Val Asp Ala Gly Thr Arg Val Val Gln Leu Gly Tyr Glu			
185	190	195	
ggc gat gaa ggc gcc gaa att gac gcg gtg att gac cgc gcg cag caa			739
Gly Asp Glu Gly Ala Glu Ile Asp Ala Val Ile Asp Arg Ala Gln Gln			
200	205	210	
gaa gtc ttc gcc gtt tcc caa aag aat cag agc gaa gac tat gca gtc			787
Glu Val Phe Ala Val Ser Gln Lys Asn Gln Ser Glu Asp Tyr Ala Val			
215	220	225	
cta gcc gat att ctg gat gaa acc atg gct gag ctg gaa atg ctc aac			835
Leu Ala Asp Ile Leu Asp Glu Thr Met Ala Glu Leu Glu Met Leu Asn			
230	235	240	245
gac ggc ggc atc gcc acc ggt att cca acc ggc ttc aaa gat ctc gat			883
Asp Gly Gly Ile Ala Thr Gly Ile Pro Thr Gly Phe Lys Asp Leu Asp			
250	255	260	
gac ctc acc aac ggt ctg cgc ggt ggc cag atg atc atc gtt gca gct			931
Asp Leu Thr Asn Gly Leu Arg Gly Gly Gln Met Ile Ile Val Ala Ala			
265	270	275	
cgt cct ggt gtg ggt aaa tcc acc atc gcc ttg gac ttc atg cgt tcg			979
Arg Pro Gly Val Gly Lys Ser Thr Ile Ala Leu Asp Phe Met Arg Ser			
280	285	290	
gca tcc atc aag aac aac atg gcg tct gtc att ttc tcc ttg gaa atg			1027
Ala Ser Ile Lys Asn Asn Met Ala Ser Val Ile Phe Ser Leu Glu Met			
295	300	305	
tcc aag tca gag atc gtg atg cgt ttg ctc tct gca gaa aca gaa atc			1075
Ser Lys Ser Glu Ile Val Met Arg Leu Leu Ser Ala Glu Thr Glu Ile			
310	315	320	325
cgc ctg gct gat atg cgt ggt gga aag atg gat gaa acc gca tgg gaa			1123
Arg Leu Ala Asp Met Arg Gly Gly Lys Met Asp Glu Thr Ala Trp Glu			
330	335	340	
aag atg gtg cag aag tta gac aag gta gcc cag gca cct ttg ttc atc			1171
Lys Met Val Gln Lys Leu Asp Lys Val Ala Gln Ala Pro Leu Phe Ile			
345	350	355	



gat gac tcc gcg aac ctc acc atg atg gaa atc cgc tcc aag gcc aga 1219  
Asp Asp Ser Ala Asn Leu Thr Met Met Glu Ile Arg Ser Lys Ala Arg  
360 365 370  
aag ctg aag cag aag cat gat ctg aaa atg atc gtg gtg gac tac ctc 1267  
Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile Val Val Asp Tyr Leu  
375 380 385  
cag ctg atg agc tcc ggt aaa cgc gtg gaa tcc cgt cag cag gaa gtc 1315  
Gln Leu Met Ser Ser Gly Lys Arg Val Glu Ser Arg Gln Gln Glu Val  
390 395 400 405  
tcc gag ttc tcc cgt cag ctc aag ctg ctg gcc aaa gaa ctc gat gtg 1363  
Ser Glu Phe Ser Arg Gln Leu Lys Leu Leu Ala Lys Glu Leu Asp Val  
410 415 420  
ccg ttg atc gcg att tcc cag ctg aac cgt gga cct gaa tcc cgt acc 1411  
Pro Leu Ile Ala Ile Ser Gln Leu Asn Arg Gly Pro Glu Ser Arg Thr  
425 430 435  
gat aag cga cca cag ctt gct gac ctt cgt gaa tcc ggc tcg ctg gag 1459  
Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Ser Leu Glu  
440 445 450  
cag gac gcc gat atc gtt atg ctg cta tac cgc cca gac tcc cag gat 1507  
Gln Asp Ala Asp Ile Val Met Leu Leu Tyr Arg Pro Asp Ser Gln Asp  
455 460 465  
aag gac gac gag cgc gcg ggc gag gcc gac atc att ttg gct aag cac 1555  
Lys Asp Asp Glu Arg Ala Gly Glu Ala Asp Ile Ile Leu Ala Lys His  
470 475 480 485  
cgt ggt ggc ccg atc gat acc gtc cag gtg gcg cac cag ctg cac tat 1603  
Arg Gly Gly Pro Ile Asp Thr Val Gln Val Ala His Gln Leu His Tyr  
490 495 500  
tca cgt ttt gtg gac atg gcg cgc ggt taagaaaagt tcatttttct 1650  
Ser Arg Phe Val Asp Met Ala Arg Gly  
505 510  
aaa 1653

&lt;210&gt; 68

&lt;211&gt; 510

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 68

Met Ala Thr Asp Thr His Ala Ala Ser Phe Asp Asp Asp Tyr Val Pro  
1 5 10 15

Pro Gln Glu Pro Ser Asp Ser Phe Ala Asp Asp Ala His Val Asp Val  
20 25 30

Pro Ala Pro Ala Phe Glu Asp Phe Ser Pro Ala Gln Ala Phe Gly Gln  
35 40 45

Gly Thr Arg Gly Gly Asp Ser Gln Gly Phe Lys Lys Arg Gly Arg Lys  
50 55 60

Asp Glu Ser Arg Glu Tyr Arg Asp Phe Arg Gln Pro Pro Tyr Asp Asn  
 65 70 75 80  
 Asp Ala Glu Met Gly Val Leu Gly Ala Met Leu Leu Ser Pro Thr Thr  
 85 90 95  
 Val Ile Asp Ile Leu Asp Ile Leu Thr Pro Glu Asp Phe Tyr Arg Pro  
 100 105 110  
 Ser His Gln Leu Ile Phe Gln Ala Ile Ile Asp Leu Phe Ser Asp Asn  
 115 120 125  
 Arg Asp Ile Asp Pro Val Ile Val Ser Gly Arg Leu Asp Arg Thr Asn  
 130 135 140  
 Asp Leu Asp Arg Val Gly Gly Gly Ala Tyr Leu His Asp Leu Ile Gln  
 145 150 155 160  
 Ser Val Pro Thr Ala Ala Asn Ala Arg Tyr Tyr Ala Glu Ile Val Ser  
 165 170 175  
 Glu Lys Ala Val Leu Arg Arg Leu Val Asp Ala Gly Thr Arg Val Val  
 180 185 190  
 Gln Leu Gly Tyr Glu Gly Asp Glu Gly Ala Glu Ile Asp Ala Val Ile  
 195 200 205  
 Asp Arg Ala Gln Gln Glu Val Phe Ala Val Ser Gln Lys Asn Gln Ser  
 210 215 220  
 Glu Asp Tyr Ala Val Leu Ala Asp Ile Leu Asp Glu Thr Met Ala Glu  
 225 230 235 240  
 Leu Glu Met Leu Asn Asp Gly Gly Ile Ala Thr Gly Ile Pro Thr Gly  
 245 250 255  
 Phe Lys Asp Leu Asp Asp Leu Thr Asn Gly Leu Arg Gly Gly Gln Met  
 260 265 270  
 Ile Ile Val Ala Ala Arg Pro Gly Val Gly Lys Ser Thr Ile Ala Leu  
 275 280 285  
 Asp Phe Met Arg Ser Ala Ser Ile Lys Asn Asn Met Ala Ser Val Ile  
 290 295 300  
 Phe Ser Leu Glu Met Ser Lys Ser Glu Ile Val Met Arg Leu Leu Ser  
 305 310 315 320  
 Ala Glu Thr Glu Ile Arg Leu Ala Asp Met Arg Gly Gly Lys Met Asp  
 325 330 335  
 Glu Thr Ala Trp Glu Lys Met Val Gln Lys Leu Asp Lys Val Ala Gln  
 340 345 350  
 Ala Pro Leu Phe Ile Asp Asp Ser Ala Asn Leu Thr Met Met Glu Ile  
 355 360 365  
 Arg Ser Lys Ala Arg Lys Leu Lys Gln Lys His Asp Leu Lys Met Ile  
 370 375 380

Val Val Asp Tyr Leu Gln Leu Met Ser Ser Gly Lys Arg Val Glu Ser  
 385 390 395 400

Arg Gln Gln Glu Val Ser Glu Phe Ser Arg Gln Leu Lys Leu Leu Ala  
 405 410 415

Lys Glu Leu Asp Val Pro Leu Ile Ala Ile Ser Gln Leu Asn Arg Gly  
 420 425 430

Pro Glu Ser Arg Thr Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu  
 435 440 445

Ser Gly Ser Leu Glu Gln Asp Ala Asp Ile Val Met Leu Leu Tyr Arg  
 450 455 460

Pro Asp Ser Gln Asp Lys Asp Asp Glu Arg Ala Gly Glu Ala Asp Ile  
 465 470 475 480

Ile Leu Ala Lys His Arg Gly Gly Pro Ile Asp Thr Val Gln Val Ala  
 485 490 495

His Gln Leu His Tyr Ser Arg Phe Val Asp Met Ala Arg Gly  
 500 505 510

&lt;210&gt; 69

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(421)

&lt;223&gt; RXA01866

&lt;400&gt; 69

accagatag tctgatcaag gaagacgctg gggcggttacg aagaagcctt tccccgacaag 60

tggattaaag ccagcctgat tcttcgatct cagctaccac ttg aaa ccc ggc cac 115  
 Leu Lys Pro Gly His  
 1 5

cgc gat gac ggc gtc aca gtc ctc atc ccc att cca gtg ctg ggt gga 163  
 Arg Asp Asp Gly Val Thr Val Leu Ile Pro Ile Pro Val Leu Gly Gly  
 10 15 20

ctt gat acc gaa ggc ttc gat tgg cta gtt cca ggc tta agg ctt gat 211  
 Leu Asp Thr Glu Gly Phe Asp Trp Leu Val Pro Gly Leu Arg Leu Asp  
 25 30 35

ttg gtg acc gag tta atc cgc acc atg cct aag gct tta cga cgc acc 259  
 Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys Ala Leu Arg Arg Thr  
 40 45 50

gtt gtc cct gcc ccg gat ttc gcc gag cgg gtc ttg ccg tta ctg cgt 307  
 Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val Leu Pro Leu Leu Arg  
 55 60 65

ccc tac atg aca cca ctg acc acc caa ctt gcc gat gca ctc cat acc 355  
 Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala Asp Ala Leu His Thr  
 70 75 80 85

ctg ggc ggc caa gga atc aac gcc tct gat ttc gat cct gcc aaa ctc 403  
 Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe Asp Pro Ala Lys Leu  
                   90                  95                  100

ccc gat cac ctg cgc att 421  
 Pro Asp His Leu Arg Ile  
                   105

<210> 70

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

Leu Lys Pro Gly His Arg Asp Asp Gly Val Thr Val Leu Ile Pro Ile  
   1                  5                  10                  15

Pro Val Leu Gly Gly Leu Asp Thr Glu Gly Phe Asp Trp Leu Val Pro  
                   20                  25                  30

Gly Leu Arg Leu Asp Leu Val Thr Glu Leu Ile Arg Thr Met Pro Lys  
                   35                  40                  45

Ala Leu Arg Arg Thr Val Val Pro Ala Pro Asp Phe Ala Glu Arg Val  
                   50                  55                  60

Leu Pro Leu Leu Arg Pro Tyr Met Thr Pro Leu Thr Thr Gln Leu Ala  
   65                  70                  75                  80

Asp Ala Leu His Thr Leu Gly Gly Gln Gly Ile Asn Ala Ser Asp Phe  
                   85                  90                  95

Asp Pro Ala Lys Leu Pro Asp His Leu Arg Ile  
                   100                  105

<210> 71

<211> 515

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(492)

<223> RXA01867

<400> 71

cca gag tgg gtg gaa aaa gca gcc ggc cca ttg ctc aag cac caa tac 48  
 Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu Leu Lys His Gln Tyr  
   1                  5                  10                  15

tct gaa ccg tat tgg tcc tca aag cgt ggc gct gcc atg gtg cac cgc 96  
 Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Ala Ala Met Val His Arg  
                   20                  25                  30

aaa tca acg ctc ttc ggt gtg aca att gtt gcc gtc aag gta gtt ccc 144  
 Lys Ser Thr Leu Phe Gly Val Thr Ile Val Ala Val Lys Val Val Pro  
                   35                  40                  45

tac cac acg gtt gat ccc gtg gct gcg cgc gat atg ttc atc cgc cat 192  
 Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His  
 50 55 60  
 gcc ctc atc gaa ggc gat tgg tcc act cac cac cgc ttc tac cac gac 240  
 Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp  
 65 70 75 80  
 aac gtg gcc aaa ttg gag gca atc gga gaa ctt gaa gcc aag gcg cgt 288  
 Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg  
 85 90 95  
 cgc cgc gac atc gtc gta gat gaa gac acc ctg ttt gat ttc tac gat 336  
 Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp  
 100 105 110  
 gcc aag ctt cca agc aac gcc acc acc acc cgc aat ttc gat tcc tgg 384  
 Ala Lys Leu Pro Ser Asn Ala Thr Thr Thr Arg Asn Phe Asp Ser Trp  
 115 120 125  
 tgg aag aaa aca tca cgc gtc aca cca gat ctt ctc gat ttc gac cca 432  
 Trp Lys Lys Thr Ser Arg Val Thr Pro Asp Leu Leu Asp Phe Asp Pro  
 130 135 140  
 gat agt ctg atc aag gaa gac gct ggg gcg tta cga aga agc ctt tcc 480  
 Asp Ser Leu Ile Lys Glu Asp Ala Gly Ala Leu Arg Arg Ser Leu Ser  
 145 150 155 160  
 cga caa gtg gat taaagccagc ctgattcttc gat 515  
 Arg Gln Val Asp

<210> 72  
 <211> 164  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 72  
 Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu Leu Lys His Gln Tyr  
 1 5 10 15  
 Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Ala Ala Met Val His Arg  
 20 25 30  
 Lys Ser Thr Leu Phe Gly Val Thr Ile Val Ala Val Lys Val Val Pro  
 35 40 45  
 Tyr His Thr Val Asp Pro Val Ala Ala Arg Asp Met Phe Ile Arg His  
 50 55 60  
 Ala Leu Ile Glu Gly Asp Trp Ser Thr His His Arg Phe Tyr His Asp  
 65 70 75 80  
 Asn Val Ala Lys Leu Glu Ala Ile Gly Glu Leu Glu Ala Lys Ala Arg  
 85 90 95  
 Arg Arg Asp Ile Val Val Asp Glu Asp Thr Leu Phe Asp Phe Tyr Asp  
 100 105 110  
 Ala Lys Leu Pro Ser Asn Ala Thr Thr Thr Arg Asn Phe Asp Ser Trp

115 120 125

Trp Lys Lys Thr Ser Arg Val Thr Pro Asp Leu Leu Asp Phe Asp Pro  
 130 135 140

Asp Ser Leu Ile Lys Glu Asp Ala Gly Ala Leu Arg Arg Ser Leu Ser  
 145 150 155 160

Arg Gln Val Asp

<210> 73  
 <211> 2358  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2335)  
 <223> RXN03166

<400> 73  
 ccctccctat agtgattagt tcacctccag actacctggc accgcgtggg ctgctttcac 60  
 ttggactttc ggcaaagaca agtagaatta gcccctagtc atg act act tct gaa 115  
 Met Thr Thr Ser Glu  
 1 5

act gcc cca tca aag gct tcc ctg tat gaa ctt tta gag ggc gta tcc 163  
 Thr Ala Pro Ser Lys Ala Ser Leu Tyr Glu Leu Leu Glu Gly Val Ser  
 10 15 20

ctc tcc gac gag cgc acg ttt agg cgc cga ctg tcc aaa gcc cgc gcg 211  
 Leu Ser Asp Glu Arg Thr Phe Arg Arg Arg Leu Ser Lys Ala Arg Ala  
 25 30 35

ccc aag gcg ctt ggt gcg att aag gct gat atc gat aag gca cgc ttg 259  
 Pro Lys Ala Leu Gly Ala Ile Lys Ala Asp Ile Asp Lys Ala Arg Leu  
 40 45 50

ctt atc gac gaa aag agc cag tta att ccg tct atc acc tac cca gaa 307  
 Leu Ile Asp Glu Lys Ser Gln Leu Ile Pro Ser Ile Thr Tyr Pro Glu  
 55 60 65

aac ctt ccg gtg agt tcc cgg cgc gat gat atc gcc gag gct atc cgt 355  
 Asn Leu Pro Val Ser Ser Arg Arg Asp Asp Ile Ala Glu Ala Ile Arg  
 70 75 80 85

gat aat cag gtg gtt att atc gcc ggt gag act ggt tcg ggt aag acg 403  
 Asp Asn Gln Val Val Ile Ile Ala Gly Glu Thr Gly Ser Gly Lys Thr  
 90 95 100

act cag att cct aag att tgt ttg gac cta ggc cgt ggc cgg cgt ggg 451  
 Thr Gln Ile Pro Lys Ile Cys Leu Asp Leu Gly Arg Gly Arg Arg Gly  
 105 110 115

ctc att ggc cac aca cag cca cgt cga tta gca gct agg acc gtc gcc 499  
 Leu Ile Gly His Thr Gln Pro Arg Arg Leu Ala Ala Arg Thr Val Ala  
 120 125 130

gag cgc atc gcc gat gaa ttg ggg caa gac atc ggc gaa tcg gtg ggt 547  
 Glu Arg Ile Ala Asp Glu Leu Gly Gln Asp Ile Gly Glu Ser Val Gly  
 135 140 145

tat gcg att cgt ttt gat gat cga gtt tcc tcg cat aca tcc gtg aag 595  
 Tyr Ala Ile Arg Phe Asp Asp Arg Val Ser Ser His Thr Ser Val Lys  
 150 155 160 165

ttg atg acg gat ggt att ttg ctt gct gaa atg cag cgg gat cgt ttc 643  
 Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met Gln Arg Asp Arg Phe  
 170 175 180

ctc aat gcg tat gac acc atc atc atc gat gag gcg cat gaa cgt tcc 691  
 Leu Asn Ala Tyr Asp Thr Ile Ile Ile Asp Glu Ala His Glu Arg Ser  
 185 190 195

ctc aac att gac ttc att ctg ggt tat ttg cgc cag ttg ttg cct aag 739  
 Leu Asn Ile Asp Phe Ile Leu Gly Tyr Leu Arg Gln Leu Leu Pro Lys  
 200 205 210

cgc cct gat ctt aaa gtc att att acc tcc gca acg att gac cct gag 787  
 Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala Thr Ile Asp Pro Glu  
 215 220 225

cgt ttc gcg gag cac ttt gct gat gct tct gga aaa cca gca cca att 835  
 Arg Phe Ala Glu His Phe Ala Asp Ala Ser Gly Lys Pro Ala Pro Ile  
 230 235 240 245

atc gag gtc tcc ggc cgc acc ttc ccg gta gag atc cgt tat cgc cca 883  
 Ile Glu Val Ser Gly Arg Thr Phe Pro Val Glu Ile Arg Tyr Arg Pro  
 250 255 260

ctt gag gta tta gac ggc gat aaa att atc gat acc gat ccc ctt gac 931  
 Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp Thr Asp Pro Leu Asp  
 265 270 275

ggc ttg tgt tct gct ttg gaa gag ctc atg gct gaa ggc gac ggc gat 979  
 Gly Leu Cys Ser Ala Leu Glu Glu Leu Met Ala Glu Gly Asp Gly Asp  
 280 285 290

atc ctc tgc ttc ttt gcc ggt gag cgt gat atc cgc gat gcc atg gag 1027  
 Ile Leu Cys Phe Phe Ala Gly Glu Arg Asp Ile Arg Asp Ala Met Glu  
 295 300 305

gca atc gag gcc cga cgc tgg aaa ggt gtg gaa gtc act ccc ctg ttt 1075  
 Ala Ile Glu Ala Arg Arg Trp Lys Gly Val Glu Val Thr Pro Leu Phe  
 310 315 320 325

ggc cgc ctg tcc aac cag gag cag cac cgt gta ttt agc ccg cac tct 1123  
 Gly Arg Leu Ser Asn Gln Glu Gln His Arg Val Phe Ser Pro His Ser  
 330 335 340

ggt cga cgc att gtg ctt tcc acc aat atc gca gag aca tcc ctg acg 1171  
 Gly Arg Arg Ile Val Leu Ser Thr Asn Ile Ala Glu Thr Ser Leu Thr  
 345 350 355

gtt ccg ggc att cac tac gtg gtt gat acc ggt acg gcg cgt atc tct 1219  
 Val Pro Gly Ile His Tyr Val Val Asp Thr Gly Thr Ala Arg Ile Ser  
 360 365 370

cgt tat tca gtg cgc acc aag gtg cag cgc ctt ccg att gag aac att 1267

Arg Tyr Ser Val Arg Thr Lys Val Gln Arg Leu Pro Ile Glu Asn Ile	
375 380 385	
tcc cag gcc agc gca aac cag cgt tct ggt cgt tgt ggt cgt gtc gca	1315
Ser Gln Ala Ser Ala Asn Gln Arg Ser Gly Arg Cys Gly Arg Val Ala	
390 395 400 405	
gac ggt att gcg att cgt ttg tat tcc gaa gat gat ttc aac tct cgc	1363
Asp Gly Ile Ala Ile Arg Leu Tyr Ser Glu Asp Asp Phe Asn Ser Arg	
410 415 420	
cca gag ttc acc gat ccg gaa att ctg cgc acc aac ttg gcg agc gtt	1411
Pro Glu Phe Thr Asp Pro Glu Ile Leu Arg Thr Asn Leu Ala Ser Val	
425 430 435	
att ttg cgc atg gcg tcg ctg cgt ctt ggc gat att aat gat ttc ccc	1459
Ile Leu Arg Met Ala Ser Leu Arg Leu Gly Asp Ile Asn Asp Phe Pro	
440 445 450	
ttc gtc caa gcc cca gag caa cgc tcc atc agg gat ggt att ttg ctg	1507
Phe Val Gln Ala Pro Glu Gln Arg Ser Ile Arg Asp Gly Ile Leu Leu	
455 460 465	
ctc cac gag ttg ggc gca ctc acc gac gac acc caa gcc gat ggt tca	1555
Leu His Glu Leu Gly Ala Leu Thr Asp Asp Thr Gln Ala Asp Gly Ser	
470 475 480 485	
ccg cag ctc acc cag atc ggt aaa gac tta gcc aac atc cca gtc gat	1603
Pro Gln Leu Thr Gln Ile Gly Lys Asp Leu Ala Asn Ile Pro Val Asp	
490 495 500	
ccc cgc atg gcc cgc atg ctc gta gaa gcc aac act cta ggc tgc ctg	1651
Pro Arg Met Ala Arg Met Leu Val Glu Ala Asn Thr Leu Gly Cys Leu	
505 510 515	
cat tct gtc atg gtc att gtg tcc gct ctg acg att caa gat gtt cgc	1699
His Ser Val Met Val Ile Val Ser Ala Leu Thr Ile Gln Asp Val Arg	
520 525 530	
gaa cgc ccc ctg gaa ttc caa gcc caa gct gat caa gcc cac gct agg	1747
Glu Arg Pro Leu Glu Phe Gln Ala Gln Ala Asp Gln Ala His Ala Arg	
535 540 545	
ttc aag gac acc acc tca gat ttc tta ggc ttt ttg aaa ctg tgg gag	1795
Phe Lys Asp Thr Thr Ser Asp Phe Leu Gly Phe Leu Lys Leu Trp Glu	
550 555 560 565	
tac atc gcc gat cag cgc aat caa agc agc ggc aat tcc ttc cgc aag	1843
Tyr Ile Ala Asp Gln Arg Asn Gln Ser Ser Gly Asn Ser Phe Arg Lys	
570 575 580	
cag atg aaa aaa gaa ttc ctc cac tac atg cgt atc cgc gag tgg tgg	1891
Gln Met Lys Lys Glu Phe Leu His Tyr Met Arg Ile Arg Glu Trp Trp	
585 590 595	
gat ttg gtg cgc caa tta gag cag att ggc cag caa ctt ggt tgg gca	1939
Asp Leu Val Arg Gln Leu Glu Gln Ile Gly Gln Gln Leu Gly Trp Ala	
600 605 610	
aag aag gag cag gtt gca ggc acc gcc agc cct gac atc att cac caa	1987
Lys Lys Glu Gln Val Ala Gly Thr Ala Ser Pro Asp Ile Ile His Gln	



615	620	625	
tcc ttg ctc acc ggt ctg ttc tcg caa atc ggt tcc cgt gat ggt gag			2035
Ser Leu Leu Thr Gly Leu Phe Ser Gln Ile Gly Ser Arg Asp Gly Glu			
630	635	640	645
agc aaa gaa ttc act gga gcc aga ggt acc aaa ttc ttg gtc ttt cct			2083
Ser Lys Glu Phe Thr Gly Ala Arg Gly Thr Lys Phe Leu Val Phe Pro			
650	655		660
ggg tct gcg cta acc aag aag ccg cca cag ttc atc atg gct ggc caa			2131
Gly Ser Ala Leu Thr Lys Lys Pro Pro Gln Phe Ile Met Ala Gly Gln			
665	670		675
ttg gta gaa acc tca cgt ttg tgg gct cgc gat gta gcc aag att gaa			2179
Leu Val Glu Thr Ser Arg Leu Trp Ala Arg Asp Val Ala Lys Ile Glu			
680	685		690
cca gag tgg gtg gaa aaa gca gcc ggc cca ttg ctc aag cac caa tac			2227
Pro Glu Trp Val Glu Lys Ala Ala Gly Pro Leu Leu Lys His Gln Tyr			
695	700		705
tct gaa ccg tat tgg tcc tca aag cgt ggc ggc tgc cat ggt gca ccg			2275
Ser Glu Pro Tyr Trp Ser Ser Lys Arg Gly Gly Cys His Gly Ala Pro			
710	715		720
caa atc aac gct ctt cgg tgt gac aat tgt tgc cgt caa ggt agt tcc			2323
Gln Ile Asn Ala Leu Arg Cys Asp Asn Cys Cys Arg Gln Gly Ser Ser			
730	735		740
cta cca cac ggt tgatcccggtg gctgcgcgcg ata			2358
Leu Pro His Gly			
745			

&lt;210&gt; 74

&lt;211&gt; 745

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 74

Met	Thr	Thr	Ser	Glu	Thr	Ala	Pro	Ser	Lys	Ala	Ser	Leu	Tyr	Glu	Leu
1				5					10					15	

Leu	Glu	Gly	Val	Ser	Leu	Ser	Asp	Glu	Arg	Thr	Phe	Arg	Arg	Arg	Leu
	20							25					30		

Ser	Lys	Ala	Arg	Ala	Pro	Lys	Ala	Leu	Gly	Ala	Ile	Lys	Ala	Asp	Ile
	35						40						45		

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 Gly Glu Ser Val Gly Tyr Ala Ile Arg Phe Asp Asp Arg Val Ser Ser  
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 His Thr Ser Val Lys Leu Met Thr Asp Gly Ile Leu Leu Ala Glu Met  
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 Gln Leu Leu Pro Lys Arg Pro Asp Leu Lys Val Ile Ile Thr Ser Ala  
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 Thr Ala Arg Ile Ser Arg Tyr Ser Val Arg Thr Lys Val Gln Arg Leu  
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 Pro Ile Glu Asn Ile Ser Gln Ala Ser Ala Asn Gln Arg Ser Gly Arg  
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 Cys Gly Arg Val Ala Asp Gly Ile Ala Ile Arg Leu Tyr Ser Glu Asp  
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 Asp Phe Asn Ser Arg Pro Glu Phe Thr Asp Pro Glu Ile Leu Arg Thr  
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Asn Leu Ala Ser Val Ile Leu Arg Met Ala Ser Leu Arg Leu Gly Asp  
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 690 695 700  
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Ser Lys Ala Ser Leu Tyr Glu Leu Leu Glu Gly Val Ser Leu Ser Asp	
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gag cgc acg ttt agg cgc cga ctg tcc aaa gcc cgc gcg ccc aag gcg	211
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Leu Gly Ala Ile Lys Ala Asp Ile Asp Lys Ala Arg Leu Leu Ile Asp	
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Val Val Ile Ile Ala Gly Glu Thr Gly Ser Gly Lys Thr Thr Gln Ile	
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Pro Lys Ile Cys Leu Asp Leu Gly Arg Gly Arg Arg Gly Leu Ile Gly	
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His Thr Gln Pro Arg Arg Leu Ala Ala Arg Thr Val Ala Glu Arg Ile	
	125                  130                  135
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Ala Asp Glu Leu Gly Gln Asp Ile Gly Glu Ser Val Gly Tyr Ala Ile	
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Arg Phe Asp Asp Arg Val Ser Ser His Thr Ser Val Lys Leu Met Thr	
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Asp Gly Ile Leu Leu Ala Glu Met Gln Arg Asp Arg Phe Leu Asn Ala	
	170                  175                  180

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Tyr Asp Thr Ile Ile Ile Asp Glu Ala His Glu Arg Ser Leu Asn Ile	
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Glu His Phe Ala Asp Ala Ser Gly Lys Pro Ala Pro Ile Ile Glu Val	
235 240 245	
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Ser Gly Arg Thr Phe Pro Val Glu Ile Arg Tyr Arg Pro Leu Glu Val	
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Leu Asp Gly Asp Lys Ile Ile Asp Thr Asp Pro Leu Asp Gly Leu Cys	
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Ser Ala Asn Gln Arg Ser Gly Arg Cys Gly Arg Val Ala Asp Gly Ile	
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 Ile Arg Tyr Arg Pro Leu Glu Val Leu Asp Gly Asp Lys Ile Ile Asp  
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200	205
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Ala Lys Gly Val Asp Trp Asp Phe Leu Asp His Met Ala Gln Lys Thr	225
215	220

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 His Asp Ala Val Thr His Ser Glu His Ser Ala Leu Ile Phe Val Pro  
 230 235 240 245

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cat aat aat gtt ttc cca ctt cat ggc caa ctc agc ccg acc gaa caa 931  
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Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys Ala Ala Ser Leu Arg	
615 620 625	
gac cga ctg aaa ttc atc cac gaa cac cgt ggc gaa ccc tgg cca gat	2035
Asp Arg Leu Lys Phe Ile His Glu His Arg Gly Glu Pro Trp Pro Asp	
630 635 640 645	
att gaa act gcg gac ccg cac ctg tgg tta tct cca gaa att gag gcg	2083
Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser Pro Glu Ile Glu Ala	
650 655 660	
ctc agc cac gga aca cga cta aac aat atc gat atg tat ccc gca ctc	2131
Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp Met Tyr Pro Ala Leu	
665 670 675	
cag cga ctt ctc ccc tgg cct gaa gca acc aac ttt gaa gaa ttc gct	2179
Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn Phe Glu Glu Phe Ala	
680 685 690	
cct tcc cac cta tcc gta ccc agc ggg aat cag cac cga cta gat tat	2227
Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln His Arg Leu Asp Tyr	
695 700 705	
tca tca ggc agg cca gtt ata cga gtg aaa tta caa gaa tgc ttc gga	2275

Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu Gln Glu Cys Phe Gly  
 710 715 720 725

tta gaa gaa tcc ccg cag ctc tgc gga atc ccg gtg caa ttt cat ctc 2323  
 Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro Val Gln Phe His Leu  
 730 735 740

ctg tca cct gcg gga aga cct ctt gca gtt acc gat gac ctg cgt agt 2371  
 Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr Asp Asp Leu Arg Ser  
 745 750 755

ttc tgg tct ggc ccg tac agc caa gtc cgt gca gaa atg cgg ggc cgg 2419  
 Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala Glu Met Arg Gly Arg  
 760 765 770

tac ccc aaa cac ccg tgg ccg gag gat cca tgg acc gct cct gcc act 2467  
 Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp Thr Ala Pro Ala Thr  
 775 780 785

gcg cgc acc aag aat cgc atg tagttttggc acgacttgat gtg 2511  
 Ala Arg Thr Lys Asn Arg Met  
 790 795

&lt;210&gt; 78

&lt;211&gt; 796

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 78

Met Ser Ser Arg Ile Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly  
 1 5 10 15

Leu Pro Val Glu Asn Ile Ile Pro His Leu Gln Glu Ala Phe Ser Ala  
 20 25 30

Gly Pro Lys Asn Leu Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr  
 35 40 45

Thr Leu Leu Pro Pro Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala  
 50 55 60

Gly Asn Ala Thr Pro Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val  
 65 70 75 80

Ala Val Arg Ala Ala Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln  
 85 90 95

Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly  
 100 105 110

Ser His Val Gln Phe Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu  
 115 120 125

Asn Asn Pro Glu Leu Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val  
 130 135 140

His Glu Arg Gln Leu Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu  
 145 150 155 160

Leu Ser Gln Leu Arg Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr

165								170							175				
Leu	Asp	Ser	Asp	Lys	Phe	Ala	Asn	Leu	Leu	Asp	Ala	Gln	Val	Leu	Ser				
			180					185					190						
Val	Glu	Ala	Pro	Ile	Phe	Pro	Leu	Asp	Ile	Ser	Tyr	Ala	Pro	Ala	Arg				
		195					200					205							
Ala	Pro	Arg	Leu	Asn	Ala	Lys	Gly	Val	Asp	Trp	Asp	Phe	Leu	Asp	His				
		210				215					220								
Met	Ala	Gln	Lys	Thr	His	Asp	Ala	Val	Thr	His	Ser	Glu	His	Ser	Ala				
225					230					235					240				
Leu	Ile	Phe	Val	Pro	Gly	Val	Arg	Glu	Ile	Asp	Arg	Val	Met	Ser	Thr				
				245					250					255					
Leu	Lys	Ser	Leu	Gly	His	Asn	Asn	Val	Phe	Pro	Leu	His	Gly	Gln	Leu				
			260					265					270						
Ser	Pro	Thr	Glu	Gln	Asp	Arg	Ala	Leu	Ala	Pro	Ser	Gln	Gln	Gln	Arg				
		275					280					285							
Ile	Ile	Val	Ser	Thr	Pro	Val	Ala	Glu	Ser	Ser	Leu	Thr	Val	Pro	Gly				
	290					295					300								
Val	Arg	Ile	Gly	Val	Asp	Ser	Gly	Leu	Ser	Arg	Ser	Pro	Lys	Arg	Asp				
305					310					315					320				
Ser	Ala	Arg	Gly	Met	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Cys	Ala	Gln	Ala				
				325					330					335					
Ser	Ala	Gly	Gln	Arg	Ala	Gly	Arg	Ala	Gly	Arg	Glu	Gly	Pro	Gly	Gln				
			340					345					350						
Ile	Ile	Arg	Cys	Tyr	Ser	Glu	Glu	Asp	Phe	Ser	His	Phe	Pro	Arg	Phe				
		355					360					365							
Val	Thr	Pro	Glu	Ile	Ser	Ser	Ala	Asp	Leu	Thr	Gln	Ala	Ala	Leu	Trp				
	370					375					380								
Leu	Ala	Gln	Trp	Gly	Thr	Ser	Pro	Ala	Asp	Leu	Pro	Leu	Leu	Asp	Gln				
385					390					395					400				
Pro	Pro	His	Ala	Ala	Trp	Thr	Ala	Ala	Gln	Gln	Ile	Leu	Arg	Leu	Ile				
				405					410					415					
Gly	Ala	Leu	Glu	Gly	Asp	Ala	Ile	Thr	Ser	Leu	Gly	His	Arg	Leu	Ser				
			420					425					430						
Thr	Leu	Pro	Leu	Cys	Pro	Gln	Leu	Ser	Ala	Ser	Leu	Leu	Arg	Phe	Gly				
		435					440					445							
Glu	Gln	Ser	Ala	Lys	Ile	Leu	Ala	Val	Val	Ser	Glu	Asn	Pro	Gln	Gly				
	450					455					460								
Asp	Val	Glu	Lys	Gln	Gln	Pro	Asp	Lys	Arg	Glu	Val	Glu	Arg	Leu	Arg				
465					470					475					480				
Arg	Leu	Ala	Pro	Ala	Ser	Val	Gly	Lys	Ala	Ser	Ala	Gly	Gln	Ile	Val				

Gly Ala Ala Phe Pro Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu  
 500 505 510  
 Tyr Leu Leu Ala Ser Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu  
 515 520 525  
 Lys Asp Ala Glu Trp Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn  
 530 535 540  
 Ser Ala Ile Ile Arg Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile  
 545 550 555 560  
 Asp Ile Ile Gly Val Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly  
 565 570 575  
 Lys Val Gln Ala Arg Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser  
 580 585 590  
 Ser Thr Pro Thr Lys Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala  
 595 600 605  
 Thr Ala Leu Ala Lys Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys  
 610 615 620  
 Ala Ala Ser Leu Arg Asp Arg Leu Lys Phe Ile His Glu His Arg Gly  
 625 630 635 640  
 Glu Pro Trp Pro Asp Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser  
 645 650 655  
 Pro Glu Ile Glu Ala Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp  
 660 665 670  
 Met Tyr Pro Ala Leu Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn  
 675 680 685  
 Phe Glu Glu Phe Ala Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln  
 690 695 700  
 His Arg Leu Asp Tyr Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu  
 705 710 715 720  
 Gln Glu Cys Phe Gly Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro  
 725 730 735  
 Val Gln Phe His Leu Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr  
 740 745 750  
 Asp Asp Leu Arg Ser Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala  
 755 760 765  
 Glu Met Arg Gly Arg Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp  
 770 775 780  
 Thr Ala Pro Ala Thr Ala Arg Thr Lys Asn Arg Met  
 785 790 795

&lt;210&gt; 79

&lt;211&gt; 2511

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2488)

&lt;223&gt; FRXA02293

&lt;400&gt; 79

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gatgtgttca ctcagcaaatt tcttaatgta caggcaattg atg agt tca aga att 115
                                         Met Ser Ser Arg Ile
                                         1 5

ggc aat ttt ctt ata aat cgc att tcc acg ggc ctg ccc gta gaa aat 163
Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly Leu Pro Val Glu Asn
                        10 15 20

att atc cct cac ctg caa gaa gct ttt tcg gcc gga cct aaa aac ctt 211
Ile Ile Pro His Leu Gln Glu Ala Phe Ser Ala Gly Pro Lys Asn Leu
                        25 30 35

gtc att cag gcc cct ccc ggc aca gga aaa acg aca ctt ctc ccc cca 259
Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr Thr Leu Leu Pro Pro
                        40 45 50

tta gta gct aac atc tta tgt aat gaa gga gcg gga aat gcc acc cca 307
Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala Gly Asn Ala Thr Pro
                        55 60 65

acc aag gtt tta gta acg gca cct cgt cgt gtg gcc gtc cga gca gca 355
Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val Ala Val Arg Ala Ala
                        70 75 80 85

gct cgc aga ctc gcc caa cta gat gat agc cag ctc gga aca aaa gtg 403
Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln Leu Gly Thr Lys Val
                        90 95 100

gga ttc agc gtg cgt ggt gaa cat att tca ggc tcc cac gtg caa ttt 451
Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly Ser His Val Gln Phe
                        105 110 115

atg acc ccc ggt gtg tta atc cgc cag ctc tta aac aac cca gaa tta 499
Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu Asn Asn Pro Glu Leu
                        120 125 130

ccc ggc atc ggc gct gtg att atc gat gaa gtc cac gaa cgt caa ctc 547
Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val His Glu Arg Gln Leu
                        135 140 145

gat tcc gat cta ctg cta gga atg ctt gct gaa ctc agt caa ctg cgc 595
Asp Ser Asp Leu Leu Gly Met Leu Ala Glu Leu Ser Gln Leu Arg
                        150 155 160 165

gac gat ttc tcc ctc atc gcc atg tcc gca acc tta gat tca gat aaa 643
Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr Leu Asp Ser Asp Lys
                        170 175 180

ttc gca aac tta tta gac gct cag gtc ctt agt gtt gaa gca ccg att 691
Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser Val Glu Ala Pro Ile

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185	190	195	
ttc ccc tta gac att tct tat gct cca gcc cgc gcg cct cgc ctc aat	739		
Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg Ala Pro Arg Leu Asn			
200	205	210	
gca aaa ggt gtc gac tgg gat ttc ctc gac cac atg gcg cag aaa act	787		
Ala Lys Gly Val Asp Trp Asp Phe Leu Asp His Met Ala Gln Lys Thr			
215	220	225	
cac gat gcg gtg aca cat tca gag cac tct gca ctc att ttc gtc cca	835		
His Asp Ala Val Thr His Ser Glu His Ser Ala Leu Ile Phe Val Pro			
230	235	240	245
ggt gtg cgt gaa att gat cga gta atg agc acg ctc aaa tcg ctc ggc	883		
Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr Leu Lys Ser Leu Gly			
250	255	260	
cat aat aat gtt ttc cca ctt cat ggc caa ctc agc ccg acc gaa caa	931		
His Asn Asn Val Phe Pro Leu His Gly Gln Leu Ser Pro Thr Glu Gln			
265	270	275	
gac cgc gcc ctc gca ccg tca caa cag cag cgc atc att gtc tcc act	979		
Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg Ile Ile Val Ser Thr			
280	285	290	
ccc gtt gcg gaa agc tcc cta act gtg cct gga gtt cgc atc ggg gtg	1027		
Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly Val Arg Ile Gly Val			
295	300	305	
gat tcc ggc ctc tca cga agc ccc aaa cga gac tct gcc cgc ggc atg	1075		
Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp Ser Ala Arg Gly Met			
310	315	320	325
aca gga ctg atc acc agc agt tgc gcg cag gct tca gca ggc caa cgc	1123		
Thr Gly Leu Ile Thr Ser Ser Cys Ala Gln Ala Ser Ala Gly Gln Arg			
330	335	340	
gca ggt cgc gct ggc cgt gaa gga cca gga caa ata atc aga tgc tat	1171		
Ala Gly Arg Ala Gly Arg Glu Gly Pro Gly Gln Ile Ile Arg Cys Tyr			
345	350	355	
tcc gaa gaa gac ttc tcc cac ttc cca cga ttt gtg aca cca gaa atc	1219		
Ser Glu Glu Asp Phe Ser His Phe Pro Arg Phe Val Thr Pro Glu Ile			
360	365	370	
agc tcc gct gac ctc acc caa gca gcc ctc tgg ctc gcc caa tgg gga	1267		
Ser Ser Ala Asp Leu Thr Gln Ala Ala Leu Trp Leu Ala Gln Trp Gly			
375	380	385	
acg tca cct gcg gat tta ccg ctt ctt gat caa ccc cct cac gca gcc	1315		
Thr Ser Pro Ala Asp Leu Pro Leu Leu Asp Gln Pro Pro His Ala Ala			
390	395	400	405
tgg acg gct gca caa cag atc ctg cgc ctc atc ggc gcg ctt gaa ggt	1363		
Trp Thr Ala Ala Gln Gln Ile Leu Arg Leu Ile Gly Ala Leu Glu Gly			
410	415	420	
gac gct atc acg agc ctg gga cat cgc tta tcg acg ctt ccc ctc tgc	1411		
Asp Ala Ile Thr Ser Leu Gly His Arg Leu Ser Thr Leu Pro Leu Cys			
425	430	435	



cct caa ctc agc gct tct ctc ctc cgc ttc ggt gaa caa tcc gca aaa 1459  
 Pro Gln Leu Ser Ala Ser Leu Leu Arg Phe Gly Glu Gln Ser Ala Lys  
 440 445 450

atc ttg gcg gtg gtg tcc gaa aac ccg cag ggg gac gtc gaa aag caa 1507  
 Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly Asp Val Glu Lys Gln  
 455 460 465

caa ccc gac aag cgt gaa gtg gaa cgc ctt cgc cgt ttg gca cct gcg 1555  
 Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg Arg Leu Ala Pro Ala  
 470 475 480 485

tcg gtt gga aaa gcg agt gcg ggg caa atc gta ggc gct gca ttc ccg 1603  
 Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val Gly Ala Ala Phe Pro  
 490 495 500

cag ctc atc ggc cga aaa ata gac aat gga gaa tac ctt tta gcc agt 1651  
 Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu Tyr Leu Leu Ala Ser  
 505 510 515

gga acc cgc gca cgc ctc atg gat tca gat ctc aaa gat gcc gaa tgg 1699  
 Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu Lys Asp Ala Glu Trp  
 520 525 530

atc tcc gtt gct gca att aac cgc tca caa aat tct gcc atc atc cgc 1747  
 Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn Ser Ala Ile Ile Arg  
 535 540 545

gcc gcc gcc cgc att tca gag gac gat gcc ata gac atc atc gga gtc 1795  
 Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile Asp Ile Ile Gly Val  
 550 555 560 565

gtg gaa gaa acc cgc gcg att ttt gtc aac gga aaa gtc caa gcc cgg 1843  
 Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly Lys Val Gln Ala Arg  
 570 575 580

aag gtc aaa gca gca ggc gcg atc gaa tta agt tcc act ccg aca aaa 1891  
 Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser Ser Thr Pro Thr Lys  
 585 590 595

cca aca ccc gcc gaa gcc tcg gaa aca atc gcc aca gcc ctt gcc aaa 1939  
 Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala Thr Ala Leu Ala Lys  
 600 605 610

ggc gga atc gac cta ttc cac ttc tcc gac aaa gcg gca tcc ttg cgt 1987  
 Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys Ala Ala Ser Leu Arg  
 615 620 625

gac cga ctg aaa ttc atc cac gaa cac cgt ggc gaa ccc tgg cca gat 2035  
 Asp Arg Leu Lys Phe Ile His Glu His Arg Gly Glu Pro Trp Pro Asp  
 630 635 640 645

att gaa act gcg gac ccg cac ctg tgg tta tct cca gaa att gag gcg 2083  
 Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser Pro Glu Ile Glu Ala  
 650 655 660

ctc agc cac gga aca cga cta aac aat atc gat atg tat ccc gca ctc 2131  
 Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp Met Tyr Pro Ala Leu  
 665 670 675

cag cga ctt ctc ccc tgg cct gaa gca acc aac ttt gaa gaa ttc gct 2179  
 Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn Phe Glu Glu Phe Ala  
 680 685 690

cct tcc cac cta tcc gta ccc agc ggg aat cag cac cga cta gat tat 2227  
 Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln His Arg Leu Asp Tyr  
 695 700 705

tca tca ggc agg cca gtt ata cga gtg aaa tta caa gaa tgc ttc gga 2275  
 Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu Gln Glu Cys Phe Gly  
 710 715 720 725

tta gaa gaa tcc ccg cag ctc tgc gga atc ccg gtg caa ttt cat ctc 2323  
 Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro Val Gln Phe His Leu  
 730 735 740

ctg tca cct gcg gga aga cct ctt gca gtt acc gat gac ctg cgt agt 2371  
 Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr Asp Asp Leu Arg Ser  
 745 750 755

ttc tgg tct ggc ccg tac agc caa gtc cgt gca gaa atg cgg ggc cgg 2419  
 Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala Glu Met Arg Gly Arg  
 760 765 770

tac ccc aaa cac ccg tgg ccg gag gat cca tgg acc gct cct gcc act 2467  
 Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp Thr Ala Pro Ala Thr  
 775 780 785

gcg cgc acc aag aat cgc atg tagttttggc acgacttgat gtg 2511  
 Ala Arg Thr Lys Asn Arg Met  
 790 795

&lt;210&gt; 80

&lt;211&gt; 796

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 80

Met Ser Ser Arg Ile Gly Asn Phe Leu Ile Asn Arg Ile Ser Thr Gly  
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Gly Pro Lys Asn Leu Val Ile Gln Ala Pro Pro Gly Thr Gly Lys Thr  
35 40 45

Thr Leu Leu Pro Pro Leu Val Ala Asn Ile Leu Cys Asn Glu Gly Ala  
50 55 60

Gly Asn Ala Thr Pro Thr Lys Val Leu Val Thr Ala Pro Arg Arg Val  
65 70 75 80

Ala Val Arg Ala Ala Ala Arg Arg Leu Ala Gln Leu Asp Asp Ser Gln  
85 90 95

Leu Gly Thr Lys Val Gly Phe Ser Val Arg Gly Glu His Ile Ser Gly  
100 105 110

Ser His Val Gln Phe Met Thr Pro Gly Val Leu Ile Arg Gln Leu Leu

115	120	125
Asn Asn Pro Glu Leu Pro Gly Ile Gly Ala Val Ile Ile Asp Glu Val 130 135 140		
His Glu Arg Gln Leu Asp Ser Asp Leu Leu Leu Gly Met Leu Ala Glu 145 150 155 160		
Leu Ser Gln Leu Arg Asp Asp Phe Ser Leu Ile Ala Met Ser Ala Thr 165 170 175		
Leu Asp Ser Asp Lys Phe Ala Asn Leu Leu Asp Ala Gln Val Leu Ser 180 185 190		
Val Glu Ala Pro Ile Phe Pro Leu Asp Ile Ser Tyr Ala Pro Ala Arg 195 200 205		
Ala Pro Arg Leu Asn Ala Lys Gly Val Asp Trp Asp Phe Leu Asp His 210 215 220		
Met Ala Gln Lys Thr His Asp Ala Val Thr His Ser Glu His Ser Ala 225 230 235 240		
Leu Ile Phe Val Pro Gly Val Arg Glu Ile Asp Arg Val Met Ser Thr 245 250 255		
Leu Lys Ser Leu Gly His Asn Asn Val Phe Pro Leu His Gly Gln Leu 260 265 270		
Ser Pro Thr Glu Gln Asp Arg Ala Leu Ala Pro Ser Gln Gln Gln Arg 275 280 285		
Ile Ile Val Ser Thr Pro Val Ala Glu Ser Ser Leu Thr Val Pro Gly 290 295 300		
Val Arg Ile Gly Val Asp Ser Gly Leu Ser Arg Ser Pro Lys Arg Asp 305 310 315 320		
Ser Ala Arg Gly Met Thr Gly Leu Ile Thr Ser Ser Cys Ala Gln Ala 325 330 335		
Ser Ala Gly Gln Arg Ala Gly Arg Ala Gly Arg Glu Gly Pro Gly Gln 340 345 350		
Ile Ile Arg Cys Tyr Ser Glu Glu Asp Phe Ser His Phe Pro Arg Phe 355 360 365		
Val Thr Pro Glu Ile Ser Ser Ala Asp Leu Thr Gln Ala Ala Leu Trp 370 375 380		
Leu Ala Gln Trp Gly Thr Ser Pro Ala Asp Leu Pro Leu Leu Asp Gln 385 390 395 400		
Pro Pro His Ala Ala Trp Thr Ala Ala Gln Gln Ile Leu Arg Leu Ile 405 410 415		
Gly Ala Leu Glu Gly Asp Ala Ile Thr Ser Leu Gly His Arg Leu Ser 420 425 430		
Thr Leu Pro Leu Cys Pro Gln Leu Ser Ala Ser Leu Leu Arg Phe Gly 435 440 445		

Glu Gln Ser Ala Lys Ile Leu Ala Val Val Ser Glu Asn Pro Gln Gly  
 450 455 460  
 Asp Val Glu Lys Gln Gln Pro Asp Lys Arg Glu Val Glu Arg Leu Arg  
 465 470 475 480  
 Arg Leu Ala Pro Ala Ser Val Gly Lys Ala Ser Ala Gly Gln Ile Val  
 485 490 495  
 Gly Ala Ala Phe Pro Gln Leu Ile Gly Arg Lys Ile Asp Asn Gly Glu  
 500 505 510  
 Tyr Leu Leu Ala Ser Gly Thr Arg Ala Arg Leu Met Asp Ser Asp Leu  
 515 520 525  
 Lys Asp Ala Glu Trp Ile Ser Val Ala Ala Ile Asn Arg Ser Gln Asn  
 530 535 540  
 Ser Ala Ile Ile Arg Ala Ala Ala Arg Ile Ser Glu Asp Asp Ala Ile  
 545 550 555 560  
 Asp Ile Ile Gly Val Val Glu Glu Thr Arg Ala Ile Phe Val Asn Gly  
 565 570 575  
 Lys Val Gln Ala Arg Lys Val Lys Ala Ala Gly Ala Ile Glu Leu Ser  
 580 585 590  
 Ser Thr Pro Thr Lys Pro Thr Pro Ala Glu Ala Ser Glu Thr Ile Ala  
 595 600 605  
 Thr Ala Leu Ala Lys Gly Gly Ile Asp Leu Phe His Phe Ser Asp Lys  
 610 615 620  
 Ala Ala Ser Leu Arg Asp Arg Leu Lys Phe Ile His Glu His Arg Gly  
 625 630 635 640  
 Glu Pro Trp Pro Asp Ile Glu Thr Ala Asp Pro His Leu Trp Leu Ser  
 645 650 655  
 Pro Glu Ile Glu Ala Leu Ser His Gly Thr Arg Leu Asn Asn Ile Asp  
 660 665 670  
 Met Tyr Pro Ala Leu Gln Arg Leu Leu Pro Trp Pro Glu Ala Thr Asn  
 675 680 685  
 Phe Glu Glu Phe Ala Pro Ser His Leu Ser Val Pro Ser Gly Asn Gln  
 690 695 700  
 His Arg Leu Asp Tyr Ser Ser Gly Arg Pro Val Ile Arg Val Lys Leu  
 705 710 715 720  
 Gln Glu Cys Phe Gly Leu Glu Glu Ser Pro Gln Leu Cys Gly Ile Pro  
 725 730 735  
 Val Gln Phe His Leu Leu Ser Pro Ala Gly Arg Pro Leu Ala Val Thr  
 740 745 750  
 Asp Asp Leu Arg Ser Phe Trp Ser Gly Pro Tyr Ser Gln Val Arg Ala  
 755 760 765

Glu Met Arg Gly Arg Tyr Pro Lys His Pro Trp Pro Glu Asp Pro Trp  
 770 775 780

Thr Ala Pro Ala Thr Ala Arg Thr Lys Asn Arg Met  
 785 790 795

<210> 81

<211> 2118

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2095)

<223> RXA02755

<400> 81

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                                         Met Ser Ala Pro Glu
                                         1 5

tca ccc aca aat acc acc cca gat ccg ctc aat gct tcc acg gaa gag 163
Ser Pro Thr Asn Thr Thr Pro Asp Pro Leu Asn Ala Ser Thr Glu Glu
              10              15              20

ttg ctt act gct gcc gtt gaa gcg ttg ggc ggt gcc cgt cgt gct gga 211
Leu Leu Thr Ala Ala Val Glu Ala Leu Gly Gly Ala Arg Arg Ala Gly
              25              30              35

cag gaa gca atg gct aag gct gtg acc aag gct ttt gat aca gag cgt 259
Gln Glu Ala Met Ala Lys Ala Val Thr Lys Ala Phe Asp Thr Glu Arg
              40              45              50

cac ttg gcg gtg cag gcg ggt acg ggt acg ggt aag tct ttg gct tat 307
His Leu Ala Val Gln Ala Gly Thr Gly Thr Gly Lys Ser Leu Ala Tyr
              55              60              65

ctt gtt ccg tcg att cgt cat gcg cag aag tct gat tcc acg gtc att 355
Leu Val Pro Ser Ile Arg His Ala Gln Lys Ser Asp Ser Thr Val Ile
              70              75              80              85

gtg tct act gcg acg atc gcg ttg cag cgc cag ttg gtc aat agg gat 403
Val Ser Thr Ala Thr Ile Ala Leu Gln Arg Gln Leu Val Asn Arg Asp
              90              95              100

ctc ccc cgc ttg gtg gat gcg ttg gaa ccc ttg atg gaa cgt cgc ccg 451
Leu Pro Arg Leu Val Asp Ala Leu Glu Pro Leu Met Glu Arg Arg Pro
              105              110              115

act ttt gcg att atg aag ggc cgt tcc aat tat ttg tgc atg aat aag 499
Thr Phe Ala Ile Met Lys Gly Arg Ser Asn Tyr Leu Cys Met Asn Lys
              120              125              130

gtt gcc cgc cag gaa gag ctg aat cag gaa gat gcc ctg att gag cag 547
Val Ala Arg Gln Glu Glu Leu Asn Gln Glu Asp Ala Leu Ile Glu Gln
              135              140              145

gag gat atc tcg tgg tta ggt aag cac att gtg cgc ctt aat gag tgg 595

```

Glu Asp Ile Ser Trp Leu Gly Lys His Ile Val Arg Leu Asn Glu Trp	
150 155 160 165	
gcc aat gag act gag act ggc gat cgt gat gat ttg gat ccg ggt gtt	643
Ala Asn Glu Thr Glu Thr Gly Asp Arg Asp Asp Leu Asp Pro Gly Val	
170 175 180	
cct gat ctt gcg tgg aag cag gta agt gtt act gcc cgt gag tgc att	691
Pro Asp Leu Ala Trp Lys Gln Val Ser Val Thr Ala Arg Glu Cys Ile	
185 190 195	
ggc gcg tca agg tgc ccg cat ggc gag gat tgt ttc gct gag att gcc	739
Gly Ala Ser Arg Cys Pro His Gly Glu Asp Cys Phe Ala Glu Ile Ala	
200 205 210	
cgc ggg aag gca aag gag gct gat gtg gtg gtc acc aac cat gcg tta	787
Arg Gly Lys Ala Lys Glu Ala Asp Val Val Val Thr Asn His Ala Leu	
215 220 225	
ctt gct att gat gcg ttg tgc gat gtt tct gtg ctt cct gaa cat gat	835
Leu Ala Ile Asp Ala Leu Ser Asp Val Ser Val Leu Pro Glu His Asp	
230 235 240 245	
gtg gtg gtc atc gat gag gcc cat gag cta gat ggt cgc atc act gct	883
Val Val Val Ile Asp Glu Ala His Glu Leu Asp Gly Arg Ile Thr Ala	
250 255 260	
gtg gcg tcg gct gag atc acg gtg aat tcg ctc aat tta gct gct cgc	931
Val Ala Ser Ala Glu Ile Thr Val Asn Ser Leu Asn Leu Ala Ala Arg	
265 270 275	
cgt gcg tcc aag ttg gat tcc gat aag cgg gaa gaa cgc gtc cag gaa	979
Arg Ala Ser Lys Leu Asp Ser Asp Lys Arg Glu Glu Arg Val Gln Glu	
280 285 290	
atc gct ggc gat ttg gaa acc ttg ttg caa acc atg cag ccg ggc cgg	1027
Ile Ala Gly Asp Leu Glu Thr Leu Leu Gln Thr Met Gln Pro Gly Arg	
295 300 305	
ttg aat gac atg gat gag ggt tcc aaa ggc aca ctg gtg gca ttg aag	1075
Trp Asn Asp Met Asp Glu Gly Ser Lys Gly Thr Leu Val Ala Leu Lys	
310 315 320 325	
gac gcg ttg tgg gca ttg cgt gct cag atc gcg gga gca cct gag ggt	1123
Asp Ala Leu Trp Ala Leu Arg Ala Gln Ile Ala Gly Ala Pro Glu Gly	
330 335 340	
gag gct gcg aat gat ccg gag cgt ttc gcc gag cga cag aat tta agc	1171
Glu Ala Ala Asn Asp Pro Glu Arg Phe Ala Glu Arg Gln Asn Leu Ser	
345 350 355	
aat cac ttg atg gaa atc cat gat gcc aac gtg cgc att ttg gag gtc	1219
Asn His Leu Met Glu Ile His Asp Ala Asn Val Arg Ile Leu Glu Val	
360 365 370	
ttc gcg gag gag gat ccc tcc aag cag tac gac gtg gtg tgg cat aac	1267
Phe Ala Glu Glu Asp Pro Ser Lys Gln Tyr Asp Val Val Trp His Asn	
375 380 385	
cac gat gat cgt cgc ggg gat tcc ctc aat gtg gcg ccg ctg tgc gtt	1315
His Asp Asp Arg Arg Gly Asp Ser Leu Asn Val Ala Pro Leu Ser Val	

390	395	400	405	
gca ggg ctg ttg cat gag aaa ctg ttc gcg gaa aac acc gtg gtt ttg				1363
Ala Gly Leu Leu His Glu Lys Leu Phe Ala Glu Asn Thr Val Val Leu	410	415	420	
gcc agt gcg acg ctg acc att ggt ggc aat ttc aac gca atg gct gcc				1411
Ala Ser Ala Thr Leu Thr Ile Gly Gly Asn Phe Asn Ala Met Ala Ala	425	430	435	
agc tgg ggt ttg ccg aaa ggg tcg tgg gat tcc atg gat gcc ggc acg				1459
Ser Trp Gly Leu Pro Lys Gly Ser Trp Asp Ser Met Asp Ala Gly Thr	440	445	450	
ccg ttt gat cca gcg aag tcg ggt att ttg tac acc gct cga cac ctt				1507
Pro Phe Asp Pro Ala Lys Ser Gly Ile Leu Tyr Thr Ala Arg His Leu	455	460	465	
ccg gac cct ggc cgc gat ggg ttg ccg gag gaa acg ctt gat gaa atc				1555
Pro Asp Pro Gly Arg Asp Gly Leu Pro Glu Glu Thr Leu Asp Glu Ile	470	475	480	485
tac gag ttg atc act gcg gcg ggt ggc cga act ttg ggg ctc ttt tcg				1603
Tyr Glu Leu Ile Thr Ala Ala Gly Gly Arg Thr Leu Gly Leu Phe Ser	490	495	500	
tcg aaa cgc gct gcg gaa caa gcc acc aag gcg atg cgt ctg cgc ctg				1651
Ser Lys Arg Ala Ala Glu Gln Ala Thr Lys Ala Met Arg Leu Arg Leu	505	510	515	
cct ttt gat gtg ctc tgc cag gga gat gac aat act gcc gcg ctg gtg				1699
Pro Phe Asp Val Leu Cys Gln Gly Asp Asp Asn Thr Ala Ala Leu Val	520	525	530	
aag aag ttt tcc gac agc gaa aac acg tgc ctt ttt ggc act ctc acg				1747
Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu Phe Gly Thr Leu Thr	535	540	545	
ctg tgg cag ggc gtc gac gtc ccc ggc cgt tcg ctg tcg ttg gtg ttg				1795
Leu Trp Gln Gly Val Asp Val Pro Gly Arg Ser Leu Ser Leu Val Leu	550	555	560	565
att gac cgc atc ccg ttc ccc cgc ccc gac gac ccg ctg ctg cag gcc				1843
Ile Asp Arg Ile Pro Phe Pro Arg Pro Asp Asp Pro Leu Leu Gln Ala	570	575	580	
cgc aag gag gcc gcc gat gcc gaa ggc cgc aac ggt ttc atg gag gtc				1891
Arg Lys Glu Ala Ala Asp Ala Glu Gly Arg Asn Gly Phe Met Glu Val	585	590	595	
gca gcc acc cac gcg gcg ttg ttg atg gcg cag ggc gcg ggc cgg ttg				1939
Ala Ala Thr His Ala Ala Leu Leu Met Ala Gln Gly Ala Gly Arg Leu	600	605	610	
ttg cgg cac gtc ggc gac cgc ggc gtg gta gca gtg cta gac cac cgc				1987
Leu Arg His Val Gly Asp Arg Gly Val Val Ala Val Leu Asp His Arg	615	620	625	
tta tcg acg aaa cgt tac ggc ggt ttc ctg cgc ttc tcc atg ccc aga				2035
Leu Ser Thr Lys Arg Tyr Gly Gly Phe Leu Arg Phe Ser Met Pro Arg	630	635	640	645

ttt tgg gaa acc acc aac cca gag acc gta cgc gcg gca ctc aaa cga 2083  
 Phe Trp Glu Thr Thr Asn Pro Glu Thr Val Arg Ala Ala Leu Lys Arg  
                     650                    655                    660

ttg gtg act aag taaaactaac tgctactgac gct 2118  
 Leu Val Thr Lys  
                     665

<210> 82

<211> 665

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Ser Ala Pro Glu Ser Pro Thr Asn Thr Thr Pro Asp Pro Leu Asn  
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Ala Ser Thr Glu Glu Leu Leu Thr Ala Ala Val Glu Ala Leu Gly Gly  
                     20                    25                    30

Ala Arg Arg Ala Gly Gln Glu Ala Met Ala Lys Ala Val Thr Lys Ala  
                     35                    40                    45

Phe Asp Thr Glu Arg His Leu Ala Val Gln Ala Gly Thr Gly Thr Gly  
                     50                    55                    60

Lys Ser Leu Ala Tyr Leu Val Pro Ser Ile Arg His Ala Gln Lys Ser  
                     65                    70                    75                    80

Asp Ser Thr Val Ile Val Ser Thr Ala Thr Ile Ala Leu Gln Arg Gln  
                     85                    90                    95

Leu Val Asn Arg Asp Leu Pro Arg Leu Val Asp Ala Leu Glu Pro Leu  
                     100                    105                    110

Met Glu Arg Arg Pro Thr Phe Ala Ile Met Lys Gly Arg Ser Asn Tyr  
                     115                    120                    125

Leu Cys Met Asn Lys Val Ala Arg Gln Glu Glu Leu Asn Gln Glu Asp  
                     130                    135                    140

Ala Leu Ile Glu Gln Glu Asp Ile Ser Trp Leu Gly Lys His Ile Val  
                     145                    150                    155                    160

Arg Leu Asn Glu Trp Ala Asn Glu Thr Glu Thr Gly Asp Arg Asp Asp  
                     165                    170                    175

Leu Asp Pro Gly Val Pro Asp Leu Ala Trp Lys Gln Val Ser Val Thr  
                     180                    185                    190

Ala Arg Glu Cys Ile Gly Ala Ser Arg Cys Pro His Gly Glu Asp Cys  
                     195                    200                    205

Phe Ala Glu Ile Ala Arg Gly Lys Ala Lys Glu Ala Asp Val Val Val  
                     210                    215                    220

Thr Asn His Ala Leu Leu Ala Ile Asp Ala Leu Ser Asp Val Ser Val  
                     225                    230                    235                    240



Leu Pro Glu His Asp Val Val Val Ile Asp Glu Ala His Glu Leu Asp  
 245 250 255  
 Gly Arg Ile Thr Ala Val Ala Ser Ala Glu Ile Thr Val Asn Ser Leu  
 260 265 270  
 Asn Leu Ala Ala Arg Arg Ala Ser Lys Leu Asp Ser Asp Lys Arg Glu  
 275 280 285  
 Glu Arg Val Gln Glu Ile Ala Gly Asp Leu Glu Thr Leu Leu Gln Thr  
 290 295 300  
 Met Gln Pro Gly Arg Trp Asn Asp Met Asp Glu Gly Ser Lys Gly Thr  
 305 310 315 320  
 Leu Val Ala Leu Lys Asp Ala Leu Trp Ala Leu Arg Ala Gln Ile Ala  
 325 330 335  
 Gly Ala Pro Glu Gly Glu Ala Ala Asn Asp Pro Glu Arg Phe Ala Glu  
 340 345 350  
 Arg Gln Asn Leu Ser Asn His Leu Met Glu Ile His Asp Ala Asn Val  
 355 360 365  
 Arg Ile Leu Glu Val Phe Ala Glu Glu Asp Pro Ser Lys Gln Tyr Asp  
 370 375 380  
 Val Val Trp His Asn His Asp Asp Arg Arg Gly Asp Ser Leu Asn Val  
 385 390 395 400  
 Ala Pro Leu Ser Val Ala Gly Leu Leu His Glu Lys Leu Phe Ala Glu  
 405 410 415  
 Asn Thr Val Val Leu Ala Ser Ala Thr Leu Thr Ile Gly Gly Asn Phe  
 420 425 430  
 Asn Ala Met Ala Ala Ser Trp Gly Leu Pro Lys Gly Ser Trp Asp Ser  
 435 440 445  
 Met Asp Ala Gly Thr Pro Phe Asp Pro Ala Lys Ser Gly Ile Leu Tyr  
 450 455 460  
 Thr Ala Arg His Leu Pro Asp Pro Gly Arg Asp Gly Leu Pro Glu Glu  
 465 470 475 480  
 Thr Leu Asp Glu Ile Tyr Glu Leu Ile Thr Ala Ala Gly Gly Arg Thr  
 485 490 495  
 Leu Gly Leu Phe Ser Ser Lys Arg Ala Ala Glu Gln Ala Thr Lys Ala  
 500 505 510  
 Met Arg Leu Arg Leu Pro Phe Asp Val Leu Cys Gln Gly Asp Asp Asn  
 515 520 525  
 Thr Ala Ala Leu Val Lys Lys Phe Ser Asp Ser Glu Asn Thr Cys Leu  
 530 535 540  
 Phe Gly Thr Leu Thr Leu Trp Gln Gly Val Asp Val Pro Gly Arg Ser  
 545 550 555 560  
 Leu Ser Leu Val Leu Ile Asp Arg Ile Pro Phe Pro Arg Pro Asp Asp

565	570	575
Pro Leu Leu Gln Ala Arg Lys Glu Ala Ala Asp Ala Glu Gly Arg Asn		
580	585	590
Gly Phe Met Glu Val Ala Ala Thr His Ala Ala Leu Leu Met Ala Gln		
595	600	605
Gly Ala Gly Arg Leu Leu Arg His Val Gly Asp Arg Gly Val Val Ala		
610	615	620
Val Leu Asp His Arg Leu Ser Thr Lys Arg Tyr Gly Gly Phe Leu Arg		
625	630	635
Phe Ser Met Pro Arg Phe Trp Glu Thr Thr Asn Pro Glu Thr Val Arg		
645	650	655
Ala Ala Leu Lys Arg Leu Val Thr Lys		
660	665	

<210> 83  
 <211> 1365  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1342)  
 <223> RXN01374

<400> 83  
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 attcgcaaat actttgttaa gacgcgttaa tctttaacct atg tct gaa tca ggt 115  
 Met Ser Glu Ser Gly  
 1 5  
 gcg cta agt tct act gac tct cta tcc ccg ggt gtc acc att gaa gtc 163  
 Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly Val Thr Ile Glu Val  
 10 15 20  
 cga gat gaa att tgg ctg gtt act cac gtt act cgc tcc aca gat ggt 211  
 Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly  
 25 30 35  
 ttt agg gtt aaa gct cgt ggt ctc tct gat tat gtg cgg gac cac gaa 259  
 Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu  
 40 45 50  
 gct acg ttc ttc acc gca ctt gat aaa gat ttg aag gtc att gac cct 307  
 Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro  
 55 60 65  
 acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc 355  
 Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser Asn Tyr Arg Arg Thr  
 70 75 80 85  
 cgc ctg tgg ttg gag gcc acc atg cgt aaa act ccg gta ccg ctc tat 403  
 Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr Pro Val Pro Leu Tyr  
 90 95 100

caa gag tca ctt tcc gtg gca gat caa atg ctc gcc gat cca ctg gag	451
Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu Ala Asp Pro Leu Glu	
105 110 115	
tac caa tta gca gcc gtg cgc aaa acc ctc tct agt gct aac ttg cgc	499
Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser Ser Ala Asn Leu Arg	
120 125 130	
ccc cgc gtg ctt att gct gat gcc gtg gga ctt ggc aaa acc cta gaa	547
Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu Gly Lys Thr Leu Glu	
135 140 145	
atg ggc atg atc ttg gcg gaa ctt atc cgc cgt ggc cgt ggt gag cgc	595
Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg Gly Arg Gly Glu Arg	
150 155 160 165	
att ttg gta gtc acc ccg cgc cac att atg gag cag ttc cag cag gaa	643
Ile Leu Val Val Thr Pro Arg His Ile Met Glu Gln Phe Gln Gln Glu	
170 175 180	
atg tgg acc cgt ttt gcc atc ccg ctc gtt cgt cta gat tcc gtg ggc	691
Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg Leu Asp Ser Val Gly	
185 190 195	
atc cag caa gtg cgc caa aaa ttg cca gca tca cgc aac cct ttt act	739
Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser Arg Asn Pro Phe Thr	
200 205 210	
tat ttc ccg cgc gtg att gtc tct atg gat act ttg aaa tct ccg aag	787
Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr Leu Lys Ser Pro Lys	
215 220 225	
tac cgc gcg caa cta gaa aag gtg cac tgg gat gcg gtg gtt ata gat	835
Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp Ala Val Val Ile Asp	
230 235 240 245	
gaa atc cac aat gca acc aat gct ggc acc caa aat aat gag cta gcc	883
Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln Asn Asn Glu Leu Ala	
250 255 260	
ggc aca ctt ggg cct act gcc gag gct ctt att ttg gcc tct gcc acc	931
Gly Thr Leu Gly Pro Thr Ala Glu Ala Leu Ile Leu Ala Ser Ala Thr	
265 270 275	
ccg cac aat ggt gat cca gaa tcc ttt aag gag atc ttg cgt ttg ctt	979
Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu Ile Leu Arg Leu Leu	
280 285 290	
gat ccc acc gct gtg atg cct gat ggc acc att gat gcc gaa gct gca	1027
Asp Pro Thr Ala Val Met Pro Asp Gly Thr Ile Asp Ala Glu Ala Ala	
295 300 305	
cag cgt ctg atc att cgt cgc cat cgc aat agc cct gag gtt tca ggt	1075
Gln Arg Leu Ile Ile Arg Arg His Arg Asn Ser Pro Glu Val Ser Gly	
310 315 320 325	
ttt gtg ggc gaa aaa tgg gct cca cgc aat gag cct cag aac ttc ctg	1123
Phe Val Gly Glu Lys Trp Ala Pro Arg Asn Glu Pro Gln Asn Phe Leu	
330 335 340	

gtc gct gcg tca aaa gaa gaa aac ggc gtt gct gca gaa ctc aac cat 1171  
 Val Ala Ala Ser Lys Glu Glu Asn Gly Val Ala Ala Glu Leu Asn His  
 345 350 355

gtg tgg att tca cca ggt gcg agc aat ccg atc aag gat cgc ctc ttc 1219  
 Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu Phe  
 360 365 370

ccc ctg gac att ggt gaa ggc ttt tct ctc ctc ccc tgc agc ctt ggg 1267  
 Pro Leu Asp Ile Gly Glu Gly Phe Ser Leu Leu Pro Cys Ser Leu Gly  
 375 380 385

cga aac agt gtc caa tcg cct caa aaa ggc ctc tgc acc aga aga aaa 1315  
 Arg Asn Ser Val Gln Ser Pro Gln Lys Gly Leu Cys Thr Arg Arg Lys  
 390 395 400 405

acg cgc cct aga aac cct ttc aca act taattctgcg atcacccccgc 1362  
 Thr Arg Pro Arg Asn Pro Phe Thr Thr  
 410

aga 1365

<210> 84  
 <211> 414  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 84  
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Val Thr Ile Glu Val Arg Asp Glu Ile Trp Leu Val Thr His Val Thr  
 20 25 30

Arg Ser Thr Asp Gly Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr  
 35 40 45

Val Arg Asp His Glu Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu  
 50 55 60

Lys Val Ile Asp Pro Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser  
 65 70 75 80

Asn Tyr Arg Arg Thr Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr  
 85 90 95

Pro Val Pro Leu Tyr Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu  
 100 105 110

Ala Asp Pro Leu Glu Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser  
 115 120 125

Ser Ala Asn Leu Arg Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu  
 130 135 140

Gly Lys Thr Leu Glu Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg  
 145 150 155 160

Gly Arg Gly Glu Arg Ile Leu Val Val Thr Pro Arg His Ile Met Glu  
 165 170 175

Gln Phe Gln Gln Glu Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg  
 180 185 190  
 Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser  
 195 200 205  
 Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr  
 210 215 220  
 Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp  
 225 230 235 240  
 Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln  
 245 250 255  
 Asn Asn Glu Leu Ala Gly Thr Leu Gly Pro Thr Ala Glu Ala Leu Ile  
 260 265 270  
 Leu Ala Ser Ala Thr Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu  
 275 280 285  
 Ile Leu Arg Leu Leu Asp Pro Thr Ala Val Met Pro Asp Gly Thr Ile  
 290 295 300  
 Asp Ala Glu Ala Ala Gln Arg Leu Ile Ile Arg Arg His Arg Asn Ser  
 305 310 315 320  
 Pro Glu Val Ser Gly Phe Val Gly Glu Lys Trp Ala Pro Arg Asn Glu  
 325 330 335  
 Pro Gln Asn Phe Leu Val Ala Ala Ser Lys Glu Glu Asn Gly Val Ala  
 340 345 350  
 Ala Glu Leu Asn His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile  
 355 360 365  
 Lys Asp Arg Leu Phe Pro Leu Asp Ile Gly Glu Gly Phe Ser Leu Leu  
 370 375 380  
 Pro Cys Ser Leu Gly Arg Asn Ser Val Gln Ser Pro Gln Lys Gly Leu  
 385 390 395 400  
 Cys Thr Arg Arg Lys Thr Arg Pro Arg Asn Pro Phe Thr Thr  
 405 410

&lt;210&gt; 85

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (982)

&lt;223&gt; FRXA01374

&lt;400&gt; 85

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attcgcaaat actttgttaa gacgcgttaa tctttaacct atg tct gaa tca ggt 115

	Met	Ser	Glu	Ser	Gly	
	1				5	
gcg cta agt tct act gac tct cta tcc ccg ggt gtc acc att gaa gtc						163
Ala Leu Ser Ser Thr Asp Ser Leu Ser Pro Gly Val Thr Ile Glu Val						
	10				20	
cga gat gaa att tgg ctg gtt act cac gtt act cgc tcc aca gat ggt						211
Arg Asp Glu Ile Trp Leu Val Thr His Val Thr Arg Ser Thr Asp Gly						
	25				35	
ttt agg gtt aaa gct cgt ggt ctc tct gat tat gtg cgg gac cac gaa						259
Phe Arg Val Lys Ala Arg Gly Leu Ser Asp Tyr Val Arg Asp His Glu						
	40				50	
gct acg ttc ttc acc gca ctt gat aaa gat ttg aag gtc att gac cct						307
Ala Thr Phe Phe Thr Ala Leu Asp Lys Asp Leu Lys Val Ile Asp Pro						
	55				65	
acc cag gtc acc gtc agt ctt gat gat tcc tcc aat tac cgt cgc acc						355
Thr Gln Val Thr Val Ser Leu Asp Asp Ser Ser Asn Tyr Arg Arg Thr						
	70				80	
cgc ctg tgg ttg gag gcc acc atg cgt aaa act ccg gta ccg ctc tat						403
Arg Leu Trp Leu Glu Ala Thr Met Arg Lys Thr Pro Val Pro Leu Tyr						
	90				100	
caa gag tca ctt tcc gtg gca gat caa atg ctc gcc gat cca ctg gag						451
Gln Glu Ser Leu Ser Val Ala Asp Gln Met Leu Ala Asp Pro Leu Glu						
	105				115	
tac caa tta gca gcc gtg cgc aaa acc ctc tct agt gct aac ttg cgc						499
Tyr Gln Leu Ala Ala Val Arg Lys Thr Leu Ser Ser Ala Asn Leu Arg						
	120				130	
ccc cgc gtg ctt att gct gat gcc gtg gga ctt ggc aaa acc cta gaa						547
Pro Arg Val Leu Ile Ala Asp Ala Val Gly Leu Gly Lys Thr Leu Glu						
	135				145	
atg ggc atg atc ttg gcg gaa ctt atc cgc cgt ggc cgt ggt gag cgc						595
Met Gly Met Ile Leu Ala Glu Leu Ile Arg Arg Gly Arg Gly Glu Arg						
	150				160	
att ttg gta gtc acc ccg cgc cac att atg gag cag ttc cag cag gaa						643
Ile Leu Val Val Thr Pro Arg His Ile Met Glu Gln Phe Gln Gln Glu						
	170				180	
atg tgg acc cgt ttt gcc atc ccg ctc gtt cgt cta gat tcc gtg ggc						691
Met Trp Thr Arg Phe Ala Ile Pro Leu Val Arg Leu Asp Ser Val Gly						
	185				195	
atc cag caa gtg cgc caa aaa ttg cca gca tca cgc aac cct ttt act						739
Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser Arg Asn Pro Phe Thr						
	200				210	
tat ttc ccg cgc gtg att gtc tct atg gat act ttg aaa tct ccg aag						787
Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr Leu Lys Ser Pro Lys						
	215				225	
tac cgc gcg caa cta gaa aag gtg cac tgg gat gcg gtg gtt ata gat						835
Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp Ala Val Val Ile Asp						

230	235	240	245	
gaa atc cac aat gca acc aat gct ggc acc caa aat aat gag cta gcc				883
Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln Asn Asn Glu Leu Ala				
	250	255	260	
cgc aca ctt gcg cct act gcc gag gct ctt att ttg gcc tct gcc acc				931
Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile Leu Ala Ser Ala Thr				
	265	270	275	
ccg cac aat ggt gat cca gaa tcc ttt aag gag atc ttg cgt ttg ctt				979
Pro His Asn Gly Asp Pro Glu Ser Phe Lys Glu Ile Leu Arg Leu Leu				
	280	285	290	
gat				982
Asp				

&lt;210&gt; 86

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 86

Met	Ser	Glu	Ser	Gly	Ala	Leu	Ser	Ser	Thr	Asp	Ser	Leu	Ser	Pro	Gly
1				5					10					15	

Val	Thr	Ile	Glu	Val	Arg	Asp	Glu	Ile	Trp	Leu	Val	Thr	His	Val	Thr
			20					25					30		

Arg	Ser	Thr	Asp	Gly	Phe	Arg	Val	Lys	Ala	Arg	Gly	Leu	Ser	Asp	Tyr
			35				40					45			

Val	Arg	Asp	His	Glu	Ala	Thr	Phe	Phe	Thr	Ala	Leu	Asp	Lys	Asp	Leu
	50					55					60				

Lys	Val	Ile	Asp	Pro	Thr	Gln	Val	Thr	Val	Ser	Leu	Asp	Asp	Ser	Ser
65					70					75					80

Asn	Tyr	Arg	Arg	Thr	Arg	Leu	Trp	Leu	Glu	Ala	Thr	Met	Arg	Lys	Thr
				85					90					95	

Pro	Val	Pro	Leu	Tyr	Gln	Glu	Ser	Leu	Ser	Val	Ala	Asp	Gln	Met	Leu
			100					105					110		

Ala	Asp	Pro	Leu	Glu	Tyr	Gln	Leu	Ala	Ala	Val	Arg	Lys	Thr	Leu	Ser
			115				120					125			

Ser	Ala	Asn	Leu	Arg	Pro	Arg	Val	Leu	Ile	Ala	Asp	Ala	Val	Gly	Leu
	130					135					140				

Gly	Lys	Thr	Leu	Glu	Met	Gly	Met	Ile	Leu	Ala	Glu	Leu	Ile	Arg	Arg
145					150					155					160

Gly	Arg	Gly	Glu	Arg	Ile	Leu	Val	Val	Thr	Pro	Arg	His	Ile	Met	Glu
			165						170					175	

Gln	Phe	Gln	Gln	Glu	Met	Trp	Thr	Arg	Phe	Ala	Ile	Pro	Leu	Val	Arg
			180					185					190		

Leu Asp Ser Val Gly Ile Gln Gln Val Arg Gln Lys Leu Pro Ala Ser  
 195 200 205  
 Arg Asn Pro Phe Thr Tyr Phe Pro Arg Val Ile Val Ser Met Asp Thr  
 210 215 220  
 Leu Lys Ser Pro Lys Tyr Arg Ala Gln Leu Glu Lys Val His Trp Asp  
 225 230 235 240  
 Ala Val Val Ile Asp Glu Ile His Asn Ala Thr Asn Ala Gly Thr Gln  
 245 250 255  
 Asn Asn Glu Leu Ala Arg Thr Leu Ala Pro Thr Ala Glu Ala Leu Ile  
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 Ile Leu Arg Leu Leu Asp  
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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN00817

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 Leu Thr Thr Pro Asp  
 1 5  
 ttt gag agt gaa aag act caa gct atg agg ccc agc ttt ggt gaa gag 163  
 Phe Glu Ser Glu Lys Thr Gln Ala Met Arg Pro Ser Phe Gly Glu Glu  
 10 15 20  
 ctg gcc gca atc gtt tcc aaa cgt tac tcc gaa tcg acg ctc act cat 211  
 Leu Ala Ala Ile Val Ser Lys Arg Tyr Ser Glu Ser Thr Leu Thr His  
 25 30 35  
 atg gtg acg ttg ccc gca tcg aaa gct aaa tac gtc gat tgg ccg agt 259  
 Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr Val Asp Trp Pro Ser  
 40 45 50  
 tgg gta cct gct agc ctg cgc gat gcg ttg gtg aat cgt ggt atc aat 307  
 Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val Asn Arg Gly Ile Asn  
 55 60 65  
 aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc 355  
 Lys Leu Phe Ser His Gln Glu Gln Thr Ala His Leu Ala Trp Asn Gly  
 70 75 80 85  
 cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt 403  
 Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly



90	95	100	
tat cag ctg ccc att ttg tca gcg ctc ggc acg gat cct acc gcc tgt			451
Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr Asp Pro Thr Ala Cys			
105	110	115	
gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc			499
Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly Ser Asp Gln Leu Thr			
120	125	130	
tcc acg tcc acg ttg ctg cgc gac att ccg gat ttc cac ccg att aat			547
Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp Phe His Pro Ile Asn			
135	140	145	
ccg gcg ccc tac gat ggc gat acc ccc tcc gag gcg cgg tcc gcc atc			595
Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu Ala Arg Ser Gly Ile			
150	155	160	165
cgc gat ttg agt cgt ttt gtg ttc acc aat ccg gat atg gtg cat gcg			643
Arg Asp Leu Ser Arg Phe Val Phe Thr Asn Pro Asp Met Val His Ala			
170	175	180	
tcg atg ctg gcg aat cat ccc cgc tgg gcc agg ttg ttg cgc cat ttg			691
Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg Leu Leu Arg His Leu			
185	190	195	
aag ttc atc gtg att gat gaa tgc cat gcc tac cgt ggt gtg ttt gcc			739
Lys Phe Ile Val Ile Asp Glu Cys His Ala Tyr Arg Gly Val Phe Gly			
200	205	210	
gcg aac gtg tcg atg gtg ctt cgt cgt cta ctg cgc atc gcc gcg ttt			787
Ala Asn Val Ser Met Val Leu Arg Arg Leu Leu Arg Ile Ala Ala Phe			
215	220	225	
tat gga tcc cac ccg acg gtc att ttg gcg tcc gcg acc agc tcc gat			835
Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser Ala Thr Ser Ser Asp			
230	235	240	245
ccg gaa att cat gct tcc aga ttg ttg ggc gcg ccg gtt aaa gca gtg			883
Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala Val			
250	255	260	
acg gaa gat ggc gcc ccg acg ggt gaa cgc acc gtt ttg ctg tgg gag			931
Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp Glu			
265	270	275	
ccc ggt ttc atc gaa ggc gcc gag ggc gag aac ggc gcg ccg gtg cgt			979
Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val Arg			
280	285	290	
cgc gca gcc agc acc gaa gca gca aac att atg gcc acg ctc att tcc			1027
Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile Ser			
295	300	305	
gag ggt gca cgc acg ttg acg ttc gtc cgt tca cgt cga caa gca gaa			1075
Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala Glu			
310	315	320	325
atc gtt gcc ctg cgc gcg cag gaa gag ctc agc acg ctg ggc cgc ccc			1123
Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser Thr Leu Gly Arg Pro			
330	335	340	

gat ttc gcc cgg cgc gtc gcg tcc tac cgg gcg ggg tac ttg gcg gag 1171  
 Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala Glu  
 345 350 355

gac cgc cgt agg ttg gag aga ttg ctt gac gac ggc acc ctc ctc ggt 1219  
 Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu Gly  
 360 365 370

gtt gct tcc acc aat gcg ctt gaa ctg ggc att gat gtc ggt gga ctg 1267  
 Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly Leu  
 375 380 385

gat gct gtg gtc acg gct ggt ttt cca gga act gtg gcg tcg ttt tgg 1315  
 Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe Trp  
 390 395 400 405

cag cag gcg ggg cga gct ggt cgg cgt ggg cag ggt tcg ttg gtg gtg 1363  
 Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln Gly Ser Leu Val Val  
 410 415 420

ctt gtt gct cgt gat gag ccg atg gat acg tat ttg gtg cat cat ccg 1411  
 Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His Pro  
 425 430 435

gca gcc ctg ttg gag aag ccg gtt gag gct gcg gtg ttt gat ccg acg 1459  
 Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro Thr  
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aat ccg cat gtt att cgg ggt cat gtt tat tgc gct gcg gtg gaa aag 1507  
 Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu Lys  
 455 460 465

cct ctg aca gag gcg gag gtc gcg gcg ttt ggt gcc caa aag gtg gtg 1555  
 Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val Val  
 470 475 480 485

gag aag ctc gag att gaa ggg ctg ttg cgc aag cgt ccg cgt ggc tgg 1603  
 Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly Trp  
 490 495 500

ttt gcg gtg gaa aag ccc atg tca gag gat ccg gat gag ctg agt cct 1651  
 Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser Pro  
 505 510 515

gat tcg gca cac cag cag gtg agt ttg cgt ggt ggg tct ggt tcg gag 1699  
 Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser Glu  
 520 525 530

ttc atg att gtt gat atc act gac ggc cgg ttg tta ggc acc atc gat 1747  
 Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile Asp  
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tcc gcg aag gcg atg tcg cag act cat ccc ggc gcg gtg tat ctc cac 1795  
 Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly Ala Val Tyr Leu His  
 550 555 560 565

cag ggt gaa tcc ttt gtc att gat gag ttg gat ttg gag gag aat ctg 1843  
 Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn Leu  
 570 575 580

gca ctg gcc agg cct gag ctg cct gat tac acc acc tat gcc aga agt 1891  
Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg Ser  
585 590 595

gac acg gac atc agg att acc tct gcc ccg ttg gag gac gag gtt ttt 1939  
Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val Phe  
600 605 610

gat gct ggt ggt ggt ttg tgg gtc gcc aac gta gag gtg cag gtc acc 1987  
Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val Thr  
615 620 625

gac cgt gtg act ggc tat gtc acc cgc ctt agt gat ggc acc acg ttg 2035  
Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr Leu  
630 635 640 645

gat gcg act ccg ttg tat ctt cct cct caa att ctt cag act cgt gcg 2083  
Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg Ala  
650 655 660

gtg gcg tac acg att gat ccg ttg gcg ttg gaa gcg atg ggc att ccc 2131  
Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile Pro  
665 670 675

gcc gct gat att ccc ggt gct ctt cac gca gcg gag cat gcg gcg att 2179  
Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala Ile  
680 685 690

ggt atg ttg ccg ctg ctt gcg acg tgt gat cgt tgg gat atc ggc ggc 2227  
Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly Gly  
695 700 705

gta tcc acg gca ctt cat gcg gat acg ggc tac ccc act gtg ttt gtc 2275  
Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe Val  
710 715 720 725

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Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe Arg  
730 735 740

cgt ttc gcc cag tgg att gag gcc aca ttt gag gtc gtc cgc agc tgt 2371  
Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser Cys  
745 750 755

agc tgt gaa tct ggg tgc ccg agc tgt gtg cag tcc ccg aaa tgc ggc 2419  
Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys Gly  
760 765 770

aat gga aac aat ccg ttg gat aag gca ggt gcc atc aag tta ctg ggt 2467  
Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu Gly  
775 780 785

gcg atg gtg acc ttg ttg gga acc tca taaaggtcct gcttttgcgt 2514  
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790 795

ggg 2517

&lt;210&gt; 88

&lt;211&gt; 798

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 88

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 Ser Thr Leu Thr His Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr  
 35 40 45  
 Val Asp Trp Pro Ser Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val  
 50 55 60  
 Asn Arg Gly Ile Asn Lys Leu Phe Ser His Gln Glu Gln Thr Ala His  
 65 70 75 80  
 Leu Ala Trp Asn Gly Gln His Val Val Ala Thr Gly Thr Ser Ser  
 85 90 95  
 Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr  
 100 105 110  
 Asp Pro Thr Ala Cys Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly  
 115 120 125  
 Ser Asp Gln Leu Thr Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp  
 130 135 140  
 Phe His Pro Ile Asn Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu  
 145 150 155 160  
 Ala Arg Ser Gly Ile Arg Asp Leu Ser Arg Phe Val Phe Thr Asn Pro  
 165 170 175  
 Asp Met Val His Ala Ser Met Leu Ala Asn His Pro Arg Trp Ala Arg  
 180 185 190  
 Leu Leu Arg His Leu Lys Phe Ile Val Ile Asp Glu Cys His Ala Tyr  
 195 200 205  
 Arg Gly Val Phe Gly Ala Asn Val Ser Met Val Leu Arg Arg Leu Leu  
 210 215 220  
 Arg Ile Ala Ala Phe Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser  
 225 230 235 240  
 Ala Thr Ser Ser Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala  
 245 250 255  
 Pro Val Lys Ala Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr  
 260 265 270  
 Val Leu Leu Trp Glu Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn  
 275 280 285  
 Gly Ala Pro Val Arg Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met  
 290 295 300

Ala Thr Leu Ile Ser Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser  
 305 310 315 320  
 Arg Arg Gln Ala Glu Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser  
 325 330 335  
 Thr Leu Gly Arg Pro Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala  
 340 345 350  
 Gly Tyr Leu Ala Glu Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp  
 355 360 365  
 Gly Thr Leu Leu Gly Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile  
 370 375 380  
 Asp Val Gly Gly Leu Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr  
 385 390 395 400  
 Val Ala Ser Phe Trp Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln  
 405 410 415  
 Gly Ser Leu Val Val Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr  
 420 425 430  
 Leu Val His His Pro Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala  
 435 440 445  
 Val Phe Asp Pro Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys  
 450 455 460  
 Ala Ala Val Glu Lys Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly  
 465 470 475 480  
 Ala Gln Lys Val Val Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys  
 485 490 495  
 Arg Pro Arg Gly Trp Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro  
 500 505 510  
 Asp Glu Leu Ser Pro Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly  
 515 520 525  
 Gly Ser Gly Ser Glu Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu  
 530 535 540  
 Leu Gly Thr Ile Asp Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly  
 545 550 555 560  
 Ala Val Tyr Leu His Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp  
 565 570 575  
 Leu Glu Glu Asn Leu Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr  
 580 585 590  
 Thr Tyr Ala Arg Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu  
 595 600 605  
 Glu Asp Glu Val Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val  
 610 615 620  
 Glu Val Gln Val Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser

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 aag ctc ttt tcc cac cag gag cag acc gca cat ctg gcg tgg aat ggc 355  
 Lys Leu Phe Ser His Gln Glu Gln Thr Ala His Leu Ala Trp Asn Gly  
 70 75 80 85  
 cag cat gtg gtg gtt gcc acc ggt aca tct tcg gga aaa tct ttg ggt 403  
 Gln His Val Val Val Ala Thr Gly Thr Ser Ser Gly Lys Ser Leu Gly  
 90 95 100  
 tat cag ctg ccc att ttg tca gcg ctc ggc acg gat cct acc gcc tgt 451  
 Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr Asp Pro Thr Ala Cys  
 105 110 115  
 gcg ttg tat cta act ccc acc aag gct ttg gga tct gat cag cta acc 499  
 Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly Ser Asp Gln Leu Thr  
 120 125 130  
 tcc acg tcc acg ttg ctg cgc gac att ccg gat ttc cac ccg att aat 547  
 Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp Phe His Pro Ile Asn  
 135 140 145  
 ccg gcg ccc tac gat ggc gat acc ccc tcc gag gcg cgg tcc ggc atc 595  
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 Arg Asp Leu Ser Arg  
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 <213> Corynebacterium glutamicum

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 20 25 30  
 Ser Thr Leu Thr His Met Val Thr Leu Pro Ala Ser Lys Ala Lys Tyr  
 35 40 45  
 Val Asp Trp Pro Ser Trp Val Pro Ala Ser Leu Arg Asp Ala Leu Val  
 50 55 60  
 Asn Arg Gly Ile Asn Lys Leu Phe Ser His Gln Glu Gln Thr Ala His  
 65 70 75 80  
 Leu Ala Trp Asn Gly Gln His Val Val Val Ala Thr Gly Thr Ser Ser  
 85 90 95  
 Gly Lys Ser Leu Gly Tyr Gln Leu Pro Ile Leu Ser Ala Leu Gly Thr  
 100 105 110

Asp Pro Thr Ala Cys Ala Leu Tyr Leu Thr Pro Thr Lys Ala Leu Gly  
 115 120 125

Ser Asp Gln Leu Thr Ser Thr Ser Thr Leu Leu Arg Asp Ile Pro Asp  
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Phe His Pro Ile Asn Pro Ala Pro Tyr Asp Gly Asp Thr Pro Ser Glu  
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Ala Arg Ser Gly Ile Arg Asp Leu Ser Arg  
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 <223> FRXA00817

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gat ccg gaa att cat gct tcc aga ttg ttg ggc gcg ccg gtt aaa gca 96  
 Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala  
 20 25 30

gtg acg gaa gat ggc gcc ccg acg ggt gaa cgc acc gtt ttg ctg tgg 144  
 Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp  
 35 40 45

gag ccc ggt ttc atc gaa ggc gcc gag ggc gag aac ggc gcg ccg gtg 192  
 Glu Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val  
 50 55 60

cgt cgc gca gcc agc acc gaa gca gca aac att atg gcc acg ctc att 240  
 Arg Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile  
 65 70 75 80

tcc gag ggt gca cgc acg ttg acg ttc gtc cgt tca cgt cga caa gca 288  
 Ser Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala  
 85 90 95

gaa atc gtt gcc ctg cgc gcg cag gaa gag ctc agc acg ctg ggc cgc 336  
 Glu Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser Thr Leu Gly Arg  
 100 105 110

ccc gat ttc gcc cgg cgc gtc gcg tcc tac cgg gcg ggg tac ttg gcg 384  
 Pro Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala  
 115 120 125

gag gac cgc cgt agg ttg gag aga ttg ctt gac gac ggc acc ctc ctc 432  
 Glu Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu  
 130 135 140

ggt gtt gct tcc acc aat gcg ctt gaa ctg ggc att gat gtc ggt gga 480



Gly Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly	145	150	155	160	
ctg gat gct gtg gtc acg gct ggt ttt cca gga act gtg gcg tcg ttt					528
Leu Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe	165		170	175	
tgg cag cag gcg ggg cga gct ggt cgg cgt ggg cag ggt tcg ttg gtg					576
Trp Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln Gly Ser Leu Val	180		185	190	
gtg ctt gtt gct cgt gat gag ccg atg gat acg tat ttg gtg cat cat					624
Val Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His	195	200		205	
ccg gca gcc ctg ttg gag aag ccg gtt gag gct gcg gtg ttt gat ccg					672
Pro Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro	210	215		220	
acg aat ccg cat gtt att cgg ggt cat gtt tat tgc gct gcg gtg gaa					720
Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu	225	230	235	240	
aag cct ctg aca gag gcg gag gtc gcg gcg ttt ggt gcc caa aag gtg					768
Lys Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val	245		250	255	
gtg gag aag ctc gag att gaa ggg ctg ttg cgc aag cgt ccg cgt ggc					816
Val Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly	260	265		270	
tgg ttt gcg gtg gaa aag ccc atg tca gag gat ccg gat gag ctg agt					864
Trp Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser	275	280		285	
cct gat tcg gca cac cag cag gtg agt ttg cgt ggt ggg tct ggt tcg					912
Pro Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser	290	295		300	
gag ttc atg att gtt gat atc act gac gcc gcg ttg tta ggc acc atc					960
Glu Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile	305	310	315	320	
gat tcc gcg aag gcg atg tcg cag act cat ccc gcc gcg gtg tat ctc					1008
Asp Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly Ala Val Tyr Leu	325		330	335	
cac cag ggt gaa tcc ttt gtc att gat gag ttg gat ttg gag gag aat					1056
His Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn	340	345		350	
ctg gca ctg gcc agg cct gag ctg cct gat tac acc acc tat gcc aga					1104
Leu Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg	355	360		365	
agt gac acg gac atc agg att acc tct gcc ccg ttg gag gac gag gtt					1152
Ser Asp Thr Asp Ile Arg Ile Thr Ser Ala Pro Leu Glu Asp Glu Val	370	375	380		
ttt gat gct ggt ggt ggt ttg tgg gtc gcc aac gta gag gtg cag gtc					1200
Phe Asp Ala Gly Gly Gly Leu Trp Val Ala Asn Val Glu Val Gln Val					

385	390	395	400	
acc gac cgt gtg act ggc tat gtc acc cgc ctt agt gat ggc acc acg				1248
Thr Asp Arg Val Thr Gly Tyr Val Thr Arg Leu Ser Asp Gly Thr Thr	405	410	415	
ttg gat gcg act ccg ttg tat ctt cct cct caa att ctt cag act cgt				1296
Leu Asp Ala Thr Pro Leu Tyr Leu Pro Pro Gln Ile Leu Gln Thr Arg	420	425	430	
gcg gtg gcg tac acg att gat ccg ttg gcg ttg gaa gcg atg ggc att				1344
Ala Val Ala Tyr Thr Ile Asp Pro Leu Ala Leu Glu Ala Met Gly Ile	435	440	445	
ccc gcc gct gat att ccc ggt gct ctt cac gca gcg gag cat gcg gcg				1392
Pro Ala Ala Asp Ile Pro Gly Ala Leu His Ala Ala Glu His Ala Ala	450	455	460	
att ggt atg ttg ccg ctg ctt gcg acg tgt gat cgt tgg gat atc ggc				1440
Ile Gly Met Leu Pro Leu Leu Ala Thr Cys Asp Arg Trp Asp Ile Gly	465	470	475	480
ggc gta tcc acg gca ctt cat gcg gat acg ggc tac ccc act gtg ttt				1488
Gly Val Ser Thr Ala Leu His Ala Asp Thr Gly Tyr Pro Thr Val Phe	485	490	495	
gtc tat gac ggt atg gac ggc gga gct ggt ttt gcg gat act ggt ttt				1536
Val Tyr Asp Gly Met Asp Gly Gly Ala Gly Phe Ala Asp Thr Gly Phe	500	505	510	
cga cgt ttc gcc cag tgg att gag gcc aca ttt gag gtc gtc cgc agc				1584
Arg Arg Phe Ala Gln Trp Ile Glu Ala Thr Phe Glu Val Val Arg Ser	515	520	525	
tgt agc tgt gaa tct ggg tgc ccg agc tgt gtg cag tcc ccg aaa tgc				1632
Cys Ser Cys Glu Ser Gly Cys Pro Ser Cys Val Gln Ser Pro Lys Cys	530	535	540	
ggc aat gga aac aat ccg ttg gat aag gca ggt gcc atc aag tta ctg				1680
Gly Asn Gly Asn Asn Pro Leu Asp Lys Ala Gly Ala Ile Lys Leu Leu	545	550	555	560
ggt gcg atg gtg acc ttg ttg gga acc tca taaaggctcct gcttttgcgt				1730
Gly Ala Met Val Thr Leu Leu Gly Thr Ser	565	570		
ggg				1733
<210> 92				
<211> 570				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 92				
Phe Tyr Gly Ser His Pro Thr Val Ile Leu Ala Ser Ala Thr Ser Ser	1	5	10	15
Asp Pro Glu Ile His Ala Ser Arg Leu Leu Gly Ala Pro Val Lys Ala	20	25	30	

Val Thr Glu Asp Gly Ala Pro Thr Gly Glu Arg Thr Val Leu Leu Trp  
 35 40 45  
 Glu Pro Gly Phe Ile Glu Gly Ala Glu Gly Glu Asn Gly Ala Pro Val  
 50 55 60  
 Arg Arg Ala Ala Ser Thr Glu Ala Ala Asn Ile Met Ala Thr Leu Ile  
 65 70 75 80  
 Ser Glu Gly Ala Arg Thr Leu Thr Phe Val Arg Ser Arg Arg Gln Ala  
 85 90 95  
 Glu Ile Val Ala Leu Arg Ala Gln Glu Glu Leu Ser Thr Leu Gly Arg  
 100 105 110  
 Pro Asp Phe Ala Arg Arg Val Ala Ser Tyr Arg Ala Gly Tyr Leu Ala  
 115 120 125  
 Glu Asp Arg Arg Arg Leu Glu Arg Leu Leu Asp Asp Gly Thr Leu Leu  
 130 135 140  
 Gly Val Ala Ser Thr Asn Ala Leu Glu Leu Gly Ile Asp Val Gly Gly  
 145 150 155 160  
 Leu Asp Ala Val Val Thr Ala Gly Phe Pro Gly Thr Val Ala Ser Phe  
 165 170 175  
 Trp Gln Gln Ala Gly Arg Ala Gly Arg Arg Gly Gln Gly Ser Leu Val  
 180 185 190  
 Val Leu Val Ala Arg Asp Glu Pro Met Asp Thr Tyr Leu Val His His  
 195 200 205  
 Pro Ala Ala Leu Leu Glu Lys Pro Val Glu Ala Ala Val Phe Asp Pro  
 210 215 220  
 Thr Asn Pro His Val Ile Arg Gly His Val Tyr Cys Ala Ala Val Glu  
 225 230 235 240  
 Lys Pro Leu Thr Glu Ala Glu Val Ala Ala Phe Gly Ala Gln Lys Val  
 245 250 255  
 Val Glu Lys Leu Glu Ile Glu Gly Leu Leu Arg Lys Arg Pro Arg Gly  
 260 265 270  
 Trp Phe Ala Val Glu Lys Pro Met Ser Glu Asp Pro Asp Glu Leu Ser  
 275 280 285  
 Pro Asp Ser Ala His Gln Gln Val Ser Leu Arg Gly Gly Ser Gly Ser  
 290 295 300  
 Glu Phe Met Ile Val Asp Ile Thr Asp Gly Arg Leu Leu Gly Thr Ile  
 305 310 315 320  
 Asp Ser Ala Lys Ala Met Ser Gln Thr His Pro Gly Ala Val Tyr Leu  
 325 330 335  
 His Gln Gly Glu Ser Phe Val Ile Asp Glu Leu Asp Leu Glu Glu Asn  
 340 345 350  
 Leu Ala Leu Ala Arg Pro Glu Leu Pro Asp Tyr Thr Thr Tyr Ala Arg

ctt tcc cga ttc cga cct caa gta gcg gag tgg ttc cgg gat gtc ttt 163  
Leu Ser Arg Phe Arg Pro Gln Val Ala Glu Trp Phe Arg Asp Val Phe

	10	15	20	
gca tct ccg acc cct gtt cag gag gga acg tgg gag gcg gta tct aag				211
Ala Ser Pro Thr Pro Val Gln Glu Gly Thr Trp Glu Ala Val Ser Lys				
	25	30	35	
ggg aag aat gcc ctc gtg gtg gcg ccg acc ggt agt ggt aaa acc ttg				259
Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly Ser Gly Lys Thr Leu				
	40	45	50	
gct gcg ttt ttg tgg gcg tta gat tcc ctc act gaa caa aca ggt caa				307
Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr Glu Gln Thr Gly Gln				
	55	60	65	
cag gtt tta gac acg gga aca ccg gtg cct gtt cgt ggt ggg aaa gtg				355
Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val Arg Gly Gly Lys Val				
	70	75	80	85
aaa gtg ctc tac att tcc cca ctc aaa gcg ctt ggc gtg gat gta gaa				403
Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu Gly Val Asp Val Glu				
	90	95	100	
aat aat ctg cgt gca ccg ttg acc ggt att gcg agg act gcc tct cgg				451
Asn Asn Leu Arg Ala Pro Leu Thr Gly Ile Ala Arg Thr Ala Ser Arg				
	105	110	115	
atg ggt ttg gat gtg ccc aat atc act gtg gcg gtt cgt tcg ggt gat				499
Met Gly Leu Asp Val Pro Asn Ile Thr Val Ala Val Arg Ser Gly Asp				
	120	125	130	
acg cca tcg gcg gag ccg gcc ccg cag gtg cgt aag cct cca gac att				547
Thr Pro Ser Ala Glu Arg Ala Arg Gln Val Arg Lys Pro Pro Asp Ile				
	135	140	145	
ttg atc acc act ccg gag tcg gcg tat ttg atg ttg acc tca aaa gcg				595
Leu Ile Thr Thr Pro Glu Ser Ala Tyr Leu Met Leu Thr Ser Lys Ala				
	150	155	160	165
ggg gcg acc ctt tcg gat gtt gat gtg gtg atc atc gat gaa atc cac				643
Gly Ala Thr Leu Ser Asp Val Asp Val Val Ile Ile Asp Glu Ile His				
	170	175	180	
gcc atg gcc gga acc aaa ccg gga gtg cat ctg gcg ttg acg ctg gag				691
Ala Met Ala Gly Thr Lys Arg Gly Val His Leu Ala Leu Thr Leu Glu				
	185	190	195	
cgt ttg gaa aag ctc gtg ggg ccg cct gtg cag cga gtt ggt ttg tct				739
Arg Leu Glu Lys Leu Val Gly Arg Pro Val Gln Arg Val Gly Leu Ser				
	200	205	210	
gca acg gtg cgt cct ttg gaa acg gtg gcg ggt ttc ttg ggc ggt ggc				787
Ala Thr Val Arg Pro Leu Glu Thr Val Ala Gly Phe Leu Gly Gly Gly				
	215	220	225	
aga ccc gtt gag att gtg gct cca cct gcg gag aaa aag tgg gat ctc				835
Arg Pro Val Glu Ile Val Ala Pro Pro Ala Glu Lys Lys Trp Asp Leu				
	230	235	240	245
act gtc act gtg ccg gtg gaa gac atg tcg gat ttg ccg gtt cag gag				883
Thr Val Thr Val Pro Val Glu Asp Met Ser Asp Leu Pro Val Gln Glu				
	250	255	260	

ccg gga tca act att ggt gaa cta gtc atg gat gat ccg ttg ggg att 931  
 Pro Gly Ser Thr Ile Gly Glu Leu Val Met Asp Asp Pro Leu Gly Ile  
 265 270 275

act ggc gaa tca gcg ctg cct act caa ggc tcg att tgg cca cac att 979  
 Thr Gly Glu Ser Ala Leu Pro Thr Gln Gly Ser Ile Trp Pro His Ile  
 280 285 290

gag cag cag gtg tac aac cag gtg atg tcg gcg aaa tcg acc atc gtg 1027  
 Glu Gln Gln Val Tyr Asn Gln Val Met Ser Ala Lys Ser Thr Ile Val  
 295 300 305

ttt gta aat tcc agg cgt tcc gcg gag cgt tta acc agt cgg ttg aat 1075  
 Phe Val Asn Ser Arg Arg Ser Ala Glu Arg Leu Thr Ser Arg Leu Asn  
 310 315 320 325

gaa atc tgg gcg atg gaa cac gat ccg gaa tcg ctg tcg ccg cag ctg 1123  
 Glu Ile Trp Ala Met Glu His Asp Pro Glu Ser Leu Ser Pro Gln Leu  
 330 335 340

cga aga gat ccg gcg cag att atg tcg tca gcg gat gtg gca gga aaa 1171  
 Arg Arg Asp Pro Ala Gln Ile Met Ser Ser Ala Asp Val Ala Gly Lys  
 345 350 355

gca cca cag gtg atc gca cgt gcg cac cac gga tcc gta tcc aaa gat 1219  
 Ala Pro Gln Val Ile Ala Arg Ala His His Gly Ser Val Ser Lys Asp  
 360 365 370

gaa cgt gcc acc acc gaa acc atg ctg aag gaa ggt cgg ttg cgc gca 1267  
 Glu Arg Ala Thr Thr Glu Thr Met Leu Lys Glu Gly Arg Leu Arg Ala  
 375 380 385

gtt att tcc acc tcc tcg ctg gag ttg ggc att gat atg ggt gcc gtg 1315  
 Val Ile Ser Thr Ser Ser Leu Glu Leu Gly Ile Asp Met Gly Ala Val  
 390 395 400 405

gac ctg gtg att cag gtg gaa tcg cca ccg tcc gtg gca agt ggc ctg 1363  
 Asp Leu Val Ile Gln Val Glu Ser Pro Pro Ser Val Ala Ser Gly Leu  
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cag cgc gtg ggg cgt gcg ggg cac acg gtg ggg gcg acg tcg ata ggc 1411  
 Gln Arg Val Gly Arg Ala Gly His Thr Val Gly Ala Thr Ser Ile Gly  
 425 430 435

tcc ttt tat ccc aag cac cgc tcc gac ttg gtg caa acc gcg gtg acc 1459  
 Ser Phe Tyr Pro Lys His Arg Ser Asp Leu Val Gln Thr Ala Val Thr  
 440 445 450

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 Val Gln Arg Met Lys Glu Gly Leu Ile Glu Glu Ile His Val Pro Lys  
 455 460 465

aac gcg ctt gat gta ctg gca cag cag acg gtg gcg gct gtc tcg att 1555  
 Asn Ala Leu Asp Val Leu Ala Gln Gln Thr Val Ala Ala Val Ser Ile  
 470 475 480 485

aaa gat gtg cag gtc gat gag tgg tac gag act att cgc aag gcg tat 1603  
 Lys Asp Val Gln Val Asp Glu Trp Tyr Glu Thr Ile Arg Lys Ala Tyr  
 490 495 500

ccg tac cgg gat ttg gcg cgc gaa gtc ttc gat tcc gtc atc gac ctg 1651  
 Pro Tyr Arg Asp Leu Ala Arg Glu Val Phe Asp Ser Val Ile Asp Leu  
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gtc agc ggt gtg tat ccc tcc aca gat ttt gcc gag ctg aag cca cgt 1699  
 Val Ser Gly Val Tyr Pro Ser Thr Asp Phe Ala Glu Leu Lys Pro Arg  
 520 525 530

gtg gtg tac gac cgg gtt tca ggc gtg ctg gag ggc cgg cca gga tcc 1747  
 Val Val Tyr Asp Arg Val Ser Gly Val Leu Glu Gly Arg Pro Gly Ser  
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caa cgc gta gca gtg acc agt ggc gga aca att ccc gat cga gga atg 1795  
 Gln Arg Val Ala Val Thr Ser Gly Gly Thr Ile Pro Asp Arg Gly Met  
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ttc gga gtc ttc ctc gtc ggc gat ggt ccc cgg cgc gtc ggc gag ctc 1843  
 Phe Gly Val Phe Leu Val Gly Asp Gly Pro Arg Arg Val Gly Glu Leu  
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 Asp Glu Glu Met Val Tyr Glu Ser Arg Val Gly Asp Val Phe Thr Leu  
 585 590 595

ggg gcg tcg agt tgg cgg att gaa gag atc acc cgc gac cag gta ctg 1939  
 Gly Ala Ser Ser Trp Arg Ile Glu Glu Ile Thr Arg Asp Gln Val Leu  
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 Val Thr Pro Ala Pro Gly His Thr Gly Arg Leu Pro Phe Trp Thr Gly  
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gat gcc gca ggc cgg ccc gct gag ctg ggt aaa gct tta ggc gct ttt 2035  
 Asp Ala Ala Gly Arg Pro Ala Glu Leu Gly Lys Ala Leu Gly Ala Phe  
 630 635 640 645

cga cgc tcg acc ctc acc gat cca tcc agc tcc ggc ttg gaa ggc tgg 2083  
 Arg Arg Ser Thr Leu Thr Asp Pro Ser Ser Gly Leu Glu Gly Trp  
 650 655 660

gcg cac gac aac ctg atc gcc ttt tta cag gag cag gaa gaa tcc acc 2131  
 Ala His Asp Asn Leu Ile Ala Phe Leu Gln Glu Gln Glu Glu Ser Thr  
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ggt gtg ttg ccg gat gag aag acg ttg gtg ttg gag cgt ttc aaa gat 2179  
 Gly Val Leu Pro Asp Glu Lys Thr Leu Val Leu Glu Arg Phe Lys Asp  
 680 685 690

gaa cta ggc gac tgg cgc att gtc ctg cac act cct tat gga cga gga 2227  
 Glu Leu Gly Asp Trp Arg Ile Val Leu His Thr Pro Tyr Gly Arg Gly  
 695 700 705

gta aac gca gca tgg gct ttg gcc gtc ggg gcg aaa atc gct gaa gag 2275  
 Val Asn Ala Ala Trp Ala Leu Ala Val Gly Ala Lys Ile Ala Glu Glu  
 710 715 720 725

acc ggc atg gat gcg caa gcc gtg gca ggt gat gat ggc att gtg ctt 2323  
 Thr Gly Met Asp Ala Gln Ala Val Ala Gly Asp Asp Gly Ile Val Leu  
 730 735 740

cgg ttg ccg gaa ggg gat gaa gat ccc agc gca gcg ttg ttt atg ttt 2371

Arg Leu Pro Glu Gly Asp Glu Asp Pro Ser Ala Ala Leu Phe Met Phe	
745 750 755	
gag gcg gaa gag atc gaa acg cta gtg aca gag cag gtg ggt aac tct	2419
Glu Ala Glu Glu Ile Glu Thr Leu Val Thr Glu Gln Val Gly Asn Ser	
760 765 770	
gcg ctg ttt gcc agc agg ttc cgt gaa tgc gcc gcg agg gcc cta ttg	2467
Ala Leu Phe Ala Ser Arg Phe Arg Glu Cys Ala Ala Arg Ala Leu Leu	
775 780 785	
ctg ccg aga cga aac ccc ggc aag cgc gca ccg ctg tgg cag caa cga	2515
Leu Pro Arg Arg Asn Pro Gly Lys Arg Ala Pro Leu Trp Gln Gln Arg	
790 795 800 805	
caa cga gca gca cag ctt ctt gat gtg gcc aga aag tac ccg agt ttc	2563
Gln Arg Ala Ala Gln Leu Leu Asp Val Ala Arg Lys Tyr Pro Ser Phe	
810 815 820	
ccg atc att ttg gaa aca gtg cgc gaa tgt ctt caa gat gtt tac gat	2611
Pro Ile Ile Leu Glu Thr Val Arg Glu Cys Leu Gln Asp Val Tyr Asp	
825 830 835	
ctg ccc gct ctg aag aat ctc att gag gat cta cag ctg cgg aag gta	2659
Leu Pro Ala Leu Lys Asn Leu Ile Glu Asp Leu Gln Leu Arg Lys Val	
840 845 850	
aga atc gcg gaa gtc acc acc cag cag ccc agt cct ttt gcc tcc gca	2707
Arg Ile Ala Glu Val Thr Gln Gln Pro Ser Pro Phe Ala Ser Ala	
855 860 865	
ttg ctg ttc aat tac acc ggt gca ttc atg tac gaa ggc gac agc ccg	2755
Leu Leu Phe Asn Tyr Thr Gly Ala Phe Met Tyr Glu Gly Asp Ser Pro	
870 875 880 885	
ctc gca gag aaa cgt gcc gca gcg ttg gcc ctg gat ccg gca ctg ttg	2803
Leu Ala Glu Lys Arg Ala Ala Ala Leu Ala Leu Asp Pro Ala Leu Leu	
890 895 900	
gcg aaa ttg ctg ggt gag gtg gag ctt cga caa tta ctg gat ccc gac	2851
Ala Lys Leu Leu Gly Glu Val Glu Leu Arg Gln Leu Leu Asp Pro Asp	
905 910 915	
atc atc gca gaa gtg cac caa caa ttg cgc agg caa ggc gat cgt gcg	2899
Ile Ile Ala Glu Val His Gln Gln Leu Arg Arg Gln Gly Asp Arg Ala	
920 925 930	
gcg aga aac aat gaa gaa ctc gca gat tct ttg agg att tta gga ccg	2947
Ala Arg Asn Asn Glu Glu Leu Ala Asp Ser Leu Arg Ile Leu Gly Pro	
935 940 945	
att cct ttg gat gaa ttg ggc gaa cac atc acc ttt gaa aac cca gac	2995
Ile Pro Leu Asp Glu Leu Gly Glu His Ile Thr Phe Glu Asn Pro Asp	
950 955 960 965	
ctg gag gat cga gca atg act gtt cgg atc aac ggt cgg gaa cat tta	3043
Leu Glu Asp Arg Ala Met Thr Val Arg Ile Asn Gly Arg Glu His Leu	
970 975 980	
gcg cag gtc ttg gat gca cct ttg ctt cga gat gcc tta ggt gtt ccc	3091
Ala Gln Val Leu Asp Ala Pro Leu Leu Arg Asp Ala Leu Gly Val Pro	



985	990	995	
gta ccg cct ggt gtg cct gcg cag gta gaa acc att acg gat gcg ttg			3139
Val Pro Pro Gly Val Pro Ala Gln Val Glu Thr Ile Thr Asp Ala Leu			
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gaa cag tta gtc aac agg tgg gtt cgt acc aga ggg cca ttt act gcg			3187
Glu Gln Leu Val Asn Arg Trp Val Arg Thr Arg Gly Pro Phe Thr Ala			
1015	1020	1025	
aat gat ttg gca gaa gcc ttt gga ctg ggc atc gcc acg gcg atc acc			3235
Asn Asp Leu Ala Glu Ala Phe Gly Leu Gly Ile Ala Thr Ala Ile Thr			
1030	1035	1040	1045
gcc ctt caa agc gca cct gtg att gaa ggc cgc tac cga caa ggc gtg			3283
Ala Leu Gln Ser Ala Pro Val Ile Glu Gly Arg Tyr Arg Gln Gly Val			
1050	1055	1060	
gac gtg cag gaa tac tgt gcg aca gaa gtg ttg tcg atc ata agg cga			3331
Asp Val Gln Glu Tyr Cys Ala Thr Glu Val Leu Ser Ile Ile Arg Arg			
1065	1070	1075	
cgc agc ctc gca gca gcg agg aaa caa acc agg ccg gta tcg caa tca			3379
Arg Ser Leu Ala Ala Ala Arg Lys Gln Thr Arg Pro Val Ser Gln Ser			
1080	1085	1090	
gcc ttt gcg cga ttc ctg ctt gat tgg caa cag atc gca ccg gtg ggc			3427
Ala Phe Ala Arg Phe Leu Leu Asp Trp Gln Gln Ile Ala Pro Val Gly			
1095	1100	1105	
gcc aca cct gaa ctt cga ggc gtt gat ggc acc tac aca gtc att gaa			3475
Ala Thr Pro Glu Leu Arg Gly Val Asp Gly Thr Tyr Thr Val Ile Glu			
1110	1115	1120	1125
caa ctc gcc ggt gta cgt ctt ccc gcc agt gcg tgg gaa gat ctc gtg			3523
Gln Leu Ala Gly Val Arg Leu Pro Ala Ser Ala Trp Glu Asp Leu Val			
1130	1135	1140	
ttg ccg cgc cgg gtt gcc gac tat tca ccg atc cat ctc gat gag ctg			3571
Leu Pro Arg Arg Val Ala Asp Tyr Ser Pro Ile His Leu Asp Glu Leu			
1145	1150	1155	
acc tcc aat ggg gaa gtc ctc atc gtg gga gcg ggc caa gcc gga agc			3619
Thr Ser Asn Gly Glu Val Leu Ile Val Gly Ala Gly Gln Ala Gly Ser			
1160	1165	1170	
cgc gat ccg tgg att agc ttg ctg ccc gtg gat tat gcg gcg cag ttg			3667
Arg Asp Pro Trp Ile Ser Leu Leu Pro Val Asp Tyr Ala Ala Gln Leu			
1175	1180	1185	
gtg ggg gag gcg tcg aca agc atg agc cca ttg cag gac gcc gtg ctt			3715
Val Gly Glu Ala Ser Thr Ser Met Ser Pro Leu Gln Asp Ala Val Leu			
1190	1195	1200	1205
gac cag ctg cgt gcg gga ggc gcc ttc ctg ttt tct gac att ctc gaa			3763
Asp Gln Leu Arg Ala Gly Gly Ala Phe Leu Phe Ser Asp Ile Leu Glu			
1210	1215	1220	
gag aat ttc ggc tac acc aca gcc cag ctg caa gaa gcg atg tgg ggg			3811
Glu Asn Phe Gly Tyr Thr Thr Ala Gln Leu Gln Glu Ala Met Trp Gly			
1225	1230	1235	

ctg gtg gaa gca ggc ctg gtc agc cct gat agc ttc gcg ccg atc cgc 3859  
 Leu Val Glu Ala Gly Leu Val Ser Pro Asp Ser Phe Ala Pro Ile Arg  
 1240 1245 1250

gcg cgc cta gcg tcg gga acc acg gcg cat cgg gcg aaa cgt cga cca 3907  
 Ala Arg Leu Ala Ser Gly Thr Thr Ala His Arg Ala Lys Arg Arg Pro  
 1255 1260 1265

gcg aga tcc cgg ctg cgc acc cgc acc agc ttc gcg agc gac gtg ccc 3955  
 Ala Arg Ser Arg Leu Arg Thr Arg Thr Ser Phe Ala Ser Asp Val Pro  
 1270 1275 1280 1285

cca gac atg cgc gga cga tgg acg ctg tcc gtg caa ccc gcc gac gcc 4003  
 Pro Asp Met Arg Gly Arg Trp Thr Leu Ser Val Gln Pro Ala Asp Ala  
 1290 1295 1300

acc agc cgc tcc gtc gca cac ggc gaa ggc tgg ctc gac cgc tac gcc 4051  
 Thr Ser Arg Ser Val Ala His Gly Glu Gly Trp Leu Asp Arg Tyr Gly  
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 Val Leu Thr Arg Gly Ser Val Val Ala Glu Asp Ile Val Gly Gly Phe  
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gcc ctg gcc tac aaa gtg ctc tcc ggc ttc gaa gaa agc ggc aaa gcg 4147  
 Ala Leu Ala Tyr Lys Val Leu Ser Gly Phe Glu Glu Ser Gly Lys Ala  
 1335 1340 1345

atg cgc ggc tac ttc atc gaa ggg ctc ggc gcc gcg caa ttc tcc acg 4195  
 Met Arg Gly Tyr Phe Ile Glu Gly Leu Gly Ala Ala Gln Phe Ser Thr  
 1350 1355 1360 1365

ccc gcc atc atc gac cgc ctc cgc ggc cac gac gat tcc ccc gac gtc 4243  
 Pro Ala Ile Ile Asp Arg Leu Arg Gly His Asp Asp Ser Pro Asp Val  
 1370 1375 1380

gaa ggc tgg ccc tcc ggc gcc acc gac cca gac gtc tac ctc ata gcc 4291  
 Glu Gly Trp Pro Ser Gly Ala Thr Asp Pro Asp Val Tyr Leu Ile Ala  
 1385 1390 1395

gcc gcc gac ccc gca aac ccc tac ggc gcc gca ctt ccc tgg cct gag 4339  
 Ala Ala Asp Pro Ala Asn Pro Tyr Gly Ala Ala Leu Pro Trp Pro Glu  
 1400 1405 1410

cag ggg ccc agc cgc gcc gcc gga gct atg gtc gtg ctt tgc gac gga 4387  
 Gln Gly Pro Ser Arg Ala Ala Gly Ala Met Val Val Leu Cys Asp Gly  
 1415 1420 1425

ctc ctc ctc gcc cac ctc acc cgc ggc ggg cgc acc ctc acc gtg ttc 4435  
 Leu Leu Leu Ala His Leu Thr Arg Gly Gly Arg Thr Leu Thr Val Phe  
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tcc gac aat atc ccc aaa atc gcg aca gcc cta atc aca tac gaa agg 4483  
 Ser Asp Asn Ile Pro Lys Ile Ala Thr Ala Leu Ile Thr Tyr Glu Arg  
 1450 1455 1460

ctc acg gta gaa aaa atc aac ggc gac aac gtc ttc gac tcc cca ctc 4531  
 Leu Thr Val Glu Lys Ile Asn Gly Asp Asn Val Phe Asp Ser Pro Leu  
 1465 1470 1475

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 Leu Glu Gln Phe Arg Lys His Gly Ala Thr Ile Thr Pro Lys Gly Met  
           1480                    1485                    1490

cga ttt cga cca cca gtg gca cgg gaa acc ccc tca gat acg ctt ccc 4627  
 Arg Phe Arg Pro Pro Val Ala Arg Glu Thr Pro Ser Asp Thr Leu Pro  
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acc agg act ttt cgt gga ggc ttc gga cgg cgc taacctgatg acatgccaga 4680  
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           1510                    1515                    1520

agg 4683

&lt;210&gt; 94

&lt;211&gt; 1520

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 94

Met Ala Lys Ser Ile Leu Ser Arg Phe Arg Pro Gln Val Ala Glu Trp  
           1                    5                    10                    15

Phe Arg Asp Val Phe Ala Ser Pro Thr Pro Val Gln Glu Gly Thr Trp  
                     20                    25                    30

Glu Ala Val Ser Lys Gly Lys Asn Ala Leu Val Val Ala Pro Thr Gly  
                     35                    40                    45

Ser Gly Lys Thr Leu Ala Ala Phe Leu Trp Ala Leu Asp Ser Leu Thr  
                     50                    55                    60

Glu Gln Thr Gly Gln Gln Val Leu Asp Thr Gly Thr Pro Val Pro Val  
                     65                    70                    75                    80

Arg Gly Gly Lys Val Lys Val Leu Tyr Ile Ser Pro Leu Lys Ala Leu  
                     85                    90                    95

Gly Val Asp Val Glu Asn Asn Leu Arg Ala Pro Leu Thr Gly Ile Ala  
                     100                    105                    110

Arg Thr Ala Ser Arg Met Gly Leu Asp Val Pro Asn Ile Thr Val Ala  
                     115                    120                    125

Val Arg Ser Gly Asp Thr Pro Ser Ala Glu Arg Ala Arg Gln Val Arg  
                     130                    135                    140

Lys Pro Pro Asp Ile Leu Ile Thr Thr Pro Glu Ser Ala Tyr Leu Met  
                     145                    150                    155                    160

Leu Thr Ser Lys Ala Gly Ala Thr Leu Ser Asp Val Asp Val Val Ile  
                     165                    170                    175

Ile Asp Glu Ile His Ala Met Ala Gly Thr Lys Arg Gly Val His Leu  
                     180                    185                    190

Ala Leu Thr Leu Glu Arg Leu Glu Lys Leu Val Gly Arg Pro Val Gln  
                     195                    200                    205

Arg Val Gly Leu Ser Ala Thr Val Arg Pro Leu Glu Thr Val Ala Gly

210						215						220					
Phe	Leu	Gly	Gly	Gly	Arg	Pro	Val	Glu	Ile	Val	Ala	Pro	Pro	Ala	Glu		
225					230					235					240		
Lys	Lys	Trp	Asp	Leu	Thr	Val	Thr	Val	Pro	Val	Glu	Asp	Met	Ser	Asp		
				245					250					255			
Leu	Pro	Val	Gln	Glu	Pro	Gly	Ser	Thr	Ile	Gly	Glu	Leu	Val	Met	Asp		
			260					265					270				
Asp	Pro	Leu	Gly	Ile	Thr	Gly	Glu	Ser	Ala	Leu	Pro	Thr	Gln	Gly	Ser		
		275					280					285					
Ile	Trp	Pro	His	Ile	Glu	Gln	Gln	Val	Tyr	Asn	Gln	Val	Met	Ser	Ala		
	290					295					300						
Lys	Ser	Thr	Ile	Val	Phe	Val	Asn	Ser	Arg	Arg	Ser	Ala	Glu	Arg	Leu		
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Thr	Ser	Arg	Leu	Asn	Glu	Ile	Trp	Ala	Met	Glu	His	Asp	Pro	Glu	Ser		
				325					330					335			
Leu	Ser	Pro	Gln	Leu	Arg	Arg	Asp	Pro	Ala	Gln	Ile	Met	Ser	Ser	Ala		
			340					345					350				
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Tyr Thr Val Ile Glu Gln Leu Ala Gly Val Arg Leu Pro Ala Ser Ala 1125	1130	1135
Trp Glu Asp Leu Val Leu Pro Arg Arg Val Ala Asp Tyr Ser Pro Ile 1140	1145	1150
His Leu Asp Glu Leu Thr Ser Asn Gly Glu Val Leu Ile Val Gly Ala 1155	1160	1165
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Glu Ala Met Trp Gly Leu Val Glu Ala Gly Leu Val Ser Pro Asp Ser 1235	1240	1245
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Gln Pro Ala Asp Ala Thr Ser Arg Ser Val Ala His Gly Glu Gly Trp 1300	1305	1310
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Ile Val Gly Gly Phe Ala Leu Ala Tyr Lys Val Leu Ser Gly Phe Glu 1330	1335	1340
Glu Ser Gly Lys Ala Met Arg Gly Tyr Phe Ile Glu Gly Leu Gly Ala 1345	1350	1355 1360
Ala Gln Phe Ser Thr Pro Ala Ile Ile Asp Arg Leu Arg Gly His Asp 1365	1370	1375
Asp Ser Pro Asp Val Glu Gly Trp Pro Ser Gly Ala Thr Asp Pro Asp 1380	1385	1390

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 Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu Trp Glu Asn Val Leu  
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 Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His His Gln Lys Ala Ala  
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Thr Ser Glu Gln Arg Ala Ala Ile Glu Gln Gly Arg Ser Val Ala Gly		570	575	580
ccg cga gga gtt gat ggc acc tca gca gtg ctg tgg ttc cat agc gcc	1891			
Pro Arg Gly Val Asp Gly Thr Ser Ala Val Leu Trp Phe His Ser Ala		585	590	595
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Ser Asn Glu Leu Ser Thr Arg Gln Pro Ser Pro Glu Glu Glu Gln Ser		600	605	610
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Gly Ser Ser Ile Ala Val Leu Thr His Phe Gly Pro Glu Ala Asp Asp		615	620	625
ctc tcc gcc aaa cag acc tgc cct tcc tgt ggt gat gtt gat tcc atc	2035			
Leu Ser Ala Lys Gln Thr Cys Pro Ser Cys Gly Asp Val Asp Ser Ile		630	635	640
cgt tat atc gga tcg gga atc tct acc ctg ctc tct gtc tca ctc tcc	2083			
Arg Tyr Ile Gly Ser Gly Ile Ser Thr Leu Leu Ser Val Ser Leu Ser		650	655	660
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Asn Leu Phe Gly Met Ala Asp Leu Asp Ser Ala Glu Lys Lys Thr Leu		665	670	675
gtc ttt gcc gat tcc gtg caa gat gcc gcg cac cgc gcc ggg tac gtc	2179			
Val Phe Ala Asp Ser Val Gln Asp Ala Ala His Arg Ala Gly Tyr Val		680	685	690
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Gln Ala Arg Ser Arg Ala Phe Ala Leu Arg Thr Tyr Thr Arg Arg Ala		695	700	705
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Val Gly Asp Asn Glu Val Thr Leu Pro Ser Ile Ser Arg Ala Leu Met		710	715	720
gat aac gcc acc tct ggg cgc acc cgt tat gag ctc cta ccc cct gac	2323			
Asp Asn Ala Thr Ser Gly Arg Thr Arg Tyr Glu Leu Leu Pro Pro Asp		730	735	740
ctg acc gat ctt gat att tac aaa cct tat tgg cac ccc gat gcc agc	2371			
Leu Thr Asp Leu Asp Ile Tyr Lys Pro Tyr Trp His Pro Asp Ala Ser		745	750	755
aag gct gag cgc cgt gag gcc tcc cgc aat gtg cat aaa cgt tta agt	2419			
Lys Ala Glu Arg Arg Glu Ala Ser Arg Asn Val His Lys Arg Leu Ser		760	765	770
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Phe Asp Leu Ala Leu Glu Phe Gly Gln Arg Ala Asp Leu Pro Arg Ser		775	780	785
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Val Ala Leu Ser Ala Ala Ala Glu Ala Leu Tyr Ala Ile Glu Val Pro	810	815	820	
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Thr Leu Asp Ile Glu Asp Glu Asn Leu Arg Leu Arg Trp Val Gln Gly	825	830	835	
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Ala Leu Glu Leu Leu Arg Ala Arg Gly Gly Ile Asn His Glu Trp Phe	840	845	850	
ggc gcc tac ctg cgc acc gat ggc aac ccc tat atg ctt aac cgc cgc				2707
Gly Ala Tyr Leu Arg Thr Asp Gly Asn Pro Tyr Met Leu Asn Arg Arg	855	860	865	
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Gln Ala Arg Ala Glu Gly Ile Pro Gly Phe Val Arg Gly Gly Ala Pro	870	875	880	885
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Glu Phe Pro Arg Val Gly Ser Ala Leu Ser Gly Ser Leu Arg Ser Ser	890	895	900	
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Thr Gly Thr Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp	905	910	915	
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Thr Ser Gln Val Leu Gly Ile Ser Thr His Asp Ala Ala Thr Ala Ile	920	925	930	
aca aag ctt ttc gac gct tta agc aac cgc agc att ctc tcc tca ata				2947
Thr Lys Leu Phe Asp Ala Leu Ser Asn Arg Ser Ile Leu Ser Ser Ile	935	940	945	
tct acc gac agc ggc gga aaa atc tac tgc ctc gag gcc gaa cgc atc				2995
Ser Thr Asp Ser Gly Gly Lys Ile Tyr Cys Leu Glu Ala Glu Arg Ile	950	955	960	965
cgt att ttt agc gaa gac cat ccc gaa gtt ctg gaa tgc agc gtg tgc				3043
Arg Ile Phe Ser Glu Asp His Pro Glu Val Leu Glu Cys Ser Val Cys	970	975	980	
cat gcc caa act ggt gta act gat cat gtg cgt gac ttc ctt gat ggc				3091
His Ala Gln Thr Gly Val Thr Asp His Val Arg Asp Phe Leu Asp Gly	985	990	995	
gct ccg tgt ttt agc cct agt tgt ggg ggc gtt ctc cat atc gag gaa				3139
Ala Pro Cys Phe Ser Pro Ser Cys Gly Gly Val Leu His Ile Glu Glu	1000	1005	1010	
gta gaa gac aac tac tac cgc agg ctt tat tcc gca att gaa ccg cgc				3187
Val Glu Asp Asn Tyr Tyr Arg Arg Leu Tyr Ser Ala Ile Glu Pro Arg	1015	1020	1025	
act gtc att gcc cgc gag cac acc agc atg ctc aag aaa aaa gac cgc				3235
Thr Val Ile Ala Arg Glu His Thr Ser Met Leu Lys Lys Lys Asp Arg	1030	1035	1040	1045

ctc gca ctc gaa caa tcc ttt aga ggt gga gaa ggc tcg gcc aaa caa 3283  
 Leu Ala Leu Glu Gln Ser Phe Arg Gly Gly Glu Gly Ser Ala Lys Gln  
 1050 1055 1060

tcc ccc gat gcg ccc aat gtg ttg gta gct acg cca acg ctg gaa atg 3331  
 Ser Pro Asp Ala Pro Asn Val Leu Val Ala Thr Pro Thr Leu Glu Met  
 1065 1070 1075

ggt att gac atc ggc gat ctc tcc acc gtg atg ctt gcg tct ttg cca 3379  
 Gly Ile Asp Ile Gly Asp Leu Ser Thr Val Met Leu Ala Ser Leu Pro  
 1080 1085 1090

aca tca gtg gcc agt tat gta cag cgt gtt ggt cgt gcc ggg cgc ctc 3427  
 Thr Ser Val Ala Ser Tyr Val Gln Arg Val Gly Arg Ala Gly Arg Leu  
 1095 1100 1105

agc gga aac tcg ttg gta ctc gcc gtg gtg cgt ggc cgc ggt gtc aca 3475  
 Ser Gly Asn Ser Leu Val Leu Ala Val Val Arg Gly Arg Gly Val Thr  
 1110 1115 1120 1125

ttg cct cgt ctt aac caa ccg ctc tcc atg atc aag gga gct att acc 3523  
 Leu Pro Arg Leu Asn Gln Pro Leu Ser Met Ile Lys Gly Ala Ile Thr  
 1130 1135 1140

cca cca gtt gcg tat ctt tcc gcc agt gaa atc ttg cac cgc caa ttc 3571  
 Pro Pro Val Ala Tyr Leu Ser Ala Ser Glu Ile Leu His Arg Gln Phe  
 1145 1150 1155

ttg gca tat gtg atc gac tgc tta gat act cgc gcc gaa ctg cca aaa 3619  
 Leu Ala Tyr Val Ile Asp Cys Leu Asp Thr Arg Ala Glu Leu Pro Lys  
 1160 1165 1170

ctc gaa aca gca att gat gtt ttt gat aat gcc gcc gga aaa aca cct 3667  
 Leu Glu Thr Ala Ile Asp Val Phe Asp Asn Ala Ala Gly Lys Thr Pro  
 1175 1180 1185

ttg gtt gca tta ctc aaa gcg cag att cac gca ggc cta gat cct ttg 3715  
 Leu Val Ala Leu Leu Lys Ala Gln Ile His Ala Gly Leu Asp Pro Leu  
 1190 1195 1200 1205

ctg gag gaa ttt gta cgc acc ctc aac atg caa atc agc att gat aat 3763  
 Leu Glu Glu Phe Val Arg Thr Leu Asn Met Gln Ile Ser Ile Asp Asn  
 1210 1215 1220

att ttc gaa ctg cgc act tgg gca tct gga aat agc aca gac tcc ctc 3811  
 Ile Phe Glu Leu Arg Thr Trp Ala Ser Gly Asn Ser Thr Asp Ser Leu  
 1225 1230 1235

ctc gcg ctg ctg gaa acc tcc caa aaa gag tgg atg gaa gaa cgc cgc 3859  
 Leu Ala Leu Leu Glu Thr Ser Gln Lys Glu Trp Met Glu Glu Arg Arg  
 1240 1245 1250

agc ctt acc gcg cgg cgg gga gaa ctc gaa aaa atc ttt gac aaa cta 3907  
 Ser Leu Thr Ala Arg Arg Gly Glu Leu Glu Lys Ile Phe Asp Lys Leu  
 1255 1260 1265

gat gcg cgc aat gat gca cat gat gaa gag cta aag gaa gaa aaa cgt 3955  
 Asp Ala Arg Asn Asp Ala His Asp Glu Glu Leu Lys Glu Glu Lys Arg  
 1270 1275 1280 1285



aaa acc gca gct tcc ctt aaa gcc gtc aaa ctt caa atc cgt gat cta 4003  
 Lys Thr Ala Ala Ser Leu Lys Ala Val Lys Leu Gln Ile Arg Asp Leu  
 1290 1295 1300

ctt ggt gaa ttc tgg atc gct gct ttg gag cgt tat ggt ctc ctg ccc 4051  
 Leu Gly Glu Phe Trp Ile Ala Ala Leu Glu Arg Tyr Gly Leu Leu Pro  
 1305 1310 1315

aac ttc acc ctg gtt gat gat tcc gta gaa ctt aat gtg gcg gtt act 4099  
 Asn Phe Thr Leu Val Asp Asp Ser Val Glu Leu Asn Val Ala Val Thr  
 1320 1325 1330

tcg ttc aac ccc cag gaa gtg gaa ttt gat acc aag aat cat gcc tac 4147  
 Ser Phe Asn Pro Gln Glu Val Glu Phe Asp Thr Lys Asn His Ala Tyr  
 1335 1340 1345

tcg cgt ggg atc tct gca gcg ctt ttt gag ctc gct ccc ggt gcg acc 4195  
 Ser Arg Gly Ile Ser Ala Ala Leu Phe Glu Leu Ala Pro Gly Ala Thr  
 1350 1355 1360 1365

ttt tat gcc caa gga att gct gcc aaa gtt gat tcc att gag att ggt 4243  
 Phe Tyr Ala Gln Gly Ile Ala Ala Lys Val Asp Ser Ile Glu Ile Gly  
 1370 1375 1380

gaa cat ggc tct gcc att gag caa tgg cgg ttg tgc ccc gtg tgc tcg 4291  
 Glu His Gly Ser Ala Ile Glu Gln Trp Arg Leu Cys Pro Val Cys Ser  
 1385 1390 1395

cac tcc gaa atc ctc cag ccg ggt gtc tct aca ccg gga tcg tgt cct 4339  
 His Ser Glu Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro  
 1400 1405 1410

acc tgt ggc tcc ccc gcc ttt gcc gat aag gga caa atc cta gag gta 4387  
 Thr Cys Gly Ser Pro Ala Phe Ala Asp Lys Gly Gln Ile Leu Glu Val  
 1415 1420 1425

gtg caa atg cgt aag gtt tcc tcc gca gtg gag aaa act cgc gct gcc 4435  
 Val Gln Met Arg Lys Val Ser Ser Ala Val Glu Lys Thr Arg Ala Ala  
 1430 1435 1440 1445

att agc gat gac cgt gaa gat cgc ttt agc acc cgc ttt aac cag cac 4483  
 Ile Ser Asp Asp Arg Glu Asp Arg Phe Ser Thr Arg Phe Asn Gln His  
 1450 1455 1460

gtc agc ttt gtc gtt cca cca gat ggc cat gga aaa tcc tgg tat ttg 4531  
 Val Ser Phe Val Val Pro Pro Asp Gly His Gly Lys Ser Trp Tyr Leu  
 1465 1470 1475

aat gat ggt ttt ggc att gag cat ctg ccc aag gtg gaa tta cgc tgg 4579  
 Asn Asp Gly Phe Gly Ile Glu His Leu Pro Lys Val Glu Leu Arg Trp  
 1480 1485 1490

ctg aac tta gga att ggc aat ggc caa aag cgt cgg ctc ggt ggc ttt 4627  
 Leu Asn Leu Gly Ile Gly Asn Gly Gln Lys Arg Arg Leu Gly Gly Phe  
 1495 1500 1505

gaa gtc acc agc cca cta ttt aat gtg tgc cgc cac tgt gga cat tta 4675  
 Glu Val Thr Ser Pro Leu Phe Asn Val Cys Arg His Cys Gly His Leu  
 1510 1515 1520 1525

gat tcc gag gca gga gct aac tca cgc tgg gat cac cga ccc tgg tgc 4723

Asp Ser Glu Ala Gly Ala Asn Ser Arg Trp Asp His Arg Pro Trp Cys	
1530 1535 1540	
cca cac cgt tat gag caa aaa gaa gat acc gta tct ttc gct ttg ggt	4771
Pro His Arg Tyr Glu Gln Lys Glu Asp Thr Val Ser Phe Ala Leu Gly	
1545 1550 1555	
cgt act ctt aaa acc caa ggc gtg ctc atg ctg ctg ccc gaa tat ttt	4819
Arg Thr Leu Lys Thr Gln Gly Val Leu Met Leu Leu Pro Glu Tyr Phe	
1560 1565 1570	
ggc agt gaa gcc gat tct atg gtg gta acc agc ctc att gct gct atc	4867
Gly Ser Glu Ala Asp Ser Met Val Val Thr Ser Leu Ile Ala Ala Ile	
1575 1580 1585	
aaa tta gga ttt cgt gag gtg ttg ggt ggc gat cct gac cac ctg gat	4915
Lys Leu Gly Phe Arg Glu Val Leu Gly Gly Asp Pro Asp His Leu Asp	
1590 1595 1600 1605	
gtc acc agt gtg cag gtc ccc cgt act tct ggc gat ggt gca ctt gat	4963
Val Thr Ser Val Gln Val Pro Arg Thr Ser Gly Asp Gly Ala Leu Asp	
1610 1615 1620	
gcc ctt ttg ctg cac gat cag gtt cca gga ggc aca ggt tat ctt aac	5011
Ala Leu Leu Leu His Asp Gln Val Pro Gly Gly Thr Gly Tyr Leu Asn	
1625 1630 1635	
caa ttt gcc gat cct aca aag gtt cct gaa ctt att tcc cga gct tgg	5059
Gln Phe Ala Asp Pro Thr Lys Val Pro Glu Leu Ile Ser Arg Ala Trp	
1640 1645 1650	
gag cgg gtg tct agg tgc caa tgc cag tat gat gaa acg ctg gcc tgc	5107
Glu Arg Val Ser Arg Cys Gln Cys Gln Tyr Asp Glu Thr Leu Ala Cys	
1655 1660 1665	
cca gaa tgt ttg ttg cct tat acc cgc act gac acg ctc ctc cat act	5155
Pro Glu Cys Leu Leu Pro Tyr Thr Arg Thr Asp Thr Leu Leu His Thr	
1670 1675 1680 1685	
ttc cgc gca act gca gaa aaa tcc ttg cgc gca att ttg ctc aat agc	5203
Phe Arg Ala Thr Ala Glu Lys Ser Leu Arg Ala Ile Leu Leu Asn Ser	
1690 1695 1700	
tcg cgc ccc gaa gaa atc act gac ctt tct gca gta ccg gac tgg act	5251
Ser Arg Pro Glu Glu Ile Thr Asp Leu Ser Ala Val Pro Asp Trp Thr	
1705 1710 1715	
ttc ttg gaa aag cgc cca gag aac act ctt ggc tct cag ttg gaa ctg	5299
Phe Leu Glu Lys Arg Pro Glu Asn Thr Leu Gly Ser Gln Leu Glu Leu	
1720 1725 1730	
cgt ttc cgc gtg atg ctg cga cgc gcc tta aaa aat cgc cat gcc aaa	5347
Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His Ala Lys	
1735 1740 1745	
ctt gtg gac cgc gtc aac ggc tca aac tct tat gtg gat att gag atg	5395
Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile Glu Met	
1750 1755 1760 1765	
agc tcc ggt gtg cgc tgg cgg atg agc gaa caa gtt gat cgt gga tat	5443
Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg Gly Tyr	

1770	1775	1780	
aca cgc cct gat ttc tgg ttt gaa ccg ctc aac ggc aac tat ccc acc			5491
Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr Pro Thr			
1785	1790	1795	
gtg gct gtt ttt acc gat ggc gct gcg ttc cat atc tct tca gct aac			5539
Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser Ala Asn			
1800	1805	1810	
tac cgt ctt gat ggc gat att cag aaa cgg atg aaa cta gcg ctc gat			5587
Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala Leu Asp			
1815	1820	1825	
cca gac aat att ttg ccg tgg aat atc act agc tta gac ctc gac cgc			5635
Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu Asp Arg			
1830	1835	1840	1845
ttt agt aat ccc gct gca caa ggt gag gaa cca gca tgg ttt agc ccc			5683
Phe Ser Asn Pro Ala Ala Gln Gly Glu Pro Ala Trp Phe Ser Pro			
1850	1855	1860	
atc ggc agg cag ctc agc aaa gca aat ttg att ctt gat cca caa tca			5731
Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro Gln Ser			
1865	1870	1875	
act gca ctc ctg gca gca acg cct atg gat caa ctc ttg gca ttt tta			5779
Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala Phe Leu			
1880	1885	1890	
gat aat ccc gcg gca tcc tcg tgg aag gag ttt gct cat atc gct gct			5827
Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile Ala Ala			
1895	1900	1905	
gct cac atg ctt ggg cat aat cca caa aaa aat ggc gac gga att gtt			5875
Ala His Met Leu Gly His Asn Pro Gln Lys Asn Gly Asp Gly Ile Val			
1910	1915	1920	1925
ggc acc ttc cgc aat aag att tcc ttg ccg gcc acc atg gtt aat cgg			5923
Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala Thr Met Val Asn Arg			
1930	1935	1940	
gaa ctg cgc gcc cgc caa ttg tgg ctt gct ccc acc act cca gaa gag			5971
Glu Leu Arg Ala Arg Gln Leu Trp Leu Ala Pro Thr Thr Pro Glu Glu			
1945	1950	1955	
ctg gaa gtg gat acc tgg act gcc ttc ctc aat ttg gcc aac ctc atg			6019
Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn Leu Met			
1960	1965	1970	
tgg ctg gca ccg gaa tcc gta tac gta agc act aat ggt tca ccg cat			6067
Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser Pro His			
1975	1980	1985	
aaa att gat att gtg cct gct cca gca gct ccg ctt gtt gtt gaa gtt			6115
Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val Glu Val			
1990	1995	2000	2005
cct gaa ttg tgg gct ccc atc ttg gat ggc ttt acc gcc gat gaa gat			6163
Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp Glu Asp			
2010	2015	2020	

gaa gaa gcc gaa ggc gct ttg cag atc ttg gct aag gaa cat gcc ctg 6211  
 Glu Glu Ala Glu Gly Ala Leu Gln Ile Leu Ala Lys Glu His Ala Leu  
 2025 2030 2035  
 gtt cca gag acc acc ggt gat gag ctc tcg agt att cct acg att gct 6259  
 Val Pro Glu Thr Thr Gly Asp Glu Leu Ser Ser Ile Pro Thr Ile Ala  
 2040 2045 2050  
 acg tgg ccg agt gtc aag atc gct ttg ctc tat gaa tct gat ccc gat 6307  
 Thr Trp Pro Ser Val Lys Ile Ala Leu Leu Tyr Glu Ser Asp Pro Asp  
 2055 2060 2065  
 gag cct ttg gag gat gat ctc aaa gct gaa ggt tgg acg ctg ctt ttt 6355  
 Glu Pro Leu Glu Asp Asp Leu Lys Ala Glu Gly Trp Thr Leu Leu Phe  
 2070 2075 2080 2085  
 gca aat gac ctc gag acc tcc gat att ccc gct gcc ctt cgt ccc 6400  
 Ala Asn Asp Leu Glu Thr Ser Asp Ile Pro Ala Ala Leu Arg Pro  
 2090 2095 2100  
 tagtacaccc aaagtttatg aaa 6423

&lt;210&gt; 98

&lt;211&gt; 2100

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 98

Met Ser Ser Leu Ile Pro Val His Ala Ala Gly Ser Ile Gln Glu Gly  
 1 5 10 15

Ile Thr Glu Tyr Leu Thr Thr Ser Phe Ser Leu Ala Asp Lys Gln Val  
 20 25 30

Ala Thr Glu Leu Lys Arg Phe Leu Gly His Gly Asp Ser Gly Met Phe  
 35 40 45

His Gly Pro Tyr Val Arg Ala Arg Leu Pro Tyr Ala Gln Ala Gln Glu  
 50 55 60

Trp Glu Asn Val Leu Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His  
 65 70 75 80

His Gln Lys Ala Ala Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly  
 85 90 95

Lys Asp Arg Arg Pro Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser  
 100 105 110

Gly Lys Thr Glu Ser Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg  
 115 120 125

Leu Arg Lys Arg Gly Gln Gln Gly Ile Lys Ala Leu Leu Tyr Pro  
 130 135 140

Met Asn Ala Leu Ala Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile  
 145 150 155 160

His Asn Asn Pro Ala Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly

165										170					175				
Glu	Ala	Lys	Gly	Asn	Arg	Thr	Gln	Met	Gly	Glu	Arg	Glu	Leu	Ile	Asn				
			180					185					190						
Asp	Pro	Gln	Ala	Met	Arg	Val	Ser	Pro	Pro	Asp	Ile	Leu	Leu	Thr	Asn				
		195					200					205							
Tyr	Lys	Met	Leu	Asp	Gln	Leu	Leu	Leu	Arg	Ser	Val	Asp	Arg	Glu	Met				
	210					215					220								
Trp	Gln	Lys	Ser	Ala	Thr	Ser	Leu	Gln	Tyr	Leu	Val	Leu	Asp	Glu	Phe				
225					230					235					240				
His	Thr	Tyr	Asp	Gly	Ala	Gln	Gly	Thr	Asp	Val	Ala	Leu	Leu	Leu	Arg				
			245					250							255				
Arg	Leu	Gly	Leu	Met	Leu	Lys	Ser	Gln	Gln	Pro	Ala	Asn	Phe	Leu	Asp				
			260					265					270						
Asp	Ser	Ala	Met	His	Arg	Pro	Leu	Gly	Ile	Ile	Thr	Pro	Val	Ala	Thr				
		275					280					285							
Ser	Ala	Thr	Leu	Gly	Ser	Gly	Asp	Ser	Gly	Ser	Pro	Met	Leu	Asp	Phe				
	290					295					300								
Ala	Tyr	Thr	Ile	Phe	Gly	Glu	Arg	Phe	Pro	Ala	Asp	Ala	Ile	Val	Gly				
305					310						315				320				
Glu	Thr	Arg	Leu	Glu	Leu	Asp	Gln	Trp	Arg	Ala	Glu	Ile	Ala	Gln	Asn				
			325					330						335					
Phe	Gly	Ala	Pro	Ala	Val	Ser	Glu	Pro	Arg	Glu	Leu	Pro	Thr	Val	Glu				
		340						345					350						
Asp	Ile	Glu	Val	Val	Leu	Asp	Thr	Ile	Ala	Thr	Ala	Gln	His	Glu	Asp				
		355					360					365							
Asp	Tyr	Ala	Gln	Leu	Cys	Phe	Arg	Val	Phe	Cys	Glu	Lys	Val	Trp	Leu				
	370					375					380								
Cys	Glu	Ala	Asp	Leu	His	Ala	Ala	Ile	Ser	Ala	Tyr	Ala	Ala	His	Asp				
385					390						395				400				
Leu	Thr	Ala	Ala	Ile	Leu	Gln	His	Ala	Ala	Asp	Ser	Thr	Pro	Leu	Ser				
			405					410						415					
Arg	Arg	Asp	Gln	Asp	Glu	Val	Thr	Ala	Leu	Pro	Glu	Leu	Val	Leu	Gly				
			420					425					430						
Ala	Thr	Ala	Arg	Ile	Leu	Gly	Glu	Val	Lys	Ala	Ala	Glu	Phe	Ile	Ser				
		435				440						445							
His	Ala	Leu	Ala	Ala	Met	Ala	Phe	Val	Arg	Ala	Glu	Tyr	Gly	Lys	Val				
	450					455					460								
Ala	Ala	Trp	Gly	Ala	Lys	Arg	Leu	Pro	Gly	Val	Glu	Thr	His	Leu	Trp				
465					470						475				480				
Val	Arg	Glu	Val	Ser	Arg	Ile	Asp	Arg	Ala	Leu	Gly	Val	Gly	Asp	Glu				
				485				490						495					

Gln Ser Met Phe Arg Trp Ser Asp Asp Gly Pro Ala Glu Asp Ala Asn  
 500 505 510  
 Thr Gln Gln Trp Leu Pro Ala Cys Tyr Cys Arg Ser Cys Gly Arg Ser  
 515 520 525  
 Gly Trp Met Val Ser Leu Glu Gln Gly Thr Asn Ile Pro Val Leu Glu  
 530 535 540  
 Glu Gln Lys Ile Arg Leu Asn Ser Phe Glu Gln Pro His Lys Gln Arg  
 545 550 555 560  
 Ala Leu Leu Asp Ala Thr Ser Glu Gln Arg Ala Ala Ile Glu Gln Gly  
 565 570 575  
 Arg Ser Val Ala Gly Pro Arg Gly Val Asp Gly Thr Ser Ala Val Leu  
 580 585 590  
 Trp Phe His Ser Ala Ser Asn Glu Leu Ser Thr Arg Gln Pro Ser Pro  
 595 600 605  
 Glu Glu Glu Gln Ser Gly Ser Ser Ile Ala Val Leu Thr His Phe Gly  
 610 615 620  
 Pro Glu Ala Asp Asp Leu Ser Ala Lys Gln Thr Cys Pro Ser Cys Gly  
 625 630 635 640  
 Asp Val Asp Ser Ile Arg Tyr Ile Gly Ser Gly Ile Ser Thr Leu Leu  
 645 650 655  
 Ser Val Ser Leu Ser Asn Leu Phe Gly Met Ala Asp Leu Asp Ser Ala  
 660 665 670  
 Glu Lys Lys Thr Leu Val Phe Ala Asp Ser Val Gln Asp Ala Ala His  
 675 680 685  
 Arg Ala Gly Tyr Val Gln Ala Arg Ser Arg Ala Phe Ala Leu Arg Thr  
 690 695 700  
 Tyr Thr Arg Arg Ala Val Gly Asp Asn Glu Val Thr Leu Pro Ser Ile  
 705 710 715 720  
 Ser Arg Ala Leu Met Asp Asn Ala Thr Ser Gly Arg Thr Arg Tyr Glu  
 725 730 735  
 Leu Leu Pro Pro Asp Leu Thr Asp Leu Asp Ile Tyr Lys Pro Tyr Trp  
 740 745 750  
 His Pro Asp Ala Ser Lys Ala Glu Arg Arg Glu Ala Ser Arg Asn Val  
 755 760 765  
 His Lys Arg Leu Ser Phe Asp Leu Ala Leu Glu Phe Gly Gln Arg Ala  
 770 775 780  
 Asp Leu Pro Arg Ser Leu Ala Leu Thr Gly Ala Leu Ser Ala Phe Val  
 785 790 795 800  
 Asp Leu Pro Lys Gly Val Ala Leu Ser Ala Ala Ala Glu Ala Leu Tyr  
 805 810 815

Ala Ile Glu Val Pro Thr Leu Asp Ile Glu Asp Glu Asn Leu Arg Leu  
 820 825 830

Arg Trp Val Gln Gly Ala Leu Glu Leu Leu Arg Ala Arg Gly Gly Ile  
 835 840 845

Asn His Glu Trp Phe Gly Ala Tyr Leu Arg Thr Asp Gly Asn Pro Tyr  
 850 855 860

Met Leu Asn Arg Arg Gln Ala Arg Ala Glu Gly Ile Pro Gly Phe Val  
 865 870 875 880

Arg Gly Gly Ala Pro Glu Phe Pro Arg Val Gly Ser Ala Leu Ser Gly  
 885 890 895

Ser Leu Arg Ser Ser Thr Gly Thr Thr Pro Leu Gly Ser Pro Arg Gly  
 900 905 910

Arg Tyr Ala Ser Trp Thr Ser Gln Val Leu Gly Ile Ser Thr His Asp  
 915 920 925

Ala Ala Thr Ala Ile Thr Lys Leu Phe Asp Ala Leu Ser Asn Arg Ser  
 930 935 940

Ile Leu Ser Ser Ile Ser Thr Asp Ser Gly Gly Lys Ile Tyr Cys Leu  
 945 950 955 960

Glu Ala Glu Arg Ile Arg Ile Phe Ser Glu Asp His Pro Glu Val Leu  
 965 970 975

Glu Cys Ser Val Cys His Ala Gln Thr Gly Val Thr Asp His Val Arg  
 980 985 990

Asp Phe Leu Asp Gly Ala Pro Cys Phe Ser Pro Ser Cys Gly Gly Val  
 995 1000 1005

Leu His Ile Glu Glu Val Glu Asp Asn Tyr Tyr Arg Arg Leu Tyr Ser  
 1010 1015 1020

Ala Ile Glu Pro Arg Thr Val Ile Ala Arg Glu His Thr Ser Met Leu  
 1025 1030 1035 1040

Lys Lys Lys Asp Arg Leu Ala Leu Glu Gln Ser Phe Arg Gly Gly Glu  
 1045 1050 1055

Gly Ser Ala Lys Gln Ser Pro Asp Ala Pro Asn Val Leu Val Ala Thr  
 1060 1065 1070

Pro Thr Leu Glu Met Gly Ile Asp Ile Gly Asp Leu Ser Thr Val Met  
 1075 1080 1085

Leu Ala Ser Leu Pro Thr Ser Val Ala Ser Tyr Val Gln Arg Val Gly  
 1090 1095 1100

Arg Ala Gly Arg Leu Ser Gly Asn Ser Leu Val Leu Ala Val Val Arg  
 1105 1110 1115 1120

Gly Arg Gly Val Thr Leu Pro Arg Leu Asn Gln Pro Leu Ser Met Ile  
 1125 1130 1135

Lys Gly Ala Ile Thr Pro Pro Val Ala Tyr Leu Ser Ala Ser Glu Ile

1140	1145	1150
Leu His Arg Gln Phe Leu Ala Tyr Val Ile Asp Cys Leu Asp Thr Arg 1155	1160	1165
Ala Glu Leu Pro Lys Leu Glu Thr Ala Ile Asp Val Phe Asp Asn Ala 1170	1175	1180
Ala Gly Lys Thr Pro Leu Val Ala Leu Leu Lys Ala Gln Ile His Ala 1185	1190	1195 1200
Gly Leu Asp Pro Leu Leu Glu Glu Phe Val Arg Thr Leu Asn Met Gln 1205	1210	1215
Ile Ser Ile Asp Asn Ile Phe Glu Leu Arg Thr Trp Ala Ser Gly Asn 1220	1225	1230
Ser Thr Asp Ser Leu Leu Ala Leu Leu Glu Thr Ser Gln Lys Glu Trp 1235	1240	1245
Met Glu Glu Arg Arg Ser Leu Thr Ala Arg Arg Gly Glu Leu Glu Lys 1250	1255	1260
Ile Phe Asp Lys Leu Asp Ala Arg Asn Asp Ala His Asp Glu Glu Leu 1265	1270	1275 1280
Lys Glu Glu Lys Arg Lys Thr Ala Ala Ser Leu Lys Ala Val Lys Leu 1285	1290	1295
Gln Ile Arg Asp Leu Leu Gly Glu Phe Trp Ile Ala Ala Leu Glu Arg 1300	1305	1310
Tyr Gly Leu Leu Pro Asn Phe Thr Leu Val Asp Asp Ser Val Glu Leu 1315	1320	1325
Asn Val Ala Val Thr Ser Phe Asn Pro Gln Glu Val Glu Phe Asp Thr 1330	1335	1340
Lys Asn His Ala Tyr Ser Arg Gly Ile Ser Ala Ala Leu Phe Glu Leu 1345	1350	1355 1360
Ala Pro Gly Ala Thr Phe Tyr Ala Gln Gly Ile Ala Ala Lys Val Asp 1365	1370	1375
Ser Ile Glu Ile Gly Glu His Gly Ser Ala Ile Glu Gln Trp Arg Leu 1380	1385	1390
Cys Pro Val Cys Ser His Ser Glu Ile Leu Gln Pro Gly Val Ser Thr 1395	1400	1405
Pro Gly Ser Cys Pro Thr Cys Gly Ser Pro Ala Phe Ala Asp Lys Gly 1410	1415	1420
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Lys Thr Arg Ala Ala Ile Ser Asp Asp Arg Glu Asp Arg Phe Ser Thr 1445	1450	1455
Arg Phe Asn Gln His Val Ser Phe Val Val Pro Pro Asp Gly His Gly 1460	1465	1470



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 Ala His Ile Ala Ala Ala His Met Leu Gly His Asn Pro Gln Lys Asn  
 1905 1910 1915 1920  
 Gly Asp Gly Ile Val Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala  
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 Thr Thr Pro Glu Glu Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn  
 1955 1960 1965  
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 1970 1975 1980  
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 Trp Glu Asn Val Leu Ser Trp Leu Pro Glu Asn Phe Val Pro Tyr His  
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 His Gln Lys Ala Ala Phe Gln Arg Leu Ser Ser Leu Asp Asn Arg Gly  
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 Lys Asp Arg Arg Pro Asp Pro Thr Leu Val Val Thr Gly Thr Gly Ser  
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 Gly Lys Thr Glu Ser Phe Leu Tyr Pro Ile Leu Asp His Ala Leu Arg  
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 Met Asn Ala Leu Ala Asn Asp Gln Ala Asp Arg Leu Ala Arg Leu Ile  
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 His Asn Asn Pro Ala Leu Lys Gly Val Thr Ala Gly Ile Tyr Thr Gly  
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 Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His  
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gcc aaa ctt gtg gac cgc gtc aac ggc tca aac tct tat gtg gat att 192  
 Ala Lys Leu Val Asp Arg Val Asn Gly Ser Asn Ser Tyr Val Asp Ile  
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 Glu Met Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg  
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 Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser  
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Glu Glu Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn				
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Leu Met Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser				
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Pro Asp Glu Pro Leu Glu Asp Asp Leu Lys Ala Glu Gly Trp Thr Leu				
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Leu Phe Ala Asn Asp Leu Glu Thr Ser Asp Ile Pro Ala Ala Leu Arg				
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Pro				

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&lt;211&gt; 401

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 102

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Glu Leu Arg Phe Arg Val Met Leu Arg Arg Ala Leu Lys Asn Arg His  
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Glu Met Ser Ser Gly Val Arg Trp Arg Met Ser Glu Gln Val Asp Arg  
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Gly Tyr Thr Arg Pro Asp Phe Trp Phe Glu Pro Leu Asn Gly Asn Tyr  
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Pro Thr Val Ala Val Phe Thr Asp Gly Ala Ala Phe His Ile Ser Ser  
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Ala Asn Tyr Arg Leu Asp Gly Asp Ile Gln Lys Arg Met Lys Leu Ala  
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Leu Asp Pro Asp Asn Ile Leu Pro Trp Asn Ile Thr Ser Leu Asp Leu  
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Asp Arg Phe Ser Asn Pro Ala Ala Gln Gly Glu Glu Pro Ala Trp Phe  
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Ser Pro Ile Gly Arg Gln Leu Ser Lys Ala Asn Leu Ile Leu Asp Pro  
 165 170 175

Gln Ser Thr Ala Leu Leu Ala Ala Thr Pro Met Asp Gln Leu Leu Ala  
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Phe Leu Asp Asn Pro Ala Ala Ser Ser Trp Lys Glu Phe Ala His Ile  
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Ala Ala Ala His Met Leu Gly His Asn Pro Gln Lys Asn Gly Asp Gly  
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Ile Val Gly Thr Phe Arg Asn Lys Ile Ser Leu Arg Ala Thr Met Val  
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Glu Glu Leu Glu Val Asp Thr Trp Thr Ala Phe Leu Asn Leu Ala Asn  
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Leu Met Trp Leu Ala Pro Glu Ser Val Tyr Val Ser Thr Asn Gly Ser  
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Pro His Lys Ile Asp Ile Val Pro Ala Pro Ala Ala Pro Leu Val Val  
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Glu Val Pro Glu Leu Trp Ala Pro Ile Leu Asp Gly Phe Thr Ala Asp  
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Pro

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 Val Phe Cys Glu Lys Val Trp Leu Cys Glu Ala Asp Leu His Ala Ala  
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 Ile Ser Ala Tyr Ala Ala His Asp Leu Thr Ala Ala Ile Leu Gln His  
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 Pro Gly Val Glu Thr His Leu Trp Val Arg Glu Val Ser Arg Ile Asp  
 130 135 140

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Val Leu Gly Ile Ser Thr His Asp Ala Ala Thr Ala Ile Thr Lys Leu	

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Phe Asp Ala Leu Ser Asn Arg Ser Ile Leu Ser Ser Ile Ser Thr Asp			
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Ser Gly Gly Lys Ile Tyr Cys Leu Glu Ala Glu Arg Ile Arg Ile Phe			
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Ser Glu Asp His Pro Glu Val Leu Glu Cys Ser Val Cys His Ala Gln			
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Thr Gly Val Thr Asp His Val Arg Asp Phe Leu Asp Gly Ala Pro Cys			
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Phe Ser Pro Ser Cys Gly Gly Val Leu His Ile Glu Glu Val Glu Asp			
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aac tac tac cgc agg ctt tat tcc gca att gaa ccg cgc act gtc att			2064
Asn Tyr Tyr Arg Arg Leu Tyr Ser Ala Ile Glu Pro Arg Thr Val Ile			
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gcc cgc gag cac acc agc atg ctc aag aaa aaa gac cgc ctc gca ctc			2112
Ala Arg Glu His Thr Ser Met Leu Lys Lys Lys Asp Arg Leu Ala Leu			
690	695	700	
gaa caa tcc ttt aga ggt gga gaa ggc tcg gcc aaa caa tcc ccc gat			2160
Glu Gln Ser Phe Arg Gly Gly Glu Gly Ser Ala Lys Gln Ser Pro Asp			
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Ala Pro Asn Val Leu Val Ala Thr Pro Thr Leu Glu Met Gly Ile Asp			
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Ile Gly Asp Leu Ser Thr Val Met Leu Ala Ser Leu Pro Thr Ser Val			
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Ala Ser Tyr Val Gln Arg Val Gly Arg Ala Gly Arg Leu Ser Gly Asn			
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Ser Leu Val Leu Ala Val Val Arg Gly Arg Gly Val Thr Leu Pro Arg			
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Leu Asn Gln Pro Leu Ser Met Ile Lys Gly Ala Ile Thr Pro Pro Val			
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Ala Tyr Leu Ser Ala Ser Glu Ile Leu His Arg Gln Phe Leu Ala Tyr			
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Val Ile Asp Cys Leu Asp Thr Arg Ala Glu Leu Pro Lys Leu Glu Thr			
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Phe Trp Ile Ala Ala Leu Glu Arg Tyr Gly Leu Leu Pro Asn Phe Thr	
965 970 975	
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Ile Leu Gln Pro Gly Val Ser Thr Pro Gly Ser Cys Pro Thr Cys Gly	
1060 1065 1070	

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 Ser Pro Ala Phe Ala Asp Lys Gly Gln Ile Leu Glu Val Val Gln Met  
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 Arg Lys Val Ser Ser Ala Val Glu Lys Thr Arg Ala Ala Ile Ser Asp  
 1090 1095 1100  
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 Asp Arg Glu Asp Arg Phe Ser Thr Arg Phe Asn Gln His Val Ser Phe  
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 Ala Leu Pro Glu Leu Val Leu Gly Ala Thr Ala Arg Ile Leu Gly Glu  
 85 90 95  
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 Val Arg Ala Glu Tyr Gly Lys Val Ala Ala Trp Gly Ala Lys Arg Leu  
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 Lys Gln Thr Cys Pro Ser Cys Gly Asp Val Asp Ser Ile Arg Tyr Ile  
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 Thr Pro Leu Gly Ser Pro Arg Gly Arg Tyr Ala Ser Trp Thr Ser Gln  
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Pro	Leu	Gln	Gln	Arg	Val	Leu	Asp	Ala	Trp	Leu	Gly	Asp	Arg	Asp	Asp		
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Glu	Lys	Ala																	

gaa aac aaa gcg gcg tac atg gtg ttc agc aat gca acg ttg atg gcg 1411  
 Glu Asn Lys Ala Ala Tyr Met Val Phe Ser Asn Ala Thr Leu Met Ala  
           425                                  430                                  435

atc gct gaa atg aac ccc acc aac gaa aac gaa ttg ctc agc gtg ccg 1459  
 Ile Ala Glu Met Asn Pro Thr Asn Glu Asn Glu Leu Leu Ser Val Pro  
           440                                  445                                  450

ggg gtg ggg ccg atg aag atc gag aac tat ggc gat gac gtg ctc gcg 1507  
 Gly Val Gly Pro Met Lys Ile Glu Asn Tyr Gly Asp Asp Val Leu Ala  
           455                                  460                                  465

att ttg gga gca ctt taggaaccta aactccaaca cat 1545  
 Ile Leu Gly Ala Leu  
 470

&lt;210&gt; 106

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106

Val Ala Glu Glu Phe Arg Gln Gln Tyr Arg Ser Phe Val Val Asp Glu  
       1                                  5                                  10                                  15

Tyr Gln Asp Val Thr Pro Leu Gln Gln Arg Val Leu Asp Ala Trp Leu  
           20                                  25                                  30

Gly Asp Arg Asp Asp Leu Thr Val Val Gly Asp Ala Asn Gln Thr Ile  
           35                                  40                                  45

Tyr Ser Phe Thr Gly Ala Thr Pro Glu Phe Leu Leu Asn Phe Ser Arg  
       50                                  55                                  60

Lys Tyr Pro Glu Ala Thr Val Val Lys Leu Gln Arg Asp Tyr Arg Ser  
       65                                  70                                  75                                  80

Thr Pro Gln Val Thr Ala Leu Ala Asn Thr Val Ile Gly Gln Ala Arg  
           85                                  90                                  95

Gly Arg Val Ala Gly Thr Arg Leu Glu Leu Gln Gly Met Arg Ile Ala  
           100                                  105                                  110

Gly Pro Glu Pro Glu Phe Ser Ala Phe Asp Asp Glu Pro Thr Glu Ala  
           115                                  120                                  125

Arg Glu Val Ala Gly Arg Ile Leu Thr Leu Leu Lys Asn Gly Val Gln  
       130                                  135                                  140

Ala Ser Glu Ile Ala Val Leu Tyr Arg Ile Asn Ala Gln Ser Ala Val  
       145                                  150                                  155                                  160

Phe Glu Gln Ala Leu Ala Asp Ala Gly Ile Val Tyr Gln Val Arg Gly  
           165                                  170                                  175

Gly Glu Gly Phe Phe Thr Arg Pro Glu Ile Arg Gln Ala Leu Ser Gln  
           180                                  185                                  190

Leu Ile Arg Thr Ser Gln Arg Asp Val Asp Glu Ser Asp Leu Val Arg

195	200	205
Leu Thr Gln Arg Thr Leu Val Pro Leu Gly Leu Ser Ser Glu Glu Pro 210 215 220		
Ser Gly Ala Gln Glu Arg Glu Arg Trp Gln Ser Leu Asn Ala Leu Val 225 230 235 240		
Asp Leu Val Lys Asp Leu Val Lys Ala Thr Pro Asp Leu Asp Leu Thr 245 250 255		
Gly Leu Leu Leu Lys Leu Arg Glu Arg Gln Glu Ala Lys His Pro Pro 260 265 270		
Thr Val Glu Gly Val Thr Leu Ala Ser Leu His Ala Ala Lys Gly Leu 275 280 285		
Glu Trp Asp Ala Val Phe Leu Val Gly Leu Val Asp Ser Thr Leu Pro 290 295 300		
Ile Ser His Ala Ile Lys Ser Gly Asp Glu Ala Ile Glu Glu Glu Arg 305 310 315 320		
Arg Leu Phe Tyr Val Gly Val Thr Arg Ala Arg Glu His Leu His Cys 325 330 335		
Ser Trp Ala Leu Ala Arg Gln Glu Gly Gly Arg Lys Ser Arg Lys Arg 340 345 350		
Ser Arg Phe Leu Asp Gly Ile Val Val Glu Met Ala Ser Glu Ser Gly 355 360 365		
Thr Pro Arg Ser Asn Arg Pro Lys Asn Cys Arg Val Cys Gly Ser Val 370 375 380		
Leu Ser Ser Pro Ala Glu Lys Ala Val Gly Arg Cys Ala Ser Cys Pro 385 390 395 400		
Ile Gln Ala Asp Glu Arg Val Phe Glu Gln Leu Arg Thr Trp Arg Asn 405 410 415		
Asp Thr Ala Lys Arg Glu Asn Lys Ala Ala Tyr Met Val Phe Ser Asn 420 425 430		
Ala Thr Leu Met Ala Ile Ala Glu Met Asn Pro Thr Asn Glu Asn Glu 435 440 445		
Leu Leu Ser Val Pro Gly Val Gly Pro Met Lys Ile Glu Asn Tyr Gly 450 455 460		
Asp Asp Val Leu Ala Ile Leu Gly Ala Leu 465 470		

&lt;210&gt; 107

&lt;211&gt; 2691

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2668)

&lt;223&gt; RXN01683

&lt;400&gt; 107

cccaaaatgg tatcgctttg ataccaattt tggggcatgc aaggcgtaa aacggcctgt 60

ggactaaaat cggtagggtt gacacgaaga aaggatgatca gtg agc gac gac aat 115  
 Val Ser Asp Asp Asn  
 1 5

acc gga caa ttt gac cgc gtt aat ccc att gat atc aat gag gaa atg 163  
 Thr Gly Gln Phe Asp Arg Val Asn Pro Ile Asp Ile Asn Glu Glu Met  
 10 15 20

cag tcg agc tac atc gac tac gcg atg tca gtc atc gtc gga cgt gcc 211  
 Gln Ser Ser Tyr Ile Asp Tyr Ala Met Ser Val Ile Val Gly Arg Ala  
 25 30 35

ctc cca gag gtg cga gac ggc ctg aag cca gtc cac cgc cgc gtc ttg 259  
 Leu Pro Glu Val Arg Asp Gly Leu Lys Pro Val His Arg Arg Val Leu  
 40 45 50

tac gcg atg ttc gac aac ggc tac cgc ccc gac cgc agc tac gtg aag 307  
 Tyr Ala Met Phe Asp Asn Gly Tyr Arg Pro Asp Arg Ser Tyr Val Lys  
 55 60 65

tct gca aaa cca gtg gca gac acc atg ggt aac ttc cac cca cac ggc 355  
 Ser Ala Lys Pro Val Ala Asp Thr Met Gly Asn Phe His Pro His Gly  
 70 75 80 85

gac acc gca att tat gac acg ttg gtg cgc atg gct cag cca tgg tcc 403  
 Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp Ser  
 90 95 100

atg cga tac ccg ctg gta gac ggc cag ggt aac ttc ggt tcc cgc ggc 451  
 Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg Gly  
 105 110 115

aac gac ggc cct gca gca atg cgt tac acc gag tgc cgc atg acc cca 499  
 Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr Pro  
 120 125 130

ctg gcc atg gag atg gtg cgc gac atc cgc gaa aac acc gtc aac ttc 547  
 Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn Phe  
 135 140 145

tca cca aac tac gac ggt aaa acc ctc gaa cca gac gtt ttg cca tcg 595  
 Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro Ser  
 150 155 160 165

cgc gtt cca aac ttg ttg atg aac ggt tcg ggc ggc att gcg gtc ggc 643  
 Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val Gly  
 170 175 180

atg gcc acc aac atc cca ccg cac aac ctc aac gag ctt gcc gac gcc 691  
 Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp Ala  
 185 190 195

atc ttc tgg ctc ctg gaa aac cca gac gcc gaa gaa tcc gaa gct ctc 739  
 Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala Leu  
 200 205 210

gaa gcc tgc atg aag ttt gtg aag ggc cca gac ttc cca acc gct ggc	787
Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala Gly	
215 220 225	
ctc atc atc ggt gac aag ggc atc cac gat gcc tac acc acc ggc cgc	835
Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly Arg	
230 235 240 245	
ggc tcc atc cgc atg cgc ggt gtc acc tcc atc gag gag gaa ggc aac	883
Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly Asn	
250 255 260	
cgc acc gtc atc gtt atc acc gag ctg cca tac cag gtc aac ccg gat	931
Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro Asp	
265 270 275	
aac ctg atc tct aat atc gcg gag cag gtg cgc gac ggc aag ctc gtg	979
Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu Val	
280 285 290	
ggc atc tcc aag att gaa gat gaa tcc tcc gac cgc gtc ggc atg cgc	1027
Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met Arg	
295 300 305	
att gtg gtc acc ctc aag cgc gac gca gtt gcc cgc gtg gtg ctg aac	1075
Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu Asn	
310 315 320 325	
aac ctg ttc aag cac tcc cag ctg caa gcc aac ttt ggt gcg aac atg	1123
Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn Met	
330 335 340	
ctc tcc atc gtc gat ggc gtg cca cgc acc ctt cgc ctg gac cag atg	1171
Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln Met	
345 350 355	
ctg cgc tac tac gtg gca cac cag atc gaa gtc atc gtg cgc cgc acc	1219
Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg Thr	
360 365 370	
caa tac cgc ctc gac aag gct gaa gag cgc gcc cac ctc ctc cgc ggc	1267
Gln Tyr Arg Leu Asp Lys Ala Glu Glu Arg Ala His Leu Leu Arg Gly	
375 380 385	
ctg gtc aag gcc ctg gac atg ctg gac gag gtc atc gcg ctc atc cgc	1315
Leu Val Lys Ala Leu Asp Met Leu Asp Glu Val Ile Ala Leu Ile Arg	
390 395 400 405	
cgc agc cca acc cca gat gaa gcc cgc acc ggc ctc atg tcg ctt ctc	1363
Arg Ser Pro Thr Pro Asp Glu Ala Arg Thr Gly Leu Met Ser Leu Leu	
410 415 420	
gac gtc gac gag gcg cag gct gac gca att ctg gca atg cag ctg cgt	1411
Asp Val Asp Glu Ala Gln Ala Asp Ala Ile Leu Ala Met Gln Leu Arg	
425 430 435	
cgc ctg gcg gca ctg gaa cgc caa aag atc atc gat gag ctc gct gaa	1459
Arg Leu Ala Ala Leu Glu Arg Gln Lys Ile Ile Asp Glu Leu Ala Glu	
440 445 450	

atc gag ctg gaa atc gct gac ctg aag gcc atc ctg gca agc cca gaa 1507  
 Ile Glu Leu Glu Ile Ala Asp Leu Lys Ala Ile Leu Ala Ser Pro Glu  
 455 460 465

cgt cag cgc acc atc gtt cgc gat gag ctg acc gaa atc gtg gaa aag 1555  
 Arg Gln Arg Thr Ile Val Arg Asp Glu Leu Thr Glu Ile Val Glu Lys  
 470 475 480 485

tac ggc gac gag cgt cgt tcc cag atc atc gct gcc acc ggc gac gtg 1603  
 Tyr Gly Asp Glu Arg Arg Ser Gln Ile Ile Ala Ala Thr Gly Asp Val  
 490 495 500

tct gaa gaa gac ctc att gcg cgt gaa aac gtt gtc atc acc att acc 1651  
 Ser Glu Glu Asp Leu Ile Ala Arg Glu Asn Val Val Ile Thr Ile Thr  
 505 510 515

tcc acc ggt tac gca aag cgc acc aag gtc gat gcc tac aag tcg caa 1699  
 Ser Thr Gly Tyr Ala Lys Arg Thr Lys Val Asp Ala Tyr Lys Ser Gln  
 520 525 530

aag cgt ggc ggc aag ggt gtt cgt ggc gca gag ctc aag caa gat gac 1747  
 Lys Arg Gly Gly Lys Gly Val Arg Gly Ala Glu Leu Lys Gln Asp Asp  
 535 540 545

att gtt cgt cac ttc ttc gtc agc tcc acc cac gac tgg att ttg ttc 1795  
 Ile Val Arg His Phe Phe Val Ser Ser Thr His Asp Trp Ile Leu Phe  
 550 555 560 565

ttc acc aac tac ggt cgc gtg tac cgc ctc aag gca ttc gaa ctt cca 1843  
 Phe Thr Asn Tyr Gly Arg Val Tyr Arg Leu Lys Ala Phe Glu Leu Pro  
 570 575 580

gag gca tcc cgc acc gca cgt gga cag cac gtg gcc aac ctt ctg gaa 1891  
 Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val Ala Asn Leu Leu Glu  
 585 590 595

ttc caa cct ggt gag caa atc gcc cag gtc atc cag ttg gaa agc tac 1939  
 Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr  
 600 605 610

aac gac ttc cca tac ctg gtg ctc gca acc gca cac ggt cgc gtg aag 1987  
 Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala His Gly Arg Val Lys  
 615 620 625

aag tcc cgc ctg ctc gac tac gaa tca gca cgt tcc ggt ggc ctc atc 2035  
 Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg Ser Gly Gly Leu Ile  
 630 635 640 645

gcc atc aac ctg aac gag gac gat cgc ctc atc ggc gcc gca ctt tgc 2083  
 Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile Gly Ala Ala Leu Cys  
 650 655 660

ggt gaa gaa gac gat ctg ctg ctg gtc tct gaa ttc gga cag tcc atc 2131  
 Gly Glu Glu Asp Asp Leu Leu Leu Val Ser Glu Phe Gly Gln Ser Ile  
 665 670 675

cgc ttc acc gcc gac gat gag cag ctc cgc ccc atg ggc cgc gcc acc 2179  
 Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro Met Gly Arg Ala Thr  
 680 685 690

gcc ggt gtc aag ggc atg cgc ttc cgc gac aac gac caa ctg ctg tcc 2227



Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn Asp Gln Leu Leu Ser  
 695 700 705

atg tcc gtg gtc cgc gac ggc gaa ttc ctc ctc gtt gcc acc tcc ggc 2275  
 Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu Val Ala Thr Ser Gly  
 710 715 720 725

ggc tac ggc aag cgc acc cca ctt gag gat tac tcc acc cag ggc cgt 2323  
 Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr Ser Thr Gln Gly Arg  
 730 735 740

ggt ggc ctc ggc gtg gtg acc ttc aag tac acc ccg aag cgc ggt cgc 2371  
 Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr Pro Lys Arg Gly Arg  
 745 750 755

ctc gtc agc gcc atc gca gtt gag gaa gat gac gag atc ttc gcc atc 2419  
 Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp Glu Ile Phe Ala Ile  
 760 765 770

acc tcc gcc ggc ggc gtt gtt cgc acc gaa gtc aag cag atc cga cca 2467  
 Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val Lys Gln Ile Arg Pro  
 775 780 785

tcc tcc cgt gca aca atg ggt gtt cga ctg gtc aac ttg gaa gaa ggt 2515  
 Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val Asn Leu Glu Glu Gly  
 790 795 800 805

gta gaa ctg ctt gcc atc gac aag aac gtc gaa gac cag ggc gaa gca 2563  
 Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu Asp Gln Gly Glu Ala  
 810 815 820

tcc gca gaa gca gta gca aag ggt gca gtc gaa gga cca gca tcc aag 2611  
 Ser Ala Glu Ala Val Ala Lys Gly Ala Val Glu Gly Pro Ala Ser Lys  
 825 830 835

act gct gcc gaa gaa acc gac tcc gtt gac aac gga tcc gac gaa aac 2659  
 Thr Ala Ala Glu Glu Thr Asp Ser Val Asp Asn Gly Ser Asp Glu Asn  
 840 845 850

ggc gag gaa taatttatgg catcccgaga agt 2691  
 Gly Glu Glu  
 855

&lt;210&gt; 108

&lt;211&gt; 856

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 108

Val Ser Asp Asp Asn Thr Gly Gln Phe Asp Arg Val Asn Pro Ile Asp  
 1 5 10 15

Ile Asn Glu Glu Met Gln Ser Ser Tyr Ile Asp Tyr Ala Met Ser Val  
 20 25 30

Ile Val Gly Arg Ala Leu Pro Glu Val Arg Asp Gly Leu Lys Pro Val  
 35 40 45

His Arg Arg Val Leu Tyr Ala Met Phe Asp Asn Gly Tyr Arg Pro Asp  
 50 55 60

Arg Ser Tyr Val Lys Ser Ala Lys Pro Val Ala Asp Thr Met Gly Asn  
 65 70 75 80  
 Phe His Pro His Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met  
 85 90 95  
 Ala Gln Pro Trp Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn  
 100 105 110  
 Phe Gly Ser Arg Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu  
 115 120 125  
 Cys Arg Met Thr Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu  
 130 135 140  
 Asn Thr Val Asn Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro  
 145 150 155 160  
 Asp Val Leu Pro Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly  
 165 170 175  
 Gly Ile Ala Val Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn  
 180 185 190  
 Glu Leu Ala Asp Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu  
 195 200 205  
 Glu Ser Glu Ala Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp  
 210 215 220  
 Phe Pro Thr Ala Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala  
 225 230 235 240  
 Tyr Thr Thr Gly Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile  
 245 250 255  
 Glu Glu Glu Gly Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr  
 260 265 270  
 Gln Val Asn Pro Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg  
 275 280 285  
 Asp Gly Lys Leu Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp  
 290 295 300  
 Arg Val Gly Met Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala  
 305 310 315 320  
 Arg Val Val Leu Asn Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn  
 325 330 335  
 Phe Gly Ala Asn Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu  
 340 345 350  
 Arg Leu Asp Gln Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val  
 355 360 365  
 Ile Val Arg Arg Thr Gln Tyr Arg Leu Asp Lys Ala Glu Glu Arg Ala  
 370 375 380

His Leu Leu Arg Gly Leu Val Lys Ala Leu Asp Met Leu Asp Glu Val  
 385 390 395 400  
 Ile Ala Leu Ile Arg Arg Ser Pro Thr Pro Asp Glu Ala Arg Thr Gly  
 405 410 415  
 Leu Met Ser Leu Leu Asp Val Asp Glu Ala Gln Ala Asp Ala Ile Leu  
 420 425 430  
 Ala Met Gln Leu Arg Arg Leu Ala Ala Leu Glu Arg Gln Lys Ile Ile  
 435 440 445  
 Asp Glu Leu Ala Glu Ile Glu Leu Glu Ile Ala Asp Leu Lys Ala Ile  
 450 455 460  
 Leu Ala Ser Pro Glu Arg Gln Arg Thr Ile Val Arg Asp Glu Leu Thr  
 465 470 475 480  
 Glu Ile Val Glu Lys Tyr Gly Asp Glu Arg Arg Ser Gln Ile Ile Ala  
 485 490 495  
 Ala Thr Gly Asp Val Ser Glu Glu Asp Leu Ile Ala Arg Glu Asn Val  
 500 505 510  
 Val Ile Thr Ile Thr Ser Thr Gly Tyr Ala Lys Arg Thr Lys Val Asp  
 515 520 525  
 Ala Tyr Lys Ser Gln Lys Arg Gly Gly Lys Gly Val Arg Gly Ala Glu  
 530 535 540  
 Leu Lys Gln Asp Asp Ile Val Arg His Phe Phe Val Ser Ser Thr His  
 545 550 555 560  
 Asp Trp Ile Leu Phe Phe Thr Asn Tyr Gly Arg Val Tyr Arg Leu Lys  
 565 570 575  
 Ala Phe Glu Leu Pro Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val  
 580 585 590  
 Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile  
 595 600 605  
 Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala  
 610 615 620  
 His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg  
 625 630 635 640  
 Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile  
 645 650 655  
 Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu Leu Leu Val Ser Glu  
 660 665 670  
 Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro  
 675 680 685  
 Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn  
 690 695 700  
 Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu

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<210> 109
<211> 257
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(234)  
<223> FRXA01682
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<400> 109																	
cgc	acc	aag	gtc	gat	gcc	tac	aag	tcg	caa	aag	cgt	ggc	ggc	aag	ggc		48
Arg	Thr	Lys	Val	Asp	Ala	Tyr	Lys	Ser	Gln	Lys	Arg	Gly	Gly	Lys	Gly		
1				5				10						15			
gtt	tgt	ggc	gca	gag	ctc	aag	caa	gat	gac	att	gtt	cgt	cac	ttc	ttc		96
Val	Cys	Gly	Ala	Glu	Leu	Lys	Gln	Asp	Asp	Ile	Val	Arg	His	Phe	Phe		
			20						25						30		
gtc	agc	tcc	acc	cac	gac	tgg	att	ttg	ttt	ctt	cac	caa	cta	cgg	tcg		144
Val	Ser	Ser	Thr	His	Asp	Trp	Ile	Leu	Phe	Leu	His	Gln	Leu	Arg	Ser		
		35				40						45					
cgt	gta	ccg	cct	caa	ggc	att	cga	act	tcc	aga	ggc	atc	ccg	cac	cgc		192
Arg	Val	Pro	Pro	Gln	Gly	Ile	Arg	Thr	Ser	Arg	Gly	Ile	Pro	His	Arg		
50						55						60					
acg	tgg	aca	gca	cgt	ggc	caa	cct	tct	gga	att	cca	acc	tgg				234
Thr	Trp	Thr	Ala	Arg	Gly	Gln	Pro	Ser	Gly	Ile	Pro	Thr	Trp				
65				70						75							

tgagcaaadc gccaggtca tcc

257

&lt;210&gt; 110

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 110

Arg Thr Lys Val Asp Ala Tyr Lys Ser Gln Lys Arg Gly Gly Lys Gly  
 1 5 10 15

Val Cys Gly Ala Glu Leu Lys Gln Asp Asp Ile Val Arg His Phe Phe  
 20 25 30

Val Ser Ser Thr His Asp Trp Ile Leu Phe Leu His Gln Leu Arg Ser  
 35 40 45

Arg Val Pro Pro Gln Gly Ile Arg Thr Ser Arg Gly Ile Pro His Arg  
 50 55 60

Thr Trp Thr Ala Arg Gly Gln Pro Ser Gly Ile Pro Thr Trp  
 65 70 75

&lt;210&gt; 111

&lt;211&gt; 850

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(850)

&lt;223&gt; FRXA01683

&lt;400&gt; 111

ggtgtttgtg ggcagagct caagcaagat gacattgttc gtcacttctt cgtcagctcc 60

accacagact ggattttggt tcttcaccaa ctacgggtcgc gtg tac cgc ctc aag 115  
 Val Tyr Arg Leu Lys  
 1 5

gca ttc gaa ctt cca gag gca tcc cgc acc gca cgt gga cag cac gtg 163  
 Ala Phe Glu Leu Pro Glu Ala Ser Arg Thr Ala Arg Gly Gln His Val  
 10 15 20

gcc aac ctt ctg gaa ttc caa cct ggt gag caa atc gcc cag gtc atc 211  
 Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln Ile Ala Gln Val Ile  
 25 30 35

cag ttg gaa agc tac aac gac ttc cca tac ctg gtg ctc gca acc gca 259  
 Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu Val Leu Ala Thr Ala  
 40 45 50

cac ggt cgc gtg aag aag tcc cgc ctg ctc gac tac gaa tca gca cgt 307  
 His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp Tyr Glu Ser Ala Arg  
 55 60 65

tcc ggt ggc ctc atc gcc atc aac ctg aac gag gac gat cgc ctc atc 355  
 Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu Asp Asp Arg Leu Ile  
 70 75 80 85

ggc gcc gca ctt tgc ggt gaa gaa gac gat ctg ctg ctg gtc tct gaa 403  
 Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu Leu Leu Val Ser Glu  
                     90                    95                    100

ttc gga cag tcc atc cgc ttc acc gcc gac gat gag cag ctc cgc ccc 451  
 Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp Glu Gln Leu Arg Pro  
                     105                    110                    115

atg ggc cgc gcc acc gcc ggt gtc aag ggc atg cgc ttc cgc gac aac 499  
 Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met Arg Phe Arg Asp Asn  
                     120                    125                    130

gac caa ctg ctg tcc atg tcc gtg gtc cgc gac ggc gaa ttc ctc ctc 547  
 Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp Gly Glu Phe Leu Leu  
                     135                    140                    145

gtt gcc acc tcc ggc ggc tac ggc aag cgc acc cca ctt gag gat tac 595  
 Val Ala Thr Ser Gly Tyr Gly Lys Arg Thr Pro Leu Glu Asp Tyr  
                     150                    155                    160                    165

tcc acc cag ggc cgt ggt ggc ctc ggc gtg gtg acc ttc aag tac acc 643  
 Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val Thr Phe Lys Tyr Thr  
                     170                    175                    180

ccg aag cgc ggt cgc ctc gtc agc gcc atc gca gtt gag gaa gat gac 691  
 Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala Val Glu Glu Asp Asp  
                     185                    190                    195

gag atc ttc gcc atc acc tcc gcc ggc ggc gtt gtt cgc acc gaa gtc 739  
 Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val Val Arg Thr Glu Val  
                     200                    205                    210

aag cag atc cga cca tcc tcc cgt gca aca atg ggt gtt cga ctg gtc 787  
 Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met Gly Val Arg Leu Val  
                     215                    220                    225

aac ttg gaa gaa ggt gta gaa ctg ctt gcc atc gac aag aac gtc gaa 835  
 Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile Asp Lys Asn Val Glu  
                     230                    235                    240                    245

gac cag ggc gaa gca 850  
 Asp Gln Gly Glu Ala  
                     250

&lt;210&gt; 112

&lt;211&gt; 250

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 112

Val Tyr Arg Leu Lys Ala Phe Glu Leu Pro Glu Ala Ser Arg Thr Ala  
     1                    5                    10                    15

Arg Gly Gln His Val Ala Asn Leu Leu Glu Phe Gln Pro Gly Glu Gln  
                     20                    25                    30

Ile Ala Gln Val Ile Gln Leu Glu Ser Tyr Asn Asp Phe Pro Tyr Leu  
                     35                    40                    45

Val Leu Ala Thr Ala His Gly Arg Val Lys Lys Ser Arg Leu Leu Asp  
50 55 60

Tyr Glu Ser Ala Arg Ser Gly Gly Leu Ile Ala Ile Asn Leu Asn Glu  
65 70 75 80

Asp Asp Arg Leu Ile Gly Ala Ala Leu Cys Gly Glu Glu Asp Asp Leu  
85 90 95

Leu Leu Val Ser Glu Phe Gly Gln Ser Ile Arg Phe Thr Ala Asp Asp  
100 105 110

Glu Gln Leu Arg Pro Met Gly Arg Ala Thr Ala Gly Val Lys Gly Met  
115 120 125

Arg Phe Arg Asp Asn Asp Gln Leu Leu Ser Met Ser Val Val Arg Asp  
130 135 140

Gly Glu Phe Leu Leu Val Ala Thr Ser Gly Gly Tyr Gly Lys Arg Thr  
145 150 155 160

Pro Leu Glu Asp Tyr Ser Thr Gln Gly Arg Gly Gly Leu Gly Val Val  
165 170 175

Thr Phe Lys Tyr Thr Pro Lys Arg Gly Arg Leu Val Ser Ala Ile Ala  
180 185 190

Val Glu Glu Asp Asp Glu Ile Phe Ala Ile Thr Ser Ala Gly Gly Val  
195 200 205

Val Arg Thr Glu Val Lys Gln Ile Arg Pro Ser Ser Arg Ala Thr Met  
210 215 220

Gly Val Arg Leu Val Asn Leu Glu Glu Gly Val Glu Leu Leu Ala Ile  
225 230 235 240

Asp Lys Asn Val Glu Asp Gln Gly Glu Ala  
245 250

<210> 113

<211> 873

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(873)

<223> FRXA01684

<400> 113

ggc gac acc gca att tat gac acg ttg gtg cgc atg gct cag cca tgg 48  
Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp  
1 5 10 15

tcc atg cga tac ccg ctg gta gac ggc cag ggt aac ttc ggt tcc cgc 96  
Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg  
20 25 30

ggc aac gac ggc cct gca gca atg cgt tac acc gag tgc cgc atg acc 144  
Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr

35	40	45	
cca ctg gcc atg gag atg gtg cgc gac atc cgc gaa aac acc gtc aac			192
Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn			
50	55	60	
ttc tca cca aac tac gac ggt aaa acc ctc gaa cca gac gtt ttg cca			240
Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro			
65	70	75	80
tcg cgc gtt cca aac ttg ttg atg aac ggt tcg ggc ggc att gcg gtc			288
Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val			
85	90	95	
ggc atg gcc acc aac atc cca ccg cac aac ctc aac gag ctt gcc gac			336
Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp			
100	105	110	
gcc atc ttc tgg ctc ctg gaa aac cca gac gcc gaa gaa tcc gaa gct			384
Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala			
115	120	125	
ctc gaa gcc tgc atg aag ttt gtg aag ggc cca gac ttc cca acc gct			432
Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala			
130	135	140	
ggc ctc atc atc ggt gac aag ggc atc cac gat gcc tac acc acc ggc			480
Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly			
145	150	155	160
cgc ggc tcc atc cgc atg cgc ggt gtc acc tcc atc gag gag gaa ggc			528
Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly			
165	170	175	
aac cgc acc gtc atc gtt atc acc gag ctg cca tac cag gtc aac ccg			576
Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro			
180	185	190	
gat aac ctg atc tct aat atc gcg gag cag gtg cgc gac ggc aag ctc			624
Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu			
195	200	205	
gtg ggc atc tcc aag att gaa gat gaa tcc tcc gac cgc gtc ggc atg			672
Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met			
210	215	220	
cgc att gtg gtc acc ctc aag cgc gac gca gtt gcc cgc gtg gtg ctg			720
Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu			
225	230	235	240
aac aac ctg ttc aag cac tcc cag ctg caa gcc aac ttt ggt gcg aac			768
Asn Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn			
245	250	255	
atg ctc tcc atc gtc gat ggc gtg cca cgc acc ctt cgc ctg gac cag			816
Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln			
260	265	270	
atg ctg cgc tac tac gtg gca cac cag atc gaa gtc atc gtg cgc cgc			864
Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg			
275	280	285	



acc caa tac  
Thr Gln Tyr  
290

<210> 114  
<211> 291  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 114  
Gly Asp Thr Ala Ile Tyr Asp Thr Leu Val Arg Met Ala Gln Pro Trp  
1 5 10 15  
Ser Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Arg  
20 25 30  
Gly Asn Asp Gly Pro Ala Ala Met Arg Tyr Thr Glu Cys Arg Met Thr  
35 40 45  
Pro Leu Ala Met Glu Met Val Arg Asp Ile Arg Glu Asn Thr Val Asn  
50 55 60  
Phe Ser Pro Asn Tyr Asp Gly Lys Thr Leu Glu Pro Asp Val Leu Pro  
65 70 75 80  
Ser Arg Val Pro Asn Leu Leu Met Asn Gly Ser Gly Gly Ile Ala Val  
85 90 95  
Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Asn Glu Leu Ala Asp  
100 105 110  
Ala Ile Phe Trp Leu Leu Glu Asn Pro Asp Ala Glu Glu Ser Glu Ala  
115 120 125  
Leu Glu Ala Cys Met Lys Phe Val Lys Gly Pro Asp Phe Pro Thr Ala  
130 135 140  
Gly Leu Ile Ile Gly Asp Lys Gly Ile His Asp Ala Tyr Thr Thr Gly  
145 150 155 160  
Arg Gly Ser Ile Arg Met Arg Gly Val Thr Ser Ile Glu Glu Glu Gly  
165 170 175  
Asn Arg Thr Val Ile Val Ile Thr Glu Leu Pro Tyr Gln Val Asn Pro  
180 185 190  
Asp Asn Leu Ile Ser Asn Ile Ala Glu Gln Val Arg Asp Gly Lys Leu  
195 200 205  
Val Gly Ile Ser Lys Ile Glu Asp Glu Ser Ser Asp Arg Val Gly Met  
210 215 220  
Arg Ile Val Val Thr Leu Lys Arg Asp Ala Val Ala Arg Val Val Leu  
225 230 235 240  
Asn Asn Leu Phe Lys His Ser Gln Leu Gln Ala Asn Phe Gly Ala Asn  
245 250 255  
Met Leu Ser Ile Val Asp Gly Val Pro Arg Thr Leu Arg Leu Asp Gln

260

265

270

Met Leu Arg Tyr Tyr Val Ala His Gln Ile Glu Val Ile Val Arg Arg  
 275 280 285

Thr Gln Tyr  
 290

&lt;210&gt; 115

&lt;211&gt; 953

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(930)

&lt;223&gt; RXN01688

&lt;400&gt; 115

cag ttc gaa ggc cag acc aaa acc aag ctg ggc aac acg gag atc aaa	48
Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys	
1 5 10 15	
tcc ttc gtg cag cgc atg gcc aac gag cac atc ggc cac tgg ttg gaa	96
Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu	
20 25 30	
gca aac cct gct gaa gcc aag gtc atc atc aac aag gct gtc ggt tcc	144
Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser	
35 40 45	
gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg	192
Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg	
50 55 60	
aag tca gca acc gat ctg ggt gga ctg ccc ggt aag ctt gcc gac tgc	240
Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys	
65 70 75 80	
cgt tcc aag gat cca gaa aag tcc gaa ctt tac atc gtg gag ggc gac	288
Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp	
85 90 95	
tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca	336
Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala	
100 105 110	
atc ctt cca ctg cga ggc aag atc ctc aac gtg gaa aag gcc cgc cta	384
Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu	
115 120 125	
gac aag gtt ctg aag aac gcc gaa gtc caa gcg atc atc acc gca ctg	432
Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu	
130 135 140	
ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac	480
Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His	
145 150 155 160	
aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca	528

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Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala
      165                      170                      175

acg ctg ctg ctc acc ctg ctt ttc cgc ttc atg cca gac ctc gtc gcc 576
Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro Asp Leu Val Ala
      180                      185                      190

gaa ggc cac gtc tac ttg gca cag cca cct ttg tac aaa ctg aag tgg 624
Glu Gly His Val Tyr Leu Ala Gln Pro Pro Leu Tyr Lys Leu Lys Trp
      195                      200                      205

cag cgc gga gag cca gga ttc gca tac tcc gat gag gag cgc gat gag 672
Gln Arg Gly Glu Pro Gly Phe Ala Tyr Ser Asp Glu Glu Arg Asp Glu
      210                      215                      220

cag ctc aac gaa ggc ctt gcc gct gga cgc aag atc aac aag gac gac 720
Gln Leu Asn Glu Gly Leu Ala Ala Gly Arg Lys Ile Asn Lys Asp Asp
      225                      230                      235                      240

ggc atc cag cgc tac aag ggt ctc ggc gag atg aac gcc agc gag ctg 768
Gly Ile Gln Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Ser Glu Leu
      245                      250                      255

tgg gaa acc acc atg gac cca act gtt cgt att ctg cgc cgc gtg gac 816
Trp Glu Thr Thr Met Asp Pro Thr Val Arg Ile Leu Arg Arg Val Asp
      260                      265                      270

atc acc gat gct cag cgt gct gat gaa ctg ttc tcc atc ttg atg ggt 864
Ile Thr Asp Ala Gln Arg Ala Asp Glu Leu Phe Ser Ile Leu Met Gly
      275                      280                      285

gac gac gtt gtg gct cgc cgc agc ttc atc acc cga aat gcc aag gat 912
Asp Asp Val Val Ala Arg Arg Ser Phe Ile Thr Arg Asn Ala Lys Asp
      290                      295                      300

gtt cgt ttc ctc gat atc taaagcgcct tacttaaccc gcc 953
Val Arg Phe Leu Asp Ile
305                      310

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&lt;210&gt; 116

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 116

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Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys
  1                      5                      10                      15

Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu
      20                      25                      30

Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser
      35                      40                      45

Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg
      50                      55                      60

Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
      65                      70                      75                      80

```

Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp  
                     85                    90                    95  
 Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala  
                     100                    105                    110  
 Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu  
                     115                    120                    125  
 Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu  
                     130                    135                    140  
 Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His  
                     145                    150                    155                    160  
 Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala  
                     165                    170                    175  
 Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro Asp Leu Val Ala  
                     180                    185                    190  
 Glu Gly His Val Tyr Leu Ala Gln Pro Pro Leu Tyr Lys Leu Lys Trp  
                     195                    200                    205  
 Gln Arg Gly Glu Pro Gly Phe Ala Tyr Ser Asp Glu Glu Arg Asp Glu  
                     210                    215                    220  
 Gln Leu Asn Glu Gly Leu Ala Ala Gly Arg Lys Ile Asn Lys Asp Asp  
                     225                    230                    235                    240  
 Gly Ile Gln Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Ser Glu Leu  
                     245                    250                    255  
 Trp Glu Thr Thr Met Asp Pro Thr Val Arg Ile Leu Arg Arg Val Asp  
                     260                    265                    270  
 Ile Thr Asp Ala Gln Arg Ala Asp Glu Leu Phe Ser Ile Leu Met Gly  
                     275                    280                    285  
 Asp Asp Val Val Ala Arg Arg Ser Phe Ile Thr Arg Asn Ala Lys Asp  
                     290                    295                    300  
 Val Arg Phe Leu Asp Ile  
                     305                    310

&lt;210&gt; 117

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(564)

&lt;223&gt; FRXA01688

&lt;400&gt; 117

cag ttc gaa ggc cag acc aaa acc aag ctg ggc aac acg gag atc aaa 48  
 Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys  
           1                    5                    10                    15

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tcc ttc gtg cag cgc atg gcc aac gag cac atc ggc cac tgg ttg gaa 96
Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu
      20          25          30

gca aac cct gct gaa gcc aag gtc atc atc aac aag gct gtc ggt tcc 144
Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser
      35          40          45

gcg cag gca cgc ctt gct gct cga aaa gcc cgt gac ctg gtc cga cgg 192
Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg
      50          55          60

aag tca gca acc gat ctg ggt gga ctg ccc ggt aag ctt gcc gac tgc 240
Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
      65          70          75

cgt tcc aag gat cca gaa aag tcc gaa ctt tac atc gtg gag ggc gac 288
Arg Ser Lys Asp Pro Glu Lys Ser Glu Leu Tyr Ile Val Glu Gly Asp
      85          90          95

tcc gca ggt ggt tct gcg aag tcc ggc cgt gac tcc atg ttc cag gca 336
Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala
      100          105          110

atc ctt cca ctg cga ggc aag atc ctc aac gtg gaa aag gcc cgc cta 384
Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Arg Leu
      115          120          125

gac aag gtt ctg aag aac gcc gaa gtc caa gcg atc atc acc gca ctg 432
Asp Lys Val Leu Lys Asn Ala Glu Val Gln Ala Ile Ile Thr Ala Leu
      130          135          140

ggt acc ggc atc cac gac gag ttc gac atc aac aag ctg cgc tac cac 480
Gly Thr Gly Ile His Asp Glu Phe Asp Ile Asn Lys Leu Arg Tyr His
      145          150          155          160

aag atc gtg ctg atg gcc gac gcc gat gtt gac ggc cag cac atc gca 528
Lys Ile Val Leu Met Ala Asp Ala Asp Val Asp Gly Gln His Ile Ala
      165          170          175

acg ctg ctg ctc acc ctg ctt ttc cgc ttc atg cca 564
Thr Leu Leu Leu Thr Leu Leu Phe Arg Phe Met Pro
      180          185

```

&lt;210&gt; 118

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 118

```

Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Ile Lys
  1          5          10          15

```

```

Ser Phe Val Gln Arg Met Ala Asn Glu His Ile Gly His Trp Leu Glu
      20          25          30

```

```

Ala Asn Pro Ala Glu Ala Lys Val Ile Ile Asn Lys Ala Val Gly Ser
      35          40          45

```

```

Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Asp Leu Val Arg Arg

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[illegible]

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<220>
<221> CDS
<222> (101)..(1216)
<223> RXN01689
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<400> 119
ttttgccgtt tctcgcggttgc tgcgtgggtac tacgtgggga cctaagcgtg taagatggaa 60

acgtctgtat cggataagta gcgaggagtg ttcgttaaaa gtg gca aac act gaa 115
Val Ala Asn Thr Glu
1 5

cac aat tat gac gct tca tgc atc acc atc ctt gaa ggt ctt gag gcg 163
His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu Glu Gly Leu Glu Ala
10 15 20

gta cgt aag cgc ccg ggc atg tac atc ggt tca act gga ccg cgt gga 211
Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser Thr Gly Pro Arg Gly
25 30 35

ctg cac cac ctg att tgg gaa gtc gtt gac aac tca gtg gat gag gcc 259
Leu His His Leu Ile Trp Glu Val Val Asp Asn Ser Val Asp Glu Ala
40 45 50

atg gct ggc cac gcc acc aag gtt gaa gtg acc ctt ctg gaa gat ggt 307
Met Ala Gly His Ala Thr Lys Val Glu Val Thr Leu Leu Glu Asp Gly
55 60 65

ggc gtt caa gtt gtc gat gac ggt cga gga att ccc gtc gat atg cac 355

```

Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile Pro Val Asp Met His	
70 75 80 85	
cca tcc ggt gca cca acc gtg cag gtt gtt atg acc cag ctg cac gcc	403
Pro Ser Gly Ala Pro Thr Val Gln Val Val Met Thr Gln Leu His Ala	
90 95 100	
ggc ggt aag ttt gac tcc gat tct tac gcc gtt tcc ggt ggt ctg cat	451
Gly Gly Lys Phe Asp Ser Asp Ser Tyr Ala Val Ser Gly Gly Leu His	
105 110 115	
ggt gtt ggt att tct gtg gtg aac gcc ctg tcc acc cgc gtg gaa gcc	499
Gly Val Gly Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala	
120 125 130	
gac atc aag ttg cac ggc aag cac tgg tac caa aac ttt gaa aag tct	547
Asp Ile Lys Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser	
135 140 145	
gtt cca gac gag ttg atc gaa ggc ggc aac gct cgc ggc acc ggt acc	595
Val Pro Asp Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr	
150 155 160 165	
acc att cgt ttt tgg cca gac gct gaa att ttc gaa acc acc gag ttt	643
Thr Ile Arg Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe	
170 175 180	
gat ttc gaa acg att tct cga cgt ctg cag gaa atg gca ttc ctt aac	691
Asp Phe Glu Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn	
185 190 195	
aag ggt ctg acc atc acc ttg acg gac aac cgc gcc acc gac gag gaa	739
Lys Gly Leu Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu	
200 205 210	
ctc gag ctc gaa gca ctc gct gag cag ggc gaa acc gca acg gaa cta	787
Leu Glu Leu Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu	
215 220 225	
tcc ctc gat gag atc gac aac gaa acc gaa ctc gtt gaa gag acc acc	835
Ser Leu Asp Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr	
230 235 240 245	
gat gct cca aag aag cca aaa aag cgt gag aag aag aaa atc ttc cac	883
Asp Ala Pro Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His	
250 255 260	
tac ccc aat ggc ctc gag gac tac gtt cac tac ctc aac cgc agc aag	931
Tyr Pro Asn Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys	
265 270 275	
acc aac atc cac cct tca atc gtg tca ttc gag gca aag gga gat gac	979
Thr Asn Ile His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp	
280 285 290	
cac gag gtt gag gtg gca atg cag tgg aac tcc tcc tac aag gaa tcc	1027
His Glu Val Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser	
295 300 305	
gtc cac acc ttc gcc aac acc att aac acc cgc gaa ggc ggc acc cac	1075
Val His Thr Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His	

310	315	320	325	
gag gaa ggt ttc cgc tct gcg ctg acc tcc ctg atg aac cgc tac gca				1123
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala				
	330	335	340	
cgt gag cac aag ctt ctg aaa gaa aag gaa gca aac ctt acc ggt gac				1171
Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala Asn Leu Thr Gly Asp				
	345	350	355	
gac tgt cgt gaa ggc ctg tcc gcg gtt att ttc cgt gcg cgt tgg				1216
Asp Cys Arg Glu Gly Leu Ser Ala Val Ile Phe Arg Ala Arg Trp				
	360	365	370	
tgacccacag ttcgaaggcc aga				1239

&lt;210&gt; 120

&lt;211&gt; 372

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 120

Val	Ala	Asn	Thr	Glu	His	Asn	Tyr	Asp	Ala	Ser	Ser	Ile	Thr	Ile	Leu
1				5					10					15	

Glu	Gly	Leu	Glu	Ala	Val	Arg	Lys	Arg	Pro	Gly	Met	Tyr	Ile	Gly	Ser
		20					25						30		

Thr	Gly	Pro	Arg	Gly	Leu	His	His	Leu	Ile	Trp	Glu	Val	Val	Asp	Asn
		35					40					45			

Ser	Val	Asp	Glu	Ala	Met	Ala	Gly	His	Ala	Thr	Lys	Val	Glu	Val	Thr
	50					55					60				

Leu	Leu	Glu	Asp	Gly	Gly	Val	Gln	Val	Val	Asp	Asp	Gly	Arg	Gly	Ile
65				70						75					80

Pro	Val	Asp	Met	His	Pro	Ser	Gly	Ala	Pro	Thr	Val	Gln	Val	Val	Met
				85					90						95

Thr	Gln	Leu	His	Ala	Gly	Gly	Lys	Phe	Asp	Ser	Asp	Ser	Tyr	Ala	Val
		100					105						110		

Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Ile	Ser	Val	Val	Asn	Ala	Leu	Ser
		115					120						125		

Thr	Arg	Val	Glu	Ala	Asp	Ile	Lys	Leu	His	Gly	Lys	His	Trp	Tyr	Gln
		130					135				140				

Asn	Phe	Glu	Lys	Ser	Val	Pro	Asp	Glu	Leu	Ile	Glu	Gly	Gly	Asn	Ala
145					150					155					160

Arg	Gly	Thr	Gly	Thr	Thr	Ile	Arg	Phe	Trp	Pro	Asp	Ala	Glu	Ile	Phe
			165						170					175	

Glu	Thr	Thr	Glu	Phe	Asp	Phe	Glu	Thr	Ile	Ser	Arg	Arg	Leu	Gln	Glu
			180					185						190	

Met	Ala	Phe	Leu	Asn	Lys	Gly	Leu	Thr	Ile	Thr	Leu	Thr	Asp	Asn	Arg
			195				200						205		



Ala Thr Asp Glu Glu Leu Glu Leu Glu Ala Leu Ala Glu Gln Gly Glu  
210 215 220

Thr Ala Thr Glu Leu Ser Leu Asp Glu Ile Asp Asn Glu Thr Glu Leu  
225 230 235 240

Val Glu Glu Thr Thr Asp Ala Pro Lys Lys Pro Lys Lys Arg Glu Lys  
245 250 255

Lys Lys Ile Phe His Tyr Pro Asn Gly Leu Glu Asp Tyr Val His Tyr  
260 265 270

Leu Asn Arg Ser Lys Thr Asn Ile His Pro Ser Ile Val Ser Phe Glu  
275 280 285

Ala Lys Gly Asp Asp His Glu Val Glu Val Ala Met Gln Trp Asn Ser  
290 295 300

Ser Tyr Lys Glu Ser Val His Thr Phe Ala Asn Thr Ile Asn Thr Arg  
305 310 315 320

Glu Gly Gly Thr His Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Leu  
325 330 335

Met Asn Arg Tyr Ala Arg Glu His Lys Leu Leu Lys Glu Lys Glu Ala  
340 345 350

Asn Leu Thr Gly Asp Asp Cys Arg Glu Gly Leu Ser Ala Val Ile Phe  
355 360 365

Arg Ala Arg Trp  
370

<210> 121

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> FRXA01689

<400> 121

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Phe Asp Ser Asp Ser Tyr Ala Val Ser Gly Gly Leu His Gly Val Gly  
1 5 10 15

att tct gtg gtg aac gcc ctg tcc acc cgc gtg gaa gcc gac atc aag 96  
Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys  
20 25 30

ttg cac ggc aag cac tgg tac caa aac ttt gaa aag tct gtt cca gac 144  
Leu His Gly Lys His Trp Tyr Gln Asn Phe Glu Lys Ser Val Pro Asp  
35 40 45

gag ttg atc gaa ggc ggc aac gct cgc ggc acc ggt acc acc att cgt 192  
Glu Leu Ile Glu Gly Gly Asn Ala Arg Gly Thr Gly Thr Thr Ile Arg  
50 55 60

ttt tgg cca gac gct gaa att ttc gaa acc acc gag ttt gat ttc gaa 240  
 Phe Trp Pro Asp Ala Glu Ile Phe Glu Thr Thr Glu Phe Asp Phe Glu  
 65 70 75 80  
 acg att tct cga cgt ctg cag gaa atg gca ttc ctt aac aag ggt ctg 288  
 Thr Ile Ser Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu  
 85 90 95  
 acc atc acc ttg acg gac aac cgc gcc acc gac gag gaa ctc gag ctc 336  
 Thr Ile Thr Leu Thr Asp Asn Arg Ala Thr Asp Glu Glu Leu Glu Leu  
 100 105 110  
 gaa gca ctc gct gag cag ggc gaa acc gca acg gaa cta tcc ctc gat 384  
 Glu Ala Leu Ala Glu Gln Gly Glu Thr Ala Thr Glu Leu Ser Leu Asp  
 115 120 125  
 gag atc gac aac gaa acc gaa ctc gtt gaa gag acc acc gat gct cca 432  
 Glu Ile Asp Asn Glu Thr Glu Leu Val Glu Glu Thr Thr Asp Ala Pro  
 130 135 140  
 aag aag cca aaa aag cgt gag aag aag aaa atc ttc cac tac ccc aat 480  
 Lys Lys Pro Lys Lys Arg Glu Lys Lys Lys Ile Phe His Tyr Pro Asn  
 145 150 155 160  
 ggc ctc gag gac tac gtt cac tac ctc aac cgc agc aag acc aac atc 528  
 Gly Leu Glu Asp Tyr Val His Tyr Leu Asn Arg Ser Lys Thr Asn Ile  
 165 170 175  
 cac cct tca atc gtg tca ttc gag gca aag gga gat gac cac gag gtt 576  
 His Pro Ser Ile Val Ser Phe Glu Ala Lys Gly Asp Asp His Glu Val  
 180 185 190  
 gag gtg gca atg cag tgg aac tcc tcc tac aag gaa tcc gtc cac acc 624  
 Glu Val Ala Met Gln Trp Asn Ser Ser Tyr Lys Glu Ser Val His Thr  
 195 200 205  
 ttc gcc aac acc att aac acc cgc gaa ggc ggc acc cac gag gaa ggt 672  
 Phe Ala Asn Thr Ile Asn Thr Arg Glu Gly Gly Thr His Glu Glu Gly  
 210 215 220  
 ttc cgc tct gcg ctg acc tcc ctg atg aac cgc tac gca cgt gag cac 720  
 Phe Arg Ser Ala Leu Thr Ser Leu Met Asn Arg Tyr Ala Arg Glu His  
 225 230 235 240  
 aag ctt 726  
 Lys Leu

&lt;210&gt; 122

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 122

Phe Asp Ser Asp Ser Tyr Ala Val Ser Gly Gly Leu His Gly Val Gly  
 1 5 10 15

Ile Ser Val Val Asn Ala Leu Ser Thr Arg Val Glu Ala Asp Ile Lys  
 20 25 30

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<400> 123
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acgtctgtat cggataagta gcgaggagtg ttcgttaaaa gtg gca aac act gaa 115
Val Ala Asn Thr Glu
      1           5

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cac aat tat gac gct tca tgc atc acc atc ctt gaa ggt ctt gag gcg 163  
 His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu Glu Gly Leu Glu Ala  
                   10                  15                  20  
  
 gta cgt aag cgc ccg ggc atg tac atc ggt tca act gga ccg cgt gga 211  
 Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser Thr Gly Pro Arg Gly  
                   25                  30                  35  
  
 ctg cac cac ctg att tgg gaa gtc gtt gac aac tca gtg gat gag gcc 259  
 Leu His His Leu Ile Trp Glu Val Val Asp Asn Ser Val Asp Glu Ala  
                   40                  45                  50  
  
 atg gct ggc cac gcc acc aag gtt gaa gtg acc ctt ctg gaa gat ggt 307  
 Met Ala Gly His Ala Thr Lys Val Glu Val Thr Leu Leu Glu Asp Gly  
                   55                  60                  65  
  
 ggc gtt caa gtt gtc gat gac ggt cga gga att ccc gtc gat atg cac 355  
 Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile Pro Val Asp Met His  
                   70                  75                  80                  85  
  
 cca tcc ggt gca cca acc gtg cag gtt 382  
 Pro Ser Gly Ala Pro Thr Val Gln Val  
                   90

<210> 124  
 <211> 94  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 124  
 Val Ala Asn Thr Glu His Asn Tyr Asp Ala Ser Ser Ile Thr Ile Leu  
   1                  5                  10                  15  
  
 Glu Gly Leu Glu Ala Val Arg Lys Arg Pro Gly Met Tyr Ile Gly Ser  
                   20                  25                  30  
  
 Thr Gly Pro Arg Gly Leu His His Leu Ile Trp Glu Val Val Asp Asn  
                   35                  40                  45  
  
 Ser Val Asp Glu Ala Met Ala Gly His Ala Thr Lys Val Glu Val Thr  
                   50                  55                  60  
  
 Leu Leu Glu Asp Gly Gly Val Gln Val Val Asp Asp Gly Arg Gly Ile  
                   65                  70                  75                  80  
  
 Pro Val Asp Met His Pro Ser Gly Ala Pro Thr Val Gln Val  
                   85                  90

<210> 125  
 <211> 1962  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1939)  
 <223> RXN03093

<400> 125

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tgaaggggggt caaggcagtt aacgagaggg atgcattccc gtg gca gat acc gca 115  
Val Ala Asp Thr Ala  
1 5

ggc acc aca gga tcg aaa aag aag tac ttg gtg atc gtc gag tcg gcg 163  
Gly Thr Thr Gly Ser Lys Lys Lys Tyr Leu Val Ile Val Glu Ser Ala  
10 15 20

acc aag gct aaa aag att cag cct tac ctt ggc aac gac tac atc gtc 211  
Thr Lys Ala Lys Lys Ile Gln Pro Tyr Leu Gly Asn Asp Tyr Ile Val  
25 30 35

gag gcc tcc gtt ggt cat att cgt gat ctg cca cgt ggc gct gct gac 259  
Glu Ala Ser Val Gly His Ile Arg Asp Leu Pro Arg Gly Ala Ala Asp  
40 45 50

atc cct gca aag tac aag aag gag cct tgg gct cgt ctt ggt gtg gac 307  
Ile Pro Ala Lys Tyr Lys Lys Glu Pro Trp Ala Arg Leu Gly Val Asp  
55 60 65

acc gat cgc ggt ttc gcg ccg ctt tat gtg gtg agc ccc gat aaa aag 355  
Thr Asp Arg Gly Phe Ala Pro Leu Tyr Val Val Ser Pro Asp Lys Lys  
70 75 80 85

aag aag gtc gct gac ctc aag gcg aag ctc aag ctc gtt gat gag ttg 403  
Lys Lys Val Ala Asp Leu Lys Ala Lys Leu Lys Leu Val Asp Glu Leu  
90 95 100

ctg ctg gca aca gac ccc gac cgt gag ggc gag gcg att gcg tgg cat 451  
Leu Leu Ala Thr Asp Pro Asp Arg Glu Gly Glu Ala Ile Ala Trp His  
105 110 115

ttg ctt gag gtg ttg aag ccg act gtt cct gtg cgt cgc atg gtg ttc 499  
Leu Leu Glu Val Leu Lys Pro Thr Val Pro Val Arg Arg Met Val Phe  
120 125 130

aat gag atc acg aag cct gcc att ttg gct gcg gcg gaa aac act cgt 547  
Asn Glu Ile Thr Lys Pro Ala Ile Leu Ala Ala Glu Asn Thr Arg  
135 140 145

gag ctg gat gag aac ctg gtg gat gcg cag gaa act cgt cgt att ctg 595  
Glu Leu Asp Glu Asn Leu Val Asp Ala Gln Glu Thr Arg Arg Ile Leu  
150 155 160 165

gac cgt ttg tac ggc tat gaa gtc tct cct gtg ctg tgg aaa aag gtc 643  
Asp Arg Leu Tyr Gly Tyr Glu Val Ser Pro Val Leu Trp Lys Lys Val  
170 175 180

atg ccg agg ttg tcg gcg ggc cgt gtg cag tcg gtg gca acc cgt gtg 691  
Met Pro Arg Leu Ser Ala Gly Arg Val Gln Ser Val Ala Thr Arg Val  
185 190 195

att gtt gag cgg gag cgc gag cgc atg gcg ttc gtg tcg gcg gat tat 739  
Ile Val Glu Arg Glu Arg Glu Arg Met Ala Phe Val Ser Ala Asp Tyr  
200 205 210

tgg gat ctg tcg gcg gag ttt aat gcg cgt gaa aac ggc aag gcg gat 787  
Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu Asn Gly Lys Ala Asp  
215 220 225

tcg gat aac ccg tcg tcg ttt act gcg cgt ttg tcc acg att gat gga 835  
 Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile Asp Gly  
 230 235 240 245

aac cgt gtt gct caa ggc cgt gat ttt aat gat cgg gga gag ctg acc 883  
 Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu Leu Thr  
 250 255 260

tcg gag gct gtc gtc gtc gat aag cag cgt gct gag gcg tta gcc gag 931  
 Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu Ala Glu  
 265 270 275

gct ttg gaa ggc cag gaa atg gcc gtc gtt ggg gtc gag gaa aag ccg 979  
 Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu Lys Pro  
 280 285 290

tac acc cgt cgc cct tat gcg ccg ttt atg acc tct acg ctg cag caa 1027  
 Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu Gln Gln  
 295 300 305

gag tct ggc cgc aag ctg cat tac act tct gag cgc acg atg cgt att 1075  
 Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met Arg Ile  
 310 315 320 325

gcg cag cgc ttg tat gaa aac ggc cat atc act tat atg cgt act gac 1123  
 Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg Thr Asp  
 330 335 340

tcg acc tcg ttg tcg gag cag ggc atg aag gct gcg cgc gat cag gcg 1171  
 Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp Gln Ala  
 345 350 355

ttg gag ctg tac ggt gcg gaa tat gtt tcg ccg agc cca cgt acc tat 1219  
 Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg Thr Tyr  
 360 365 370

gac cgc aag gtg aag aac tcc cag gag gcc cac gag gcg att cgc cca 1267  
 Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile Arg Pro  
 375 380 385

gct ggt gaa act ttt gcg acc ccg ggc cag ctg cat ggc cag ttg gat 1315  
 Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln Leu Asp  
 390 395 400 405

gcg gaa gaa ttt aag ctc tat gag ctg att tgg cag cgc act gtg gcc 1363  
 Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr Val Ala  
 410 415 420

tcc cag atg gcc gat gcc aag ggc acg tcc atg aag gtc acc atc ggt 1411  
 Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr Ile Gly  
 425 430 435

ggc acc gcg aag acc ggc gag aag act gag ttc aac gcg acc ggc cgc 1459  
 Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr Gly Arg  
 440 445 450

acg ctg act ttc cct ggc ttc ctg cgc gct tac gtg gaa acc acc cgc 1507  
 Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr Thr Arg  
 455 460 465

acc gcc gat ggc cgc gac gta gct gac aac gcc gaa aag cgt ctg cca 1555  
 Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg Leu Pro  
 470 475 480 485

ctg ctg tct gag ggc gat ctg ctc aag gtt ttg agc atc gaa gcc gat 1603  
 Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu Ala Asp  
 490 495 500

ggt cac agc acc aat cca cct gcg cgc tac aca gag gcg tcg ctg gtg 1651  
 Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser Leu Val  
 505 510 515

aag aag atg gaa gat ctg ggc atc ggc cgt cct tcc act tat gca tcg 1699  
 Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr Ala Ser  
 520 525 530

atc att aag acg att cag gat cga ggc tac gtt tat tcg cgt ggc aat 1747  
 Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg Gly Asn  
 535 540 545

gcg ctg gtg ccg tcc tgg gtc gcg ttc gcc gtg gtc gga ttg ctt gaa 1795  
 Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu Leu Glu  
 550 555 560 565

gcc aac ttc acc tcg ctg gtg gat tac gat ttc acc tcc tcc atg gaa 1843  
 Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser Met Glu  
 570 575 580

gat gag ctg gac aac atc gcc gca ggt cgc gag ggc cgc acg gag tgg 1891  
 Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr Glu Trp  
 585 590 595

ctc aac ggt ttc tac ttc ggg cga tgc cga agc gga tca gtc cat ggc 1939  
 Leu Asn Gly Phe Tyr Phe Gly Arg Cys Arg Ser Gly Ser Val His Gly  
 600 605 610

tgaatcagtt gcccgccagg gcg 1962

&lt;210&gt; 126

&lt;211&gt; 613

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 126

Val Ala Asp Thr Ala Gly Thr Thr Gly Ser Lys Lys Lys Tyr Leu Val  
 1 5 10 15

Ile Val Glu Ser Ala Thr Lys Ala Lys Lys Ile Gln Pro Tyr Leu Gly  
 20 25 30

Asn Asp Tyr Ile Val Glu Ala Ser Val Gly His Ile Arg Asp Leu Pro  
 35 40 45

Arg Gly Ala Ala Asp Ile Pro Ala Lys Tyr Lys Lys Glu Pro Trp Ala  
 50 55 60

Arg Leu Gly Val Asp Thr Asp Arg Gly Phe Ala Pro Leu Tyr Val Val  
 65 70 75 80

Ser Pro Asp Lys Lys Lys Lys Val Ala Asp Leu Lys Ala Lys Leu Lys

[illegible]



Gln Arg Thr Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met  
420 425 430

Lys Val Thr Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe  
435 440 445

Asn Ala Thr Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr  
450 455 460

Val Glu Thr Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala  
465 470 475 480

Glu Lys Arg Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu  
485 490 495

Ser Ile Glu Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr  
500 505 510

Glu Ala Ser Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro  
515 520 525

Ser Thr Tyr Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val  
530 535 540

Tyr Ser Arg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val  
545 550 555 560

Val Gly Leu Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe  
565 570 575

Thr Ser Ser Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu  
580 585 590

Gly Arg Thr Glu Trp Leu Asn Gly Phe Tyr Phe Gly Arg Cys Arg Ser  
595 600 605

Gly Ser Val His Gly  
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<210> 127

<211> 2378

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2355)

<223> FRXA00798

<400> 127

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1 5 10 15

gcg gat tcg gat aac ccg tcg tcg ttt act gcg cgt ttg tcc acg att 96  
Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile  
20 25 30

gat gga aac cgt gtt gct caa ggc cgt gat ttt aat gat cgg gga gag 144

Asp Gly Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu	
35 40 45	
ctg acc tcg gag gct gtc gtc gtc gat aag cag cgt gct gag gcg tta	192
Leu Thr Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu	
50 55 60	
gcc gag gct ttg gaa ggc cag gaa atg gcc gtc gtt ggg gtc gag gaa	240
Ala Glu Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu	
65 70 75 80	
aag ccg tac acc cgt cgc cct tat gcg ccg ttt atg acc tct acg ctg	288
Lys Pro Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu	
85 90 95	
cag caa gag tct ggc cgc aag ctg cat tac act tct gag cgc acg atg	336
Gln Gln Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met	
100 105 110	
cgt att gcg cag cgc ttg tat gaa aac ggc cat atc act tat atg cgt	384
Arg Ile Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg	
115 120 125	
act gac tcg acc tcg ttg tcg gag cag ggc atg aag gct gcg cgc gat	432
Thr Asp Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp	
130 135 140	
cag gcg ttg gag ctg tac ggt gcg gaa tat gtt tcg ccg agc cca cgt	480
Gln Ala Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg	
145 150 155 160	
acc tat gac cgc aag gtg aag aac tcc cag gag gcc cac gag gcg att	528
Thr Tyr Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile	
165 170 175	
cgc cca gct ggt gaa act ttt gcg acc ccg ggc cag ctg cat ggc cag	576
Arg Pro Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln	
180 185 190	
ttg gat gcg gaa gaa ttt aag ctc tat gag ctg att tgg cag cgc act	624
Leu Asp Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr	
195 200 205	
gtg gcc tcc cag atg gcc gat gcc aag ggc acg tcc atg aag gtc acc	672
Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr	
210 215 220	
atc ggt ggc acc gcg aag acc ggc gag aag act gag ttc aac gcg acc	720
Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr	
225 230 235 240	
ggc cgc acg ctg act ttc cct ggc ttc ctg cgc gct tac gtg gaa acc	768
Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr	
245 250 255	
acc cgc acc gcc gat ggc cgc gac gta gct gac aac gcc gaa aag cgt	816
Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg	
260 265 270	
ctg cca ctg ctg tct gag ggc gat ctg ctc aag gtt ttg agc atc gaa	864
Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu	

275	280	285	
gcc gat ggt cac agc acc aat cca cct gcg cgc tac aca gag gcg tcg Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser 290 295 300			912
ctg gtg aag aag atg gaa gat ctg ggc atc ggc cgt cct tcc act tat Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr 305 310 315 320			960
gca tcg atc att aag acg att cag gat cga ggc tac gtt tat tcg cgt Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg 325 330 335			1008
ggc aat gcg ctg gtg ccg tcc tgg gtc gcg ttc gcc gtg gtc gga ttg Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu 340 345 350			1056
ctt gaa gcc aac ttc acc tcg ctg gtg gat tac gat ttc acc tcc tcc Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser 355 360 365			1104
atg gaa gat gag ctg gac aac atc gcc gca ggt cgc gag ggc cgc acg Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr 370 375 380			1152
gag tgg ctc aac ggt ttc tac ttc ggc gat gcc gaa gcg gat cag tcc Glu Trp Leu Asn Gly Phe Tyr Phe Gly Asp Ala Glu Ala Asp Gln Ser 385 390 395 400			1200
atg gct gaa tca gtt gcc cgc cag ggc ggt ttg aag gcg ctt gtc gac Met Ala Glu Ser Val Ala Arg Gln Gly Gly Leu Lys Ala Leu Val Asp 405 410 415			1248
gcg aac ctg gag cac atc gac gcg cgt tca gta aac tca ctc aag ctt Ala Asn Leu Glu His Ile Asp Ala Arg Ser Val Asn Ser Leu Lys Leu 420 425 430			1296
ttc gac gac gcc gaa ggc cgt gcc gtg aac gtt cga gtc gga cgc tac Phe Asp Asp Ala Glu Gly Arg Ala Val Asn Val Arg Val Gly Arg Tyr 435 440 445			1344
ggt ccg tac atc gag cgc atc gtg ggc acc acc gcg gaa ggc gag cca Gly Pro Tyr Ile Glu Arg Ile Val Gly Thr Thr Ala Glu Gly Glu Pro 450 455 460			1392
gaa ttt cag cgc gcc aac cta cct gag gaa acc acg cct gat gag ctg Glu Phe Gln Arg Ala Asn Leu Pro Glu Glu Thr Thr Pro Asp Glu Leu 465 470 475 480			1440
acc ctc gag gtc gct gag aag ctt ttc gct acc cca caa ggt gga cgt Thr Leu Glu Val Ala Glu Lys Leu Phe Ala Thr Pro Gln Gly Gly Arg 485 490 495			1488
gaa ctg ggc att aac cca gca aac ggt cgc atg gtg gtg gct aag gaa Glu Leu Gly Ile Asn Pro Ala Asn Gly Arg Met Val Val Ala Lys Glu 500 505 510			1536
ggc cgc ttt ggt cca tac gtg atc gag cag gtc acg gac tca gag cgc Gly Arg Phe Gly Pro Tyr Val Ile Glu Gln Val Thr Asp Ser Glu Arg 515 520 525			1584

gct ggc gcc gaa gcc caa gca gaa gaa gtc gtt gca gcg gaa cga aaa 1632  
 Ala Gly Ala Glu Ala Gln Ala Glu Glu Val Val Ala Ala Glu Arg Lys  
 530 535 540

gct gaa gac gaa caa cgt gcc acc gat gga atg cga ccc aag aac tgg 1680  
 Ala Glu Asp Glu Gln Arg Ala Thr Asp Gly Met Arg Pro Lys Asn Trp  
 545 550 555 560

gaa acc aag act gcc gca aac cag aag gaa aag cgc atc aac cag ctg 1728  
 Glu Thr Lys Thr Ala Ala Asn Gln Lys Glu Lys Arg Ile Asn Gln Leu  
 565 570 575

gtt gag gaa aac ctc aag cca gcg acc gca tcc ctg ttc agc ggc atg 1776  
 Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met  
 580 585 590

gaa cct gca gcc gtg acc ctg gaa gaa gcc ctc aag ctg ctg tcc ctg 1824  
 Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu  
 595 600 605

cca cgc gaa gta ggt gtc gat cct tcc gac aac gaa gtg atc acc gct 1872  
 Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala  
 610 615 620

caa aac gga cga tac ggc cct tat ctg aag aag ggt agc gac tcc cgt 1920  
 Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg  
 625 630 635 640

tcc ctc aac agc gaa gag cag atc ttc acc gtc act ttg gat gag gct 1968  
 Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Glu Ala  
 645 650 655

cgc cgc atc tac gcc gaa cca aag cgt cgt gga cgc gcc gct gct cag 2016  
 Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Gln  
 660 665 670

cca cca ctg aag caa ctt ggc gac aat gac gtt tcc ggc aaa cca atg 2064  
 Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met  
 675 680 685

acc gtc aag gac gga cgt ttc ggc cca tac gtc acc gac ggc acc acc 2112  
 Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr  
 690 695 700

aac gcg tca ctg cgc aag ggc gat gtt cca gag tcc ctg acc gat gcg 2160  
 Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala  
 705 710 715 720

cgt gcc aac gag tta ctt tcc gag cgt cgt gcc aag gaa gca gca gat 2208  
 Arg Ala Asn Glu Leu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp  
 725 730 735

ggc gga gct cct gcg aag aag acg tcc act aaa aag act gca gcc aag 2256  
 Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys  
 740 745 750

aag acc acg gct aaa aag aca aca gct aag aaa acc gtg agg aag gct 2304  
 Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala  
 755 760 765

ccg ccg aaa acc acc aaa aac gtg gtg aag gcc ggc gct aag aag aag 2352  
 Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys  
 770 775 780

tcc taaaacatgc tgaacgggtt cgt 2378  
 Ser  
 785

<210> 128  
 <211> 785  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 128  
 Asp Tyr Trp Asp Leu Ser Ala Glu Phe Asn Ala Arg Glu Asn Gly Lys  
 1 5 10 15  
 Ala Asp Ser Asp Asn Pro Ser Ser Phe Thr Ala Arg Leu Ser Thr Ile  
 20 25 30  
 Asp Gly Asn Arg Val Ala Gln Gly Arg Asp Phe Asn Asp Arg Gly Glu  
 35 40 45  
 Leu Thr Ser Glu Ala Val Val Val Asp Lys Gln Arg Ala Glu Ala Leu  
 50 55 60  
 Ala Glu Ala Leu Glu Gly Gln Glu Met Ala Val Val Gly Val Glu Glu  
 65 70 75 80  
 Lys Pro Tyr Thr Arg Arg Pro Tyr Ala Pro Phe Met Thr Ser Thr Leu  
 85 90 95  
 Gln Gln Glu Ser Gly Arg Lys Leu His Tyr Thr Ser Glu Arg Thr Met  
 100 105 110  
 Arg Ile Ala Gln Arg Leu Tyr Glu Asn Gly His Ile Thr Tyr Met Arg  
 115 120 125  
 Thr Asp Ser Thr Ser Leu Ser Glu Gln Gly Met Lys Ala Ala Arg Asp  
 130 135 140  
 Gln Ala Leu Glu Leu Tyr Gly Ala Glu Tyr Val Ser Pro Ser Pro Arg  
 145 150 155 160  
 Thr Tyr Asp Arg Lys Val Lys Asn Ser Gln Glu Ala His Glu Ala Ile  
 165 170 175  
 Arg Pro Ala Gly Glu Thr Phe Ala Thr Pro Gly Gln Leu His Gly Gln  
 180 185 190  
 Leu Asp Ala Glu Glu Phe Lys Leu Tyr Glu Leu Ile Trp Gln Arg Thr  
 195 200 205  
 Val Ala Ser Gln Met Ala Asp Ala Lys Gly Thr Ser Met Lys Val Thr  
 210 215 220  
 Ile Gly Gly Thr Ala Lys Thr Gly Glu Lys Thr Glu Phe Asn Ala Thr  
 225 230 235 240  
 Gly Arg Thr Leu Thr Phe Pro Gly Phe Leu Arg Ala Tyr Val Glu Thr

245	250	255
Thr Arg Thr Ala Asp Gly Arg Asp Val Ala Asp Asn Ala Glu Lys Arg 260 265 270		
Leu Pro Leu Leu Ser Glu Gly Asp Leu Leu Lys Val Leu Ser Ile Glu 275 280 285		
Ala Asp Gly His Ser Thr Asn Pro Pro Ala Arg Tyr Thr Glu Ala Ser 290 295 300		
Leu Val Lys Lys Met Glu Asp Leu Gly Ile Gly Arg Pro Ser Thr Tyr 305 310 315 320		
Ala Ser Ile Ile Lys Thr Ile Gln Asp Arg Gly Tyr Val Tyr Ser Arg 325 330 335		
Gly Asn Ala Leu Val Pro Ser Trp Val Ala Phe Ala Val Val Gly Leu 340 345 350		
Leu Glu Ala Asn Phe Thr Ser Leu Val Asp Tyr Asp Phe Thr Ser Ser 355 360 365		
Met Glu Asp Glu Leu Asp Asn Ile Ala Ala Gly Arg Glu Gly Arg Thr 370 375 380		
Glu Trp Leu Asn Gly Phe Tyr Phe Gly Asp Ala Glu Ala Asp Gln Ser 385 390 395 400		
Met Ala Glu Ser Val Ala Arg Gln Gly Gly Leu Lys Ala Leu Val Asp 405 410 415		
Ala Asn Leu Glu His Ile Asp Ala Arg Ser Val Asn Ser Leu Lys Leu 420 425 430		
Phe Asp Asp Ala Glu Gly Arg Ala Val Asn Val Arg Val Gly Arg Tyr 435 440 445		
Gly Pro Tyr Ile Glu Arg Ile Val Gly Thr Thr Ala Glu Gly Glu Pro 450 455 460		
Glu Phe Gln Arg Ala Asn Leu Pro Glu Glu Thr Thr Pro Asp Glu Leu 465 470 475 480		
Thr Leu Glu Val Ala Glu Lys Leu Phe Ala Thr Pro Gln Gly Gly Arg 485 490 495		
Glu Leu Gly Ile Asn Pro Ala Asn Gly Arg Met Val Val Ala Lys Glu 500 505 510		
Gly Arg Phe Gly Pro Tyr Val Ile Glu Gln Val Thr Asp Ser Glu Arg 515 520 525		
Ala Gly Ala Glu Ala Gln Ala Glu Glu Val Val Ala Ala Glu Arg Lys 530 535 540		
Ala Glu Asp Glu Gln Arg Ala Thr Asp Gly Met Arg Pro Lys Asn Trp 545 550 555 560		
Glu Thr Lys Thr Ala Ala Asn Gln Lys Glu Lys Arg Ile Asn Gln Leu 565 570 575		

Val Glu Glu Asn Leu Lys Pro Ala Thr Ala Ser Leu Phe Ser Gly Met  
 580 585 590

Glu Pro Ala Ala Val Thr Leu Glu Glu Ala Leu Lys Leu Leu Ser Leu  
 595 600 605

Pro Arg Glu Val Gly Val Asp Pro Ser Asp Asn Glu Val Ile Thr Ala  
 610 615 620

Gln Asn Gly Arg Tyr Gly Pro Tyr Leu Lys Lys Gly Ser Asp Ser Arg  
 625 630 635 640

Ser Leu Asn Ser Glu Glu Gln Ile Phe Thr Val Thr Leu Asp Glu Ala  
 645 650 655

Arg Arg Ile Tyr Ala Glu Pro Lys Arg Arg Gly Arg Ala Ala Ala Gln  
 660 665 670

Pro Pro Leu Lys Gln Leu Gly Asp Asn Asp Val Ser Gly Lys Pro Met  
 675 680 685

Thr Val Lys Asp Gly Arg Phe Gly Pro Tyr Val Thr Asp Gly Thr Thr  
 690 695 700

Asn Ala Ser Leu Arg Lys Gly Asp Val Pro Glu Ser Leu Thr Asp Ala  
 705 710 715 720

Arg Ala Asn Glu Leu Leu Ser Glu Arg Arg Ala Lys Glu Ala Ala Asp  
 725 730 735

Gly Gly Ala Pro Ala Lys Lys Thr Ser Thr Lys Lys Thr Ala Ala Lys  
 740 745 750

Lys Thr Thr Ala Lys Lys Thr Thr Ala Lys Lys Thr Val Arg Lys Ala  
 755 760 765

Pro Pro Lys Thr Thr Lys Asn Val Val Lys Ala Gly Ala Lys Lys Lys  
 770 775 780

Ser  
 785

&lt;210&gt; 129

&lt;211&gt; 488

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(465)

&lt;223&gt; RXN00990

&lt;400&gt; 129

atc ccc gtc ttg gtg gcc acc gat atc gcc gcc cgt ggc att gac gtg 48  
 Ile Pro Val Leu Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val  
 1 5 10 15

gat gac gtc tcg ctt gtt gtg cac gtt gat ccc cca gca gaa cac aaa 96  
 Asp Asp Val Ser Leu Val Val His Val Asp Pro Pro Ala Glu His Lys

20	25	30	
gcg tat ttg cac cgc gct ggt cgt act gca cga gcc gga act tcc ggt			144
Ala Tyr Leu His Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly			
35	40	45	
aca gtt gtg act cta gta atg gac gaa caa atc aag gaa gtc cgt gaa			192
Thr Val Val Thr Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu			
50	55	60	
ctt ttc caa aaa gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa			240
Leu Phe Gln Lys Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu			
65	70	75	80
aac tca cct gaa ttg gct aaa att act ggt gca cga cgc ccg tca ggc			288
Asn Ser Pro Glu Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly			
85	90	95	
gtt gct ctt cca gca cct gga cag cag cag cca aag cgg gaa caa aaa			336
Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys			
100	105	110	
aat acc cat aat cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc			384
Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg			
115	120	125	
agg cgc gga caa agc gga tcc aga tca acg ggc cgc tcc aac ccg agg			432
Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg			
130	135	140	
cgt cag act tca agg aaa gac ggt ccc aag agc taaaactccc ccacggcacg			485
Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser			
145	150	155	
cga			488

&lt;210&gt; 130

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 130

Ile	Pro	Val	Leu	Val	Ala	Thr	Asp	Ile	Ala	Ala	Arg	Gly	Ile	Asp	Val
1				5					10					15	

Asp	Asp	Val	Ser	Leu	Val	Val	His	Val	Asp	Pro	Pro	Ala	Glu	His	Lys
		20						25					30		

Ala	Tyr	Leu	His	Arg	Ala	Gly	Arg	Thr	Ala	Arg	Ala	Gly	Thr	Ser	Gly
		35					40					45			

Thr	Val	Val	Thr	Leu	Val	Met	Asp	Glu	Gln	Ile	Lys	Glu	Val	Arg	Glu
		50				55					60				

Leu	Phe	Gln	Lys	Ala	Gly	Val	Thr	Ala	Ala	Glu	Val	Lys	Val	Asn	Glu
	65				70					75				80	

Asn	Ser	Pro	Glu	Leu	Ala	Lys	Ile	Thr	Gly	Ala	Arg	Arg	Pro	Ser	Gly
				85					90					95	



Val Ala Leu Pro Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys  
100 105 110

Asn Thr His Asn Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg  
115 120 125

Arg Arg Gly Gln Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg  
130 135 140

Arg Gln Thr Ser Arg Lys Asp Gly Pro Lys Ser  
145 150 155

<210> 131

<211> 476

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(453)

<223> FRXA00990

<400> 131

gtg gcc acc gat atc gcc gcc cgt ggc att gac gtg gat gac gtc tcg 48  
Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val Asp Asp Val Ser  
1 5 10 15

ctt gtt gtg cac gtt gat ccc cca gca gaa cac aaa gcg tat ttg cac 96  
Leu Val Val His Val Asp Pro Pro Ala Glu His Lys Ala Tyr Leu His  
20 25 30

cgc gct ggt cgt act gca cga gcc gga act tcc ggt aca gtt gtg act 144  
Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr  
35 40 45

cta gta atg gac gaa caa atc aag gaa gtc cgt gaa ctt ttc caa aaa 192  
Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys  
50 55 60

gca ggc gtg aca gcc gct gag gta aaa gtc aac gaa aac tca cct gaa 240  
Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu  
65 70 75 80

ttg gct aaa att act ggt gca cga cgc ccg tca ggc gtt gct ctt cca 288  
Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro  
85 90 95

gca cct gga cag cag cag cca aag cgg gaa caa aaa aat acc cat aat 336  
Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn  
100 105 110

cgt tct gat tcc aga ggt tcc agc cgg aat cca cgc agg cgc gga caa 384  
Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln  
115 120 125

agc gga tcc aga tca acg ggc cgc tcc aac ccg agg cgt cag act tca 432  
Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser  
130 135 140

agg aaa gac ggt ccc aag agc taaaactccc ccacggcacg cga 476

Arg Lys Asp Gly Pro Lys Ser  
145 150

<210> 132

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Val Ala Thr Asp Ile Ala Ala Arg Gly Ile Asp Val Asp Asp Val Ser  
1 5 10 15

Leu Val Val His Val Asp Pro Pro Ala Glu His Lys Ala Tyr Leu His  
20 25 30

Arg Ala Gly Arg Thr Ala Arg Ala Gly Thr Ser Gly Thr Val Val Thr  
35 40 45

Leu Val Met Asp Glu Gln Ile Lys Glu Val Arg Glu Leu Phe Gln Lys  
50 55 60

Ala Gly Val Thr Ala Ala Glu Val Lys Val Asn Glu Asn Ser Pro Glu  
65 70 75 80

Leu Ala Lys Ile Thr Gly Ala Arg Arg Pro Ser Gly Val Ala Leu Pro  
85 90 95

Ala Pro Gly Gln Gln Gln Pro Lys Arg Glu Gln Lys Asn Thr His Asn  
100 105 110

Arg Ser Asp Ser Arg Gly Ser Ser Arg Asn Pro Arg Arg Arg Gly Gln  
115 120 125

Ser Gly Ser Arg Ser Thr Gly Arg Ser Asn Pro Arg Arg Gln Thr Ser  
130 135 140

Arg Lys Asp Gly Pro Lys Ser  
145 150

<210> 133

<211> 451

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (451)

<223> RXN00994

<400> 133

taatcaacat tcgcaagagg tgtgtcgcaa aagcactagc tcagcgatta aaagttccca 60

tgatcacttt tcaaccagca ccgactagag ttagtgggca atg act acc ttt cta 115  
Met Thr Thr Phe Leu  
1 5

gaa ctc aag ctt ccc gac gag att gtg cgc gaa ctt cgc agt cag gga 163  
Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu Leu Arg Ser Gln Gly  
10 15 20

atc acc gag gca ttc ccc atc caa gaa gca gcc atc ccc gat gcg ctc 211  
 Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala Ile Pro Asp Ala Leu  
           25                          30                          35  
  
 gct ggc aaa gat gtc ctc ggc cgt gga ccc acc ggc tct ggt aaa acc 259  
 Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr Gly Ser Gly Lys Thr  
           40                          45                          50  
  
 ttc acc ttt ggg ctt ccc atg atc acc cga ctc gcg cgc tcg ggc gcc 307  
 Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu Ala Arg Ser Gly Ala  
           55                          60                          65  
  
 tcc aaa cca ggt cgc ccc cgc ggg ctt gtc ctg gtt ccc acc cgt gaa 355  
 Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu Val Pro Thr Arg Glu  
           70                          75                          80                          85  
  
 cta gca gct cag gtg cgt gaa cgc ctc gac gat ccc gcc cgc gtt atg 403  
 Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp Pro Ala Arg Val Met  
                           90                          95                          100  
  
 ggt ctg cgc gtc ctc gag gtg gtc ggt ggc gtc aac atc aac cgc aac 451  
 Gly Leu Arg Val Leu Glu Val Val Gly Gly Val Asn Ile Asn Arg Asn  
           105                          110                          115

&lt;210&gt; 134

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 134

Met Thr Thr Phe Leu Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu  
   1                          5                          10                          15  
  
 Leu Arg Ser Gln Gly Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala  
           20                          25                          30  
  
 Ile Pro Asp Ala Leu Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr  
           35                          40                          45  
  
 Gly Ser Gly Lys Thr Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu  
           50                          55                          60  
  
 Ala Arg Ser Gly Ala Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu  
           65                          70                          75                          80  
  
 Val Pro Thr Arg Glu Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp  
           85                          90                          95  
  
 Pro Ala Arg Val Met Gly Leu Arg Val Leu Glu Val Val Gly Gly Val  
           100                          105                          110  
  
 Asn Ile Asn Arg Asn  
           115

&lt;210&gt; 135

&lt;211&gt; 442

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(442)

&lt;223&gt; FRXA00994

&lt;400&gt; 135

taatcaacat tcgcaagagg tgtgtcgcaa aagcactagc tcagcgatta aaagttccca 60

tgatcacttt tcaaccagca ccgactagag ttagtgggca atg act acc ttt cta 115  
Met Thr Thr Phe Leu  
1 5

gaa ctc aag ctt ccc gac gag att gtg cgc gaa ctt cgc agt cag gga 163  
Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu Leu Arg Ser Gln Gly  
10 15 20

atc acc gag gca ttc ccc atc caa gaa gca gcc atc ccc gat gcg ctc 211  
Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala Ile Pro Asp Ala Leu  
25 30 35

gct ggc aaa gat gtc ctc ggc cgt gga ccc acc ggc tct ggt aaa acc 259  
Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr Gly Ser Gly Lys Thr  
40 45 50

ttc acc ttt ggg ctt ccc atg atc acc cga ctc gcg cgc tcg ggc gcc 307  
Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu Ala Arg Ser Gly Ala  
55 60 65

tcc aaa cca ggt cgc ccc cgc ggg ctt gtc ctg gtt ccc acc cgt gaa 355  
Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu Val Pro Thr Arg Glu  
70 75 80 85

cta gca gct cag gtg cgt gaa cgc ctc gac gat ccc gcc cgc gtt atg 403  
Leu Ala Ala Gln Val Arg Glu Arg Leu Asp Asp Pro Ala Arg Val Met  
90 95 100

ggt ctg cgc gtc ctc gag gtg gtc ggt ggc gtc aac atc 442  
Gly Leu Arg Val Leu Glu Val Val Gly Gly Val Asn Ile  
105 110

&lt;210&gt; 136

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 136

Met Thr Thr Phe Leu Glu Leu Lys Leu Pro Asp Glu Ile Val Arg Glu  
1 5 10 15

Leu Arg Ser Gln Gly Ile Thr Glu Ala Phe Pro Ile Gln Glu Ala Ala  
20 25 30

Ile Pro Asp Ala Leu Ala Gly Lys Asp Val Leu Gly Arg Gly Pro Thr  
35 40 45

Gly Ser Gly Lys Thr Phe Thr Phe Gly Leu Pro Met Ile Thr Arg Leu  
50 55 60

Ala Arg Ser Gly Ala Ser Lys Pro Gly Arg Pro Arg Gly Leu Val Leu

Pro Ala Arg Val Met Gly Leu Arg Val Leu Glu Val Val Gly Gly Val  
100 105 110

Asn Ile

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<210> 137
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1324)  
<223> RXN02468
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<400> 137  
tcgttgatt ggaatgaccc tattgtaacc gtgcaacgat agtatctaag ttgtgtcttc 60

tgaaagcccc agacctacgt tcacagagct cggcgttgcg gtg gaa atc acc gac 115  
Val Glu Ile Thr Asp  
1 5

gca ctc gaa gcc ctc ggc atc aac cga act ttc gcg atc cag gag tac 163  
Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe Ala Ile Gln Glu Tyr  
10 15 20

aca ctt ccc atc gcg ctc gac ggc cac gac ttc atc ggc caa gcc cgc 211  
Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe Ile Gly Gln Ala Arg  
25 30 35

acc ggc atg ggc aaa acc tac gga ttc ggt gtc cca ctc ctc gat aga 259  
Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val Pro Leu Leu Asp Arg  
40 45 50

gtc ttc gac tca gcc gac gtc gca gaa acc gac ggt acc ccc cga gcc 307  
Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp Gly Thr Pro Arg Ala  
55 60 65

ctc gtc atc gtg ccc acc cga gaa ctc gca gtc caa gtc ggc gac gac 355  
Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val Gln Val Gly Asp Asp  
70 75 80 85

ctc caa cgc gca gca acc aac ctg ccg cta aag atc ttc acc ttc tac 403  
Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys Ile Phe Thr Phe Tyr  
90 95 100

ggc ggc acc ccc tac gaa gaa cag atc gac gca ctc aaa gtc ggc gtc 451  
Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala Leu Lys Val Gly Val  
105 110 115

gac gtt gtc gta ggc aca ccc gga cga tta ctc gac ctg cac aaa cga 499  
Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu Asp Leu His Lys Arg  
120 125 130

ggc gcg cta tcg ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc 547  
 Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala  
 135 140 145

gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc 595  
 Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu  
 150 155 160 165

cgt gcc ctc acc cac cag cat caa acc atg ctg ttc tct gcc acg atg 643  
 Arg Ala Leu Thr His Gln His Gln Thr Met Leu Phe Ser Ala Thr Met  
 170 175 180

ccc ggc gcg atc ctc aca ctc gca cgc agc ttc ctg aac aaa cca gtg 691  
 Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe Leu Asn Lys Pro Val  
 185 190 195

cac atc cga gcc gag aca tcg gac gcc tca gca aca cac aaa acc acc 739  
 His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala Thr His Lys Thr Thr  
 200 205 210

aga caa gtg gtt ttt cag gca cac aaa atg gac aag gaa gcc atc acc 787  
 Arg Gln Val Val Phe Gln Ala His Lys Met Asp Lys Glu Ala Ile Thr  
 215 220 225

gcg aaa att ctg cag tcg aaa gat cgc ggc aaa acg atc atc ttc gcc 835  
 Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys Thr Ile Ile Phe Ala  
 230 235 240 245

cgc acg aaa cgc acc gca gcg caa gtt gcc gaa gac cta gcc tcc aga 883  
 Arg Thr Lys Arg Thr Ala Ala Gln Val Ala Glu Asp Leu Ala Ser Arg  
 250 255 260

gga ttc tcc gtc gga tca gtg cac ggc gac atg ggc caa cca gcc cgc 931  
 Gly Phe Ser Val Gly Ser Val His Gly Asp Met Gly Gln Pro Ala Arg  
 265 270 275

gag aaa tca ctc aac gca ttc cgc aca gga aaa att gac atc ctt gta 979  
 Glu Lys Ser Leu Asn Ala Phe Arg Thr Gly Lys Ile Asp Ile Leu Val  
 280 285 290

gcc aca gac gta gcc gcc cga ggc atc gat gtt gat gac gtc acc cac 1027  
 Ala Thr Asp Val Ala Ala Arg Gly Ile Asp Val Asp Asp Val Thr His  
 295 300 305

gtg atc aac tac caa acc ccc gac gat cct atg acc tac gtc cat cgt 1075  
 Val Ile Asn Tyr Gln Thr Pro Asp Asp Pro Met Thr Tyr Val His Arg  
 310 315 320 325

atc gga cgc acg gga cgc gca ggg cac aac gga aca gcc gtc act ctt 1123  
 Ile Gly Arg Thr Gly Arg Ala Gly His Asn Gly Thr Ala Val Thr Leu  
 330 335 340

gtc ggg tac gac gaa acc ctc aaa tgg act gtc atc gac aac gaa ctc 1171  
 Val Gly Tyr Asp Glu Thr Leu Lys Trp Thr Val Ile Asp Asn Glu Leu  
 345 350 355

gaa ctc ggc caa cca aac cca cca caa tgg ttc tcc acc tca cca gag 1219  
 Glu Leu Gly Gln Pro Asn Pro Pro Gln Trp Phe Ser Thr Ser Pro Glu  
 360 365 370

ctg ctt gaa aca ctc gac atc cca gaa ggt gtc acc gaa cga gtc gga 1267

Leu Leu Glu Thr Leu Asp Ile Pro Glu Gly Val Thr Glu Arg Val Gly  
 375 380 385  
 cca cca acc aaa gtt cta ggc gga aca gcc cca cga cca cca cgc cgc 1315  
 Pro Pro Thr Lys Val Leu Gly Gly Thr Ala Pro Arg Pro Pro Arg Arg  
 390 395 400 405  
 acc cgg aaa taacttatgg cagcaaagct tca 1347  
 Thr Arg Lys

<210> 138  
 <211> 408  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 138  
 Val Glu Ile Thr Asp Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe  
 1 5 10 15  
 Ala Ile Gln Glu Tyr Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe  
 20 25 30  
 Ile Gly Gln Ala Arg Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val  
 35 40 45  
 Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp  
 50 55 60  
 Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val  
 65 70 75 80  
 Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys  
 85 90 95  
 Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala  
 100 105 110  
 Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu  
 115 120 125  
 Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu  
 130 135 140  
 Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp  
 145 150 155 160  
 Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu  
 165 170 175  
 Phe Ser Ala Thr Met Pro Gly Ala Ile Leu Thr Leu Ala Arg Ser Phe  
 180 185 190  
 Leu Asn Lys Pro Val His Ile Arg Ala Glu Thr Ser Asp Ala Ser Ala  
 195 200 205  
 Thr His Lys Thr Thr Arg Gln Val Val Phe Gln Ala His Lys Met Asp  
 210 215 220  
 Lys Glu Ala Ile Thr Ala Lys Ile Leu Gln Ser Lys Asp Arg Gly Lys

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<210> 139
<211> 237
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(214)
<223> FRXA02463
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<400> 139
nnnnnaaaant gacatccttg tagccacaga cgtagccgcc cnaggnntnt atnttnatna 60

cnttaccacac gtnattaaat accaaanccc cgncgatacct atg acc tac gtt cat 115
Met Thr Tyr Val His
1 5

tgt atn gga cgc acg gga cgc gca ggg cac aac gga aca gcc gtc act 163
Cys Xaa Gly Arg Thr Gly Arg Ala Gly His Asn Gly Thr Ala Val Thr
10 15 20

ctt gtc ggg ttc nac gaa acc ctn aaa tgg act gnc atn gac aac gaa 211
Leu Val Gly Phe Xaa Glu Thr Leu Lys Trp Thr Xaa Xaa Asp Asn Glu
25 30 35

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237

ctn naactcgggc aaccaaacc acc  
Leu

<210> 140  
<211> 38  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 140  
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Gly Thr Ala Val Thr Leu Val Gly Phe Xaa Glu Thr Leu Lys Trp Thr  
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Xaa Xaa Asp Asn Glu Leu  
35

<210> 141  
<211> 631  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(631)  
<223> FRXA02468

<400> 141  
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Val Glu Ile Thr Asp  
1 5  
gca ctc gaa gcc ctc ggc atc aac cga act ttc gcg atc cag gag tac 163  
Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe Ala Ile Gln Glu Tyr  
10 15 20  
aca ctt ccc atc gcg ctc gac ggc cac gac ttc atc ggc caa gcc cgc 211  
Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe Ile Gly Gln Ala Arg  
25 30 35  
acc ggc atg ggc aaa acc tac gga ttc ggt gtc cca ctc ctc gat aga 259  
Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val Pro Leu Leu Asp Arg  
40 45 50  
gtc ttc gac tca gcc gac gtc gca gaa acc gac ggt acc ccc cga gcc 307  
Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp Gly Thr Pro Arg Ala  
55 60 65  
ctc gtc atc gtg ccc acc cga gaa ctc gca gtc caa gtc ggc gac gac 355  
Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val Gln Val Gly Asp Asp  
70 75 80 85  
ctc caa cgc gca gca acc aac ctg ccg cta aag atc ttc acc ttc tac 403  
Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys Ile Phe Thr Phe Tyr  
90 95 100

ggc ggc acc ccc tac gaa gaa cag atc gac gca ctc aaa gtc ggc gtc 451  
 Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala Leu Lys Val Gly Val  
 105 110 115  
 gac gtt gtc gta ggc aca ccc gga cga tta ctc gac ctg cac aaa cga 499  
 Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu Asp Leu His Lys Arg  
 120 125 130  
 ggc gcg cta tcg ctc gac aaa gta gcg atc tta gtc ctc gat gaa gcc 547  
 Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu Val Leu Asp Glu Ala  
 135 140 145  
 gac gaa atg ctc gat ctg ggc ttt ctg ccc gac atc gaa aaa atc ctc 595  
 Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp Ile Glu Lys Ile Leu  
 150 155 160 165  
 cgt gcc ctc acc cac cag cat caa acc atg ctg ttc 631  
 Arg Ala Leu Thr His Gln His Gln Thr Met Leu Phe  
 170 175

&lt;210&gt; 142

&lt;211&gt; 177

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 142

Val Glu Ile Thr Asp Ala Leu Glu Ala Leu Gly Ile Asn Arg Thr Phe  
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Ala Ile Gln Glu Tyr Thr Leu Pro Ile Ala Leu Asp Gly His Asp Phe  
 20 25 30

Ile Gly Gln Ala Arg Thr Gly Met Gly Lys Thr Tyr Gly Phe Gly Val  
 35 40 45

Pro Leu Leu Asp Arg Val Phe Asp Ser Ala Asp Val Ala Glu Thr Asp  
 50 55 60

Gly Thr Pro Arg Ala Leu Val Ile Val Pro Thr Arg Glu Leu Ala Val  
 65 70 75 80

Gln Val Gly Asp Asp Leu Gln Arg Ala Ala Thr Asn Leu Pro Leu Lys  
 85 90 95

Ile Phe Thr Phe Tyr Gly Gly Thr Pro Tyr Glu Glu Gln Ile Asp Ala  
 100 105 110

Leu Lys Val Gly Val Asp Val Val Val Gly Thr Pro Gly Arg Leu Leu  
 115 120 125

Asp Leu His Lys Arg Gly Ala Leu Ser Leu Asp Lys Val Ala Ile Leu  
 130 135 140

Val Leu Asp Glu Ala Asp Glu Met Leu Asp Leu Gly Phe Leu Pro Asp  
 145 150 155 160

Ile Glu Lys Ile Leu Arg Ala Leu Thr His Gln His Gln Thr Met Leu  
 165 170 175

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<210> 143
<211> 2319
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(2296)  
<223> RXA00050
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ctg gca ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc	691
Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val	
185 190 195	
ggg ggc ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att	739
Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile	
200 205 210	
cag ctc tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca	787
Gln Leu Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro	
215 220 225	
ggc cga atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga	835
Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly	
230 235 240 245	
ctg cgc ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc	883
Leu Arg Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly	
250 255 260	
ttc cag gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag	931
Phe Gln Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys	
265 270 275	
cag gtt gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg	979
Gln Val Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu	
280 285 290	
tcc aag cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag	1027
Ser Lys Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu	
295 300 305	
acc agg act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac	1075
Thr Arg Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His	
310 315 320 325	
cgc aac aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt	1123
Arg Asn Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe	
330 335 340	
gaa gca atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt	1171
Glu Ala Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val	
345 350 355	
gct gaa aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc	1219
Ala Glu Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly	
360 365 370	
gac att gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac	1267
Asp Ile Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp	
375 380 385	
ggc cgc ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt	1315
Gly Arg Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu	
390 395 400 405	
gac gtt gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac	1363

Asp Val Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp	
410 415 420	
acc gag tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt	1411
Thr Glu Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg	
425 430 435	
acc ggc gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt	1459
Thr Gly Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu	
440 445 450	
cgc tcc atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg	1507
Arg Ser Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu	
455 460 465	
cca acc gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gct gac	1555
Pro Thr Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp	
470 475 480 485	
tcc atc acc aag tcc ctg gag gac aag cag atg gac ctg ttc cgc acc	1603
Ser Ile Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr	
490 495 500	
ctg gtc aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc	1651
Leu Val Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile	
505 510 515	
gca gcg gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctg aag	1699
Ala Ala Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys	
520 525 530	
gag ctg cca cca gag cgc cgt gag cgc aac gac cgc cgt cgt gac cgt	1747
Glu Leu Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Asp Arg	
535 540 545	
gac ttc gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac	1795
Asp Phe Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Asp	
550 555 560 565	
cgc gga gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca	1843
Arg Gly Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala	
570 575 580	
acc tac cgc ctg gca gtg ggc aag cgc cag cac atc cgc cca ggc gca	1891
Thr Tyr Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala	
585 590 595	
atc gtt ggt gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc	1939
Ile Val Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe	
600 605 610	
ggc cgc atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag	1987
Gly Arg Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys	
615 620 625	
gat ctg cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc	2035
Asp Leu Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser	
630 635 640 645	
ggc cag ctg atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc	2083
Gly Gln Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg	

650	655	660	
cgc ttc gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac			2131
Arg Phe Glu Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Asp			
665	670	675	
cgt gat gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc			2179
Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Asp Arg Gly Ser			
680	685	690	
cgt gga ggt ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc			2227
Arg Gly Gly Phe Arg Gly Gly Arg Asp Arg Asp Asp Arg Gly Gly Arg			
695	700	705	
ggt gga ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc			2275
Gly Gly Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly			
710	715	720	725
ggt tac cgt ggc gga cgc gac taagagttcg ttttagcttc agc			2319
Gly Tyr Arg Gly Gly Arg Asp			
730			

&lt;210&gt; 144

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 144

Met	Ser	Asn	Thr	Glu	Asn	Val	Asn	Gly	Asp	Val	Glu	Gln	Pro	Asn	Asn
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Val	Ile	Ser	Ser	Glu	Ser	Gln	Glu	Thr	Pro	Gln	Gly	Asp	Ser	Ala	Ser
		20						25					30		

Ala	Asp	Phe	Ala	Leu	Glu	Thr	Pro	Thr	Asn	Thr	Val	Glu	Asp	Ala	Pro
	35						40					45			

Ala	Ser	Glu	Gly	Ser	Glu	Glu	Ile	Thr	Arg	Val	Ala	Asp	Thr	Ser	Glu
	50					55					60				

Asp	Ala	Asp	Ser	Ala	Asp	Ala	Asp	Asn	Ala	Ser	Asn	Val	Ile	Asn	Glu
65				70						75				80	

Asn	Glu	Asp	Ser	Ser	Glu	Gly	Ala	Asn	Gln	Pro	Ser	Asn	Glu	Ser	Ser
			85					90					95		

Ser	Thr	Glu	Ala	Lys	Ser	Gly	Phe	Asp	Ala	Leu	Gly	Leu	Pro	Glu	Arg
		100						105					110		

Val	Leu	Asp	Ala	Val	Arg	Lys	Val	Gly	Tyr	Glu	Thr	Pro	Ser	Pro	Ile
	115						120					125			

Gln	Ala	Gln	Thr	Ile	Pro	Ile	Leu	Met	Glu	Gly	Gln	Asp	Val	Val	Gly
	130					135					140				

Leu	Ala	Gln	Thr	Gly	Thr	Gly	Lys	Thr	Ala	Ala	Phe	Ala	Leu	Pro	Ile
145				150					155					160	

Leu	Ala	Arg	Ile	Asp	Lys	Ser	Val	Arg	Ser	Pro	Gln	Ala	Leu	Val	Leu
			165					170					175		

Ala Pro Thr Arg Glu Leu Ala Leu Gln Val Ala Asp Ser Phe Gln Ser  
 180 185 190  
 Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro Ile Tyr Gly Gly  
 195 200 205  
 Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg Gly Ala His Ile  
 210 215 220  
 Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu Glu Lys Gly Ser  
 225 230 235 240  
 Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp Glu Ala Asp Glu  
 245 250 255  
 Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg Ile Leu Glu Asp  
 260 265 270  
 Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala Thr Met Pro Asn  
 275 280 285  
 Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn Pro Ala Glu Ile  
 290 295 300  
 Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile Thr Gln Arg Phe  
 305 310 315 320  
 Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu Thr Arg Ile Leu  
 325 330 335  
 Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val Arg Thr Lys His  
 340 345 350  
 Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg Gly Phe Ser Ala  
 355 360 365  
 Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg Glu Arg Thr Val  
 370 375 380  
 Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val Ala Thr Asp Val  
 385 390 395 400  
 Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His Val Leu Asn Phe  
 405 410 415  
 Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg Ile Gly Arg Thr  
 420 425 430  
 Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe Val Thr Pro Arg  
 435 440 445  
 Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr Asn Ala Pro Leu  
 450 455 460  
 His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn Asp Phe Arg Lys  
 465 470 475 480  
 Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu Asp Lys Gln Met  
 485 490 495

Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln Ala Asn Asp Val  
 500 505 510  
 Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln Ala Gln Ser Gly  
 515 520 525  
 Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg Glu Arg Asn Asp  
 530 535 540  
 Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly Arg Gly Arg Asp  
 545 550 555 560  
 Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg Phe Asp Arg Asp  
 565 570 575  
 Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly Lys Arg Gln His  
 580 585 590  
 Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn Glu Gly Gly Leu  
 595 600 605  
 Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala Asp His Thr Leu  
 610 615 620  
 Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu Asp Asn Leu Arg  
 625 630 635 640  
 Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu Arg Asp Ser Gly  
 645 650 655  
 Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg Gly Gly Arg Gly  
 660 665 670  
 Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg  
 675 680 685  
 Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly Arg Asp Arg Asp  
 690 695 700  
 Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp Asp Arg Gly Asp  
 705 710 715 720  
 Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp  
 725 730

&lt;210&gt; 145

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(427)

&lt;223&gt; RXA02682

&lt;400&gt; 145

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 gagaatacga attcggtttac ctctagaaag gcactttccc atg tct tac cac gat 115  
 Met Ser Tyr His Asp



1 5  
 cac agc gac atc gaa tac ctc aag aag atc ggc gcc aac tcc cct gac 163  
 His Ser Asp Ile Glu Tyr Leu Lys Lys Ile Gly Ala Asn Ser Pro Asp  
 10 15 20  
 gcc ttc aaa gct ttt gtc cat ttt gat gag gca gct ctc cgc ggc ccg 211  
 Ala Phe Lys Ala Phe Val His Phe Asp Glu Ala Ala Leu Arg Gly Pro  
 25 30 35  
 aac aag aaa atc cca cgc aac tac acc gaa atg atc gca ctt gcg gtc 259  
 Asn Lys Lys Ile Pro Arg Asn Tyr Thr Glu Met Ile Ala Leu Ala Val  
 40 45 50  
 gca ttc aca acc caa tgc gcc tac tgc atc gac atc cac act gcc gct 307  
 Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp Ile His Thr Ala Ala  
 55 60 65  
 gcg aag aag gaa ggt gtc acc acc gag gag ctc gct gag gtt gcg ctc 355  
 Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu Ala Glu Val Ala Leu  
 70 75 80 85  
 atc gcc gca gca ctt cgg gca ggc ggc gcc atg acg cac ggc gca ctt 403  
 Ile Ala Ala Ala Leu Arg Ala Gly Gly Ala Met Thr His Gly Ala Leu  
 90 95 100  
 gcc atg aag ctt tac gac gaa aac tagaagcgat tctgcacatt ttt 450  
 Ala Met Lys Leu Tyr Asp Glu Asn  
 105

&lt;210&gt; 146

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 146

Met Ser Tyr His Asp His Ser Asp Ile Glu Tyr Leu Lys Lys Ile Gly  
 1 5 10 15  
 Ala Asn Ser Pro Asp Ala Phe Lys Ala Phe Val His Phe Asp Glu Ala  
 20 25 30  
 Ala Leu Arg Gly Pro Asn Lys Lys Ile Pro Arg Asn Tyr Thr Glu Met  
 35 40 45  
 Ile Ala Leu Ala Val Ala Phe Thr Thr Gln Cys Ala Tyr Cys Ile Asp  
 50 55 60  
 Ile His Thr Ala Ala Ala Lys Lys Glu Gly Val Thr Thr Glu Glu Leu  
 65 70 75 80  
 Ala Glu Val Ala Leu Ile Ala Ala Ala Leu Arg Ala Gly Gly Ala Met  
 85 90 95  
 Thr His Gly Ala Leu Ala Met Lys Leu Tyr Asp Glu Asn  
 100 105

&lt;210&gt; 147

&lt;211&gt; 798

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(775)

&lt;223&gt; RXN00542

&lt;400&gt; 147

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cgatcgtggt ctgaacctga atgatgggtgt cctgcgcacc aagggttctgc gactcgacaa 60

gtaaagaact ttaaggctct agagaggttag ttgaaggatt atg gca atc gga gat 115
                Met Ala Ile Gly Asp
                1 5

act aac atc acc gtc gtt ggc aac att gtt gct gac ccg gaa ctc cgc 163
Thr Asn Ile Thr Val Val Gly Asn Ile Val Ala Asp Pro Glu Leu Arg
                10 15 20

ttc acc cca tcg ggt gca gca gtg gct aac ttc cgc att gca tca act 211
Phe Thr Pro Ser Gly Ala Ala Val Ala Asn Phe Arg Ile Ala Ser Thr
                25 30 35

ccc cgc tcg ttc aac cgc caa acc aac cag tgg gaa gac ggc gaa gcc 259
Pro Arg Ser Phe Asn Arg Gln Thr Asn Gln Trp Glu Asp Gly Glu Ala
                40 45 50

ctc ttt ctc acc gtt aac gtt tgg cgt cag gca gct gaa aac gtt gca 307
Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val Ala
                55 60 65

gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc aag 355
Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu Lys
                70 75 80 85

cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt gag 403
Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe Glu
                90 95 100

gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca gat 451
Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala Asp
                105 110 115

gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt ggc 499
Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly Gly
                120 125 130

ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa ggt 547
Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln Gly
                135 140 145

gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc aac 595
Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly Asn
                150 155 160 165

cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag tcc 643
Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln Ser
                170 175 180

cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca cag 691
Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro Gln

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185 190 195  
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 Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly Ser  
 200 205 210  
 ggc ggg ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt 785  
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 <213> Corynebacterium glutamicum  
  
 <400> 148  
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 Arg Ile Ala Ser Thr Pro Arg Ser Phe Asn Arg Gln Thr Asn Gln Trp  
 35 40 45  
 Glu Asp Gly Glu Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala  
 50 55 60  
 Ala Glu Asn Val Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val  
 65 70 75 80  
 Thr Gly Arg Leu Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys  
 85 90 95  
 Arg Ser Val Phe Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr  
 100 105 110  
 Phe Ala Lys Ala Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly  
 115 120 125  
 Gly Asn Tyr Gly Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln  
 130 135 140  
 Gly Asn Gln Gln Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly  
 145 150 155 160  
 Gly Asn Gln Gly Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly  
 165 170 175  
 Asn Gln Asn Gln Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly  
 180 185 190  
 Gly Gly Ser Pro Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala  
 195 200 205  
 Pro Pro Ala Gly Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro  
 210 215 220

Phe  
225

<210> 149  
<211> 542  
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<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (1)..(519)  
<223> FRXA00542

<400> 149  
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Ala Leu Phe Leu Thr Val Asn Val Trp Arg Gln Ala Ala Glu Asn Val  
1 5 10 15  
  
gca gag tcc ctg tcc aag ggt atg cgc gtt atc gtc acc ggt cgc ctc 96  
Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu  
20 25 30  
  
aag cag cgc tcc tat gaa acc cgt gag ggc gaa aag cgc agc gtt ttt 144  
Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe  
35 40 45  
  
gag gtc gaa gcg gat gaa gtc gga cca tca cta aca ttt gcc aag gca 192  
Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala  
50 55 60  
  
gat gtc cag cgc aca ccg cgc ggt gga aac tct ggc gga aac tac ggt 240  
Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly  
65 70 75 80  
  
ggc ggc aac caa ggt ggt ggc ctc ggt gga aac caa ggc aac cag caa 288  
Gly Gly Asn Gln Gly Gly Gly Leu Gly Asn Gln Gly Asn Gln Gln  
85 90 95  
  
ggt gga ttc agc aac cag aac tct ggc ggc ttc ggt gga aac caa ggc 336  
Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly  
100 105 110  
  
aac cag cag caa agc aac cag ggc gga ttt ggt gga aac caa aac cag 384  
Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln  
115 120 125  
  
tcc cag ggt aac aac ttc aac caa ggt gga ttt ggc gga ggc agc cca 432  
Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro  
130 135 140  
  
cag gca gca ccg gac aat gac cct tgg aat tct gca cca cca gct ggc 480  
Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly  
145 150 155 160  
  
tcc ggc ggg ttc ggc ggc gca gac gat gag cca ccg ttc taaagctttt 529  
Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe  
165 170  
  
cttttctaaa aca 542

<210> 150  
 <211> 173  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 150  
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 Ala Glu Ser Leu Ser Lys Gly Met Arg Val Ile Val Thr Gly Arg Leu  
                   20                  25                  30  
 Lys Gln Arg Ser Tyr Glu Thr Arg Glu Gly Glu Lys Arg Ser Val Phe  
                   35                  40                  45  
 Glu Val Glu Ala Asp Glu Val Gly Pro Ser Leu Thr Phe Ala Lys Ala  
                   50                  55                  60  
 Asp Val Gln Arg Thr Pro Arg Gly Gly Asn Ser Gly Gly Asn Tyr Gly  
   65                  70                  75                  80  
 Gly Gly Asn Gln Gly Gly Gly Leu Gly Gly Asn Gln Gly Asn Gln Gln  
                   85                  90                  95  
 Gly Gly Phe Ser Asn Gln Asn Ser Gly Gly Phe Gly Gly Asn Gln Gly  
                   100                  105                  110  
 Asn Gln Gln Gln Ser Asn Gln Gly Gly Phe Gly Gly Asn Gln Asn Gln  
                   115                  120                  125  
 Ser Gln Gly Asn Asn Phe Asn Gln Gly Gly Phe Gly Gly Gly Ser Pro  
   130                  135                  140  
 Gln Ala Ala Pro Asp Asn Asp Pro Trp Asn Ser Ala Pro Pro Ala Gly  
   145                  150                  155                  160  
 Ser Gly Gly Phe Gly Gly Ala Asp Asp Glu Pro Pro Phe  
                   165                  170

<210> 151  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN02833

<400> 151  
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 aaaggagata cctaacatag tgagccagaa ctcatcttct ttg ctc gaa acc tgg 115  
   Leu Leu Glu Thr Trp  
   1                  5  
 cgc caa gtt gtt gcc gat ctc aca act ttg agc cag caa gcg gac agt 163  
 Arg Gln Val Val Ala Asp Leu Thr Thr Leu Ser Gln Gln Ala Asp Ser  
                   10                  15                  20

gga ttc gac cca ttg acg cca act caa cgt gca tat ttg aac ctg acg 211  
 Gly Phe Asp Pro Leu Thr Pro Thr Gln Arg Ala Tyr Leu Asn Leu Thr  
                   25                                  30                                  35

aag ccg att gcc atc gtc gat ggc tac gcc gtg ctg tcc aca ccc aac 259  
 Lys Pro Ile Ala Ile Val Asp Gly Tyr Ala Val Leu Ser Thr Pro Asn  
                   40                                  45                                  50

gcg atg gca aaa aat gtc att gaa aac gat ttg ggc gat gct ttg acc 307  
 Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu Gly Asp Ala Leu Thr  
                   55                                  60                                  65

cgt gtg ttg tcg ctg cgc atg ggc cga tca ttc agc ttg gct gtc agt 355  
 Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val Ser  
                   70                                  75                                  80                                  85

gtg gag cct gag cag gaa att cca gaa acc cca gct cag cag gag ttt 403  
 Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro Ala Gln Gln Glu Phe  
                                   90                                  95                                  100

aaa tat cag cct gac gca cct gtg atc tct tcc aac aag gcg cca aag 451  
 Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser Asn Lys Ala Pro Lys  
                                   105                                  110                                  115

cag tat gaa gtt ggt ggt cgg gga gag gcg tcg aca agc gac ggc tgg 499  
 Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly Trp  
                   120                                  125                                  130

gaa cgt acc cac tct gca ccg gct ccc gag ccg cac ccg gca cct atc 547  
 Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro Ile  
                   135                                  140                                  145

gcc gat cgt gag cca gag ctg gcc acc ccg cag cgc att ccg cgc gaa 595  
 Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg Glu  
                   150                                  155                                  160                                  165

acc cca gct cac aac cct aat cgg gaa gtg tcc ctc aac ccg aaa tac 643  
 Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys Tyr  
                                   170                                  175                                  180

act ttt gaa agc ttc gtg atc ggg ccg ttc aac cgt ttc gcc aat gca 691  
 Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn Ala  
                   185                                  190                                  195

gcc gca gtt gct gtg gcg gaa agc cca gcg aaa gct ttc aac ccg ctg 739  
 Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro Leu  
                   200                                  205                                  210

ttt att tcc ggc ggt tcc ggc ttg ggc aaa act cac ctg ctg cac gca 787  
 Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His Ala  
                   215                                  220                                  225

gta gga aat tat gct caa gaa ttg cag cct ggc ccg cgg att aag tac 835  
 Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys Tyr  
                   230                                  235                                  240                                  245

gtc tca agt gag gaa tat cac caa cga cta cat caa ctc cgt gcg aga 883  
 Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala Arg  
                   250                                  255                                  260

tgaccgccag gaaaccttca agc

<210> 152

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Leu Leu Glu Thr Trp Arg Gln Val Val Ala Asp Leu Thr Thr Leu Ser  
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Gln Gln Ala Asp Ser Gly Phe Asp Pro Leu Thr Pro Thr Gln Arg Ala  
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Tyr Leu Asn Leu Thr Lys Pro Ile Ala Ile Val Asp Gly Tyr Ala Val  
35 40 45

Leu Ser Thr Pro Asn Ala Met Ala Lys Asn Val Ile Glu Asn Asp Leu  
50 55 60

Gly Asp Ala Leu Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe  
65 70 75 80

Ser Leu Ala Val Ser Val Glu Pro Glu Gln Glu Ile Pro Glu Thr Pro  
85 90 95

Ala Gln Gln Glu Phe Lys Tyr Gln Pro Asp Ala Pro Val Ile Ser Ser  
100 105 110

Asn Lys Ala Pro Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser  
115 120 125

Thr Ser Asp Gly Trp Glu Arg Thr His Ser Ala Pro Ala Pro Glu Pro  
130 135 140

His Pro Ala Pro Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln  
145 150 155 160

Arg Ile Pro Arg Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser  
165 170 175

Leu Asn Pro Lys Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn  
180 185 190

Arg Phe Ala Asn Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys  
195 200 205

Ala Phe Asn Pro Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr  
210 215 220

His Leu Leu His Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly  
225 230 235 240

Pro Arg Ile Lys Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His  
245 250 255

Gln Leu Arg Ala Arg  
260

<210> 153  
 <211> 602  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
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 <222> (1)..(579)  
 <223> FRXA02833

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 Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val  
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agt gtg gag cct gag cag gaa att cca aaa ccc cag ctc aag cag gag 96  
 Ser Val Glu Pro Glu Gln Glu Ile Pro Lys Pro Gln Leu Lys Gln Glu  
 20 25 30

ttt aaa tat cag cct gac gca ctt gtg ttt tct tcc aac aag gcg cca 144  
 Phe Lys Tyr Gln Pro Asp Ala Leu Val Phe Ser Ser Asn Lys Ala Pro  
 35 40 45

aag cag tat gaa gtt ggt ggt cgg gga gag gcg tcg aca agc gac ggt 192  
 Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly  
 50 55 60

tgg gaa ggt acc cac tct gca ccg gct ccc gag ccg cac ccg gca cct 240  
 Trp Glu Gly Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro  
 65 70 75 80

atc gcc gat cgt gag cca gag ctg gcc acc ccg cag cgc att ccg cgc 288  
 Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg  
 85 90 95

gaa acc cca gct cac aac cct aat cgg gaa gtg tcc ctc aac ccg aaa 336  
 Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys  
 100 105 110

tac act ttt gaa agc ttc gtg atc ggg ccg ttc aac cgt ttc gcc aat 384  
 Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn  
 115 120 125

gca gcc gca gtt gct gtg gcg gaa agc cca gcg aaa gct ttc aac ccg 432  
 Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro  
 130 135 140

ctg ttt att tcc ggc ggt tcc ggc ttg ggc aaa act cac ctg ctg cac 480  
 Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His  
 145 150 155 160

gca gta gga aat tat gct caa gaa ttg cag cct ggc ccg cgg att aag 528  
 Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys  
 165 170 175

tac gtc tca agt gag gaa tat cac caa cga cta cat caa ctc cgt gcg 576  
 Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala  
 180 185 190

aga tgaccgccag gaaaccttca agc 602  
 Arg



<210> 154  
 <211> 193  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 154  
 Thr Arg Val Leu Ser Leu Arg Met Gly Arg Ser Phe Ser Leu Ala Val  
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 Ser Val Glu Pro Glu Gln Glu Ile Pro Lys Pro Gln Leu Lys Gln Glu  
 20 25 30  
 Phe Lys Tyr Gln Pro Asp Ala Leu Val Phe Ser Ser Asn Lys Ala Pro  
 35 40 45  
 Lys Gln Tyr Glu Val Gly Gly Arg Gly Glu Ala Ser Thr Ser Asp Gly  
 50 55 60  
 Trp Glu Gly Thr His Ser Ala Pro Ala Pro Glu Pro His Pro Ala Pro  
 65 70 75 80  
 Ile Ala Asp Arg Glu Pro Glu Leu Ala Thr Pro Gln Arg Ile Pro Arg  
 85 90 95  
 Glu Thr Pro Ala His Asn Pro Asn Arg Glu Val Ser Leu Asn Pro Lys  
 100 105 110  
 Tyr Thr Phe Glu Ser Phe Val Ile Gly Pro Phe Asn Arg Phe Ala Asn  
 115 120 125  
 Ala Ala Ala Val Ala Val Ala Glu Ser Pro Ala Lys Ala Phe Asn Pro  
 130 135 140  
 Leu Phe Ile Ser Gly Gly Ser Gly Leu Gly Lys Thr His Leu Leu His  
 145 150 155 160  
 Ala Val Gly Asn Tyr Ala Gln Glu Leu Gln Pro Gly Pro Arg Ile Lys  
 165 170 175  
 Tyr Val Ser Ser Glu Glu Tyr His Gln Arg Leu His Gln Leu Arg Ala  
 180 185 190  
 Arg

<210> 155  
 <211> 2016  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1993)  
 <223> RXA01480

<400> 155  
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caatataggc acactaaagg gacggggctaa agtgatggtc	atg gca aag gga cgt	115
	Met Ala Lys Gly Arg	
	1 5	
att ccg gaa agt gac att cag gca atc cgc gag cgc acc ccg atc gag		163
Ile Pro Glu Ser Asp Ile Gln Ala Ile Arg Glu Arg Thr Pro Ile Glu		
	10 15 20	
gag atc gtg ggt gat tat gtg cag ctg aaa tcg gca ggt gct gat tcg		211
Glu Ile Val Gly Asp Tyr Val Gln Leu Lys Ser Ala Gly Ala Asp Ser		
	25 30 35	
ctc aag ggg ctt tct ccc ttt aaa gat gaa aaa aca cca tcg ttc cat		259
Leu Lys Gly Leu Ser Pro Phe Lys Asp Glu Lys Thr Pro Ser Phe His		
	40 45 50	
gtg cgc ccc aac cgt ggt tac tac cac tgt ttc tcc acc ggc aaa ggt		307
Val Arg Pro Asn Arg Gly Tyr Tyr His Cys Phe Ser Thr Gly Lys Gly		
	55 60 65	
gga gat gtg ttc tcc ttc ctc atg gag atg gaa cac atc tct ttc cct		355
Gly Asp Val Phe Ser Phe Leu Met Glu Met Glu His Ile Ser Phe Pro		
	70 75 80 85	
gag gct gtg gaa gtg tgt gcg gag aaa att ggt tat cag atc aat tac		403
Glu Ala Val Glu Val Cys Ala Glu Lys Ile Gly Tyr Gln Ile Asn Tyr		
	90 95 100	
caa ggt ggt ggc ccg ggg cgc cgt gag gaa cct gga act cgc cag cgc		451
Gln Gly Gly Gly Pro Gly Arg Arg Glu Glu Pro Gly Thr Arg Gln Arg		
	105 110 115	
ctt att ttg gct aat aag gct gcg cac cag ttt tat cgc gag caa tta		499
Leu Ile Leu Ala Asn Lys Ala Ala His Gln Phe Tyr Arg Glu Gln Leu		
	120 125 130	
gaa acc ccc gaa gca caa cct ggc agg gag ttt ttg ctg cag cgt gga		547
Glu Thr Pro Glu Ala Gln Pro Gly Arg Glu Phe Leu Leu Gln Arg Gly		
	135 140 145	
ttc gga cag cag cac att tat cat ttc gaa tgt ggc tat gcg cct gcc		595
Phe Gly Gln Gln His Ile Tyr His Phe Glu Cys Gly Tyr Ala Pro Ala		
	150 155 160 165	
ggc tgg gat acc ttg acc aag cat ttg ctg aag aag ggc ttt gag ttc		643
Gly Trp Asp Thr Leu Thr Lys His Leu Leu Lys Lys Gly Phe Glu Phe		
	170 175 180	
aag gaa tta gaa gct gcc ggt cta agc aag atg ggt aag cgc ggt ccg		691
Lys Glu Leu Glu Ala Ala Gly Leu Ser Lys Met Gly Lys Arg Gly Pro		
	185 190 195	
att gat cag ttc cag cgc agg ttg ctg tgg ccg atc aag aac ctg tct		739
Ile Asp Gln Phe Gln Arg Arg Leu Leu Trp Pro Ile Lys Asn Leu Ser		
	200 205 210	
ggg gat gtc att ggt ttt ggc gcc cgc aag ctt ttc gat gac gac aaa		787
Gly Asp Val Ile Gly Phe Gly Ala Arg Lys Leu Phe Asp Asp Asp Lys		
	215 220 225	

atg ggc aag tac atg aat acg cct gag acg ttg ttg tac aaa aag tcc	835
Met Gly Lys Tyr Met Asn Thr Pro Glu Thr Leu Leu Tyr Lys Lys Ser	
230 235 240 245	
aag gtg ctc ttt ggt cta gat tct gca aag aag gcc att gca gct ggc	883
Lys Val Leu Phe Gly Leu Asp Ser Ala Lys Lys Ala Ile Ala Ala Gly	
250 255 260	
cac caa gca gta gtg gtg gaa ggc tac acc gat gtg atg gcc atg cat	931
His Gln Ala Val Val Val Glu Gly Tyr Thr Asp Val Met Ala Met His	
265 270 275	
gcc gcg ggc att gat aca gcc gtg gca tcg tgt ggc act gcg ttt ggt	979
Ala Ala Gly Ile Asp Thr Ala Val Ala Ser Cys Gly Thr Ala Phe Gly	
280 285 290	
gaa gaa cac ttg cag atg ctt cgt cga ctc atg ctg gat gat aac tac	1027
Glu Glu His Leu Gln Met Leu Arg Arg Leu Met Leu Asp Asp Asn Tyr	
295 300 305	
ttc cgc ggt gaa ctg att tac acc ttc gat ggt gat gag gcc ggc cag	1075
Phe Arg Gly Glu Leu Ile Tyr Thr Phe Asp Gly Asp Glu Ala Gly Gln	
310 315 320 325	
aag gcc gcc atg cgt gcc ttt gag ggc gat cag aag ttc aca gga caa	1123
Lys Ala Ala Met Arg Ala Phe Glu Gly Asp Gln Lys Phe Thr Gly Gln	
330 335 340	
tca ttt gtg tct gtg gca ccc aac ggc atg gat ccg tgt gat ctg cgc	1171
Ser Phe Val Ser Val Ala Pro Asn Gly Met Asp Pro Cys Asp Leu Arg	
345 350 355	
ctt gag cgt ggc gat gcg gcg gtg cgt gat ctt gtg gca cga cgc atc	1219
Leu Glu Arg Gly Asp Ala Ala Val Arg Asp Leu Val Ala Arg Arg Ile	
360 365 370	
ccg atg ttt gag ttc gtc atc caa tcg atc atc agc gaa tac acc ctc	1267
Pro Met Phe Glu Phe Val Ile Gln Ser Ile Ile Ser Glu Tyr Thr Leu	
375 380 385	
gac acc gtg gaa ggc cgt ctg gct gcg ctt cgt cgg gca gtc ccc atc	1315
Asp Thr Val Glu Gly Arg Leu Ala Ala Leu Arg Arg Ala Val Pro Ile	
390 395 400 405	
gtg gcg gat att cgc gat aag acg ctg cag tct gaa tac gcc cgc ctg	1363
Val Ala Asp Ile Arg Asp Lys Thr Leu Gln Ser Glu Tyr Ala Arg Leu	
410 415 420	
ctg tct ggt tgg gtc ggc tgg tct gat cct tca gag gtg ctg cgt cag	1411
Leu Ser Gly Trp Val Gly Trp Ser Asp Pro Ser Glu Val Leu Arg Gln	
425 430 435	
gtt cac gag gaa gca cgt cgc ccc aag cgc gat aag aag cct gtg cgt	1459
Val His Glu Glu Ala Arg Arg Pro Lys Arg Asp Lys Lys Pro Val Arg	
440 445 450	
gca aag cgt ttc gat caa ccg ctc gag gat caa agc ctg cga ccc acc	1507
Ala Lys Arg Phe Asp Gln Pro Leu Glu Asp Gln Ser Leu Arg Pro Thr	
455 460 465	
atg gcg ctg cct aat ccg cgg aac cct gtg ctg tgg cag gaa cgg gaa	1555

Met Ala Leu Pro Asn Pro Arg Asn Pro Val Leu Trp Gln Glu Arg Glu  
 470 475 480 485

tca ctc aag atc gcc ctg caa tat ccg gag ctc gcg gga tcg tac ttt 1603  
 Ser Leu Lys Ile Ala Leu Gln Tyr Pro Glu Leu Ala Gly Ser Tyr Phe  
 490 495 500

gat gga ctg cca acc gat agc ttc acc aac cct gcc tac cgc atg gta 1651  
 Asp Gly Leu Pro Thr Asp Ser Phe Thr Asn Pro Ala Tyr Arg Met Val  
 505 510 515

cgc gat gcc att tcg gct gct ggg gga tgt gaa cgt gcc ctc gat ggc 1699  
 Arg Asp Ala Ile Ser Ala Ala Gly Gly Cys Glu Arg Ala Leu Asp Gly  
 520 525 530

act gat tgg ttg cct gcc gta tcg gaa aat atg act gat att ttg ggc 1747  
 Thr Asp Trp Leu Pro Ala Val Ser Glu Asn Met Thr Asp Ile Leu Gly  
 535 540 545

acg tcg ttg gtg tca gag ctg gcg atg gaa ccc atc gag gtg gaa gcg 1795  
 Thr Ser Leu Val Ser Glu Leu Ala Met Glu Pro Ile Glu Val Glu Ala  
 550 555 560 565

caa gac ctg gaa tca tat acc gat ggt gtg ttg tcc agg ctg cag gaa 1843  
 Gln Asp Leu Glu Ser Tyr Thr Asp Gly Val Leu Ser Arg Leu Gln Glu  
 570 575 580

aca cga gtg ggc aac cag atc gcc atc ttg aaa gga cag ctg caa aga 1891  
 Thr Arg Val Gly Asn Gln Ile Ala Ile Leu Lys Gly Gln Leu Gln Arg  
 585 590 595

atg cgt ccg tct gaa gat gag caa gcc tac aac tcg ctg ttt tcc gat 1939  
 Met Arg Pro Ser Glu Asp Glu Gln Ala Tyr Asn Ser Leu Phe Ser Asp  
 600 605 610

ctg gtt gcc ctg gaa cag gcg cgc cgg gag ctg ttg gcc cgg gcg ttt 1987  
 Leu Val Ala Leu Glu Gln Ala Arg Arg Glu Leu Leu Ala Arg Ala Phe  
 615 620 625

aga ggg taatttagtc ctggtcttgc tcg 2016  
 Arg Gly  
 630

&lt;210&gt; 156

&lt;211&gt; 631

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 156

Met Ala Lys Gly Arg Ile Pro Glu Ser Asp Ile Gln Ala Ile Arg Glu  
 1 5 10 15

Arg Thr Pro Ile Glu Glu Ile Val Gly Asp Tyr Val Gln Leu Lys Ser  
 20 25 30

Ala Gly Ala Asp Ser Leu Lys Gly Leu Ser Pro Phe Lys Asp Glu Lys  
 35 40 45

Thr Pro Ser Phe His Val Arg Pro Asn Arg Gly Tyr Tyr His Cys Phe  
 50 55 60

Ser Thr Gly Lys Gly Gly Asp Val Phe Ser Phe Leu Met Glu Met Glu  
 65 70 75 80  
 His Ile Ser Phe Pro Glu Ala Val Glu Val Cys Ala Glu Lys Ile Gly  
 85 90 95  
 Tyr Gln Ile Asn Tyr Gln Gly Gly Gly Pro Gly Arg Arg Glu Glu Pro  
 100 105 110  
 Gly Thr Arg Gln Arg Leu Ile Leu Ala Asn Lys Ala Ala His Gln Phe  
 115 120 125  
 Tyr Arg Glu Gln Leu Glu Thr Pro Glu Ala Gln Pro Gly Arg Glu Phe  
 130 135 140  
 Leu Leu Gln Arg Gly Phe Gly Gln Gln His Ile Tyr His Phe Glu Cys  
 145 150 155 160  
 Gly Tyr Ala Pro Ala Gly Trp Asp Thr Leu Thr Lys His Leu Leu Lys  
 165 170 175  
 Lys Gly Phe Glu Phe Lys Glu Leu Glu Ala Ala Gly Leu Ser Lys Met  
 180 185 190  
 Gly Lys Arg Gly Pro Ile Asp Gln Phe Gln Arg Arg Leu Leu Trp Pro  
 195 200 205  
 Ile Lys Asn Leu Ser Gly Asp Val Ile Gly Phe Gly Ala Arg Lys Leu  
 210 215 220  
 Phe Asp Asp Asp Lys Met Gly Lys Tyr Met Asn Thr Pro Glu Thr Leu  
 225 230 235 240  
 Leu Tyr Lys Lys Ser Lys Val Leu Phe Gly Leu Asp Ser Ala Lys Lys  
 245 250 255  
 Ala Ile Ala Ala Gly His Gln Ala Val Val Val Glu Gly Tyr Thr Asp  
 260 265 270  
 Val Met Ala Met His Ala Ala Gly Ile Asp Thr Ala Val Ala Ser Cys  
 275 280 285  
 Gly Thr Ala Phe Gly Glu Glu His Leu Gln Met Leu Arg Arg Leu Met  
 290 295 300  
 Leu Asp Asp Asn Tyr Phe Arg Gly Glu Leu Ile Tyr Thr Phe Asp Gly  
 305 310 315 320  
 Asp Glu Ala Gly Gln Lys Ala Ala Met Arg Ala Phe Glu Gly Asp Gln  
 325 330 335  
 Lys Phe Thr Gly Gln Ser Phe Val Ser Val Ala Pro Asn Gly Met Asp  
 340 345 350  
 Pro Cys Asp Leu Arg Leu Glu Arg Gly Asp Ala Ala Val Arg Asp Leu  
 355 360 365  
 Val Ala Arg Arg Ile Pro Met Phe Glu Phe Val Ile Gln Ser Ile Ile  
 370 375 380

Ser Glu Tyr Thr Leu Asp Thr Val Glu Gly Arg Leu Ala Ala Leu Arg  
 385 390 395 400  
 Arg Ala Val Pro Ile Val Ala Asp Ile Arg Asp Lys Thr Leu Gln Ser  
 405 410 415  
 Glu Tyr Ala Arg Leu Leu Ser Gly Trp Val Gly Trp Ser Asp Pro Ser  
 420 425 430  
 Glu Val Leu Arg Gln Val His Glu Glu Ala Arg Arg Pro Lys Arg Asp  
 435 440 445  
 Lys Lys Pro Val Arg Ala Lys Arg Phe Asp Gln Pro Leu Glu Asp Gln  
 450 455 460  
 Ser Leu Arg Pro Thr Met Ala Leu Pro Asn Pro Arg Asn Pro Val Leu  
 465 470 475 480  
 Trp Gln Glu Arg Glu Ser Leu Lys Ile Ala Leu Gln Tyr Pro Glu Leu  
 485 490 495  
 Ala Gly Ser Tyr Phe Asp Gly Leu Pro Thr Asp Ser Phe Thr Asn Pro  
 500 505 510  
 Ala Tyr Arg Met Val Arg Asp Ala Ile Ser Ala Ala Gly Gly Cys Glu  
 515 520 525  
 Arg Ala Leu Asp Gly Thr Asp Trp Leu Pro Ala Val Ser Glu Asn Met  
 530 535 540  
 Thr Asp Ile Leu Gly Thr Ser Leu Val Ser Glu Leu Ala Met Glu Pro  
 545 550 555 560  
 Ile Glu Val Glu Ala Gln Asp Leu Glu Ser Tyr Thr Asp Gly Val Leu  
 565 570 575  
 Ser Arg Leu Gln Glu Thr Arg Val Gly Asn Gln Ile Ala Ile Leu Lys  
 580 585 590  
 Gly Gln Leu Gln Arg Met Arg Pro Ser Glu Asp Glu Gln Ala Tyr Asn  
 595 600 605  
 Ser Leu Phe Ser Asp Leu Val Ala Leu Glu Gln Ala Arg Arg Glu Leu  
 610 615 620  
 Leu Ala Arg Ala Phe Arg Gly  
 625 630

&lt;210&gt; 157

&lt;211&gt; 1597

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1597)

&lt;223&gt; RXN03163

&lt;400&gt; 157

gcactgattt ggaccttctt tgggaggcta tcgaccgcgt tgatgaactt cgcgagccc 60

tcaagttggc ctaaaaatct gatgtagtat cttcggattc atg gca aaa acc cgc	115
Met Ala Lys Thr Arg	
1 5	
gtc ccc gct cct gaa aag tcg gtg gcg cgg gtt tta cct ctt ttg ggg	163
Val Pro Ala Pro Glu Lys Ser Val Ala Arg Val Leu Pro Leu Leu Gly	
10 15 20	
tta cct cac ctg gat cga ctg ttt gat tac cgc atc agc gaa gac caa	211
Leu Pro His Leu Asp Arg Leu Phe Asp Tyr Arg Ile Ser Glu Asp Gln	
25 30 35	
cac gat gat gtg caa cct ggc gtg cgg gtg cgc gtg cgt ttt ggt gga	259
His Asp Asp Val Gln Pro Gly Val Arg Val Arg Val Arg Phe Gly Gly	
40 45 50	
cgt tta gtt gat gcc atc gtg atg tca cgc acc gcg caa acc tcg cac	307
Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr Ala Gln Thr Ser His	
55 60 65	
gag gga aag ctg atg tgg ctg gat cgg gtg att tcg ccg atc gtg gtg	355
Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile Ser Pro Ile Val Val	
70 75 80 85	
tat cca cct caa aca gca aag cta att gag caa ctc agt gat cgc tat	403
Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln Leu Ser Asp Arg Tyr	
90 95 100	
ggc ggg gta cgt tcg gat ctc atc cgt tcg gcg cta ccg gcg cgg cat	451
Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala Leu Pro Ala Arg His	
105 110 115	
gct ggg gca gaa gag gca gat acc tcc acg tcg tgg gag tca ttg ggt	499
Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser Trp Glu Ser Leu Gly	
120 125 130	
gag gtt aaa gaa ccc gat tta tcg tcg tgg tct gcg tat cag cat ggt	547
Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser Ala Tyr Gln His Gly	
135 140 145	
caa tca ttt gtt gac gcc gtc ttg gcg gga aca act gcg cgg gcg tca	595
Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr Thr Ala Arg Ala Ser	
150 155 160 165	
tgg cag att gct ccc gga gat gat tgg gcg ctg gct ttg gct tct ttg	643
Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu Ala Leu Ala Ser Leu	
170 175 180	
gcg gtc aag gtt gtc aaa gac ggc ggc gga gcg ctt ctc gta gtg cct	691
Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala Leu Leu Val Val Pro	
185 190 195	
gat cag cgc gat ctc gac cgc ttg gaa gct gcg ctt cga ggt ttg gtt	739
Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala Leu Arg Gly Leu Val	
200 205 210	
gcg gcg aaa caa atc act gtg ctt aat tca ggt ctt ggt ccg cag gca	787
Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly Leu Gly Pro Gln Ala	
215 220 225	

cga tat cgg cgt ttc cta tcg gta ctc agt ggg cag gga cga ctg att 835  
 Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly Gln Gly Arg Leu Ile  
 230 235 240 245

att gga acc aga agt gcc gct ttt gca ccc gtg aag gat ctg aaa ctg 883  
 Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val Lys Asp Leu Lys Leu  
 250 255 260

gcc gtc att tta aat gat ggc gac gac aac ctc gtt gat cct aga gcg 931  
 Ala Val Ile Leu Asn Asp Gly Asp Asn Leu Val Asp Pro Arg Ala  
 265 270 275

ccc tat gcc cac gcc agg gaa gtg ctg acc acg cgt tcc agt ttg gaa 979  
 Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr Arg Ser Ser Leu Glu  
 280 285 290

gca agc tcc ttg att att gcg gga cat gcg cgg acc gcg gaa acc caa 1027  
 Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg Thr Ala Glu Thr Gln  
 295 300 305

ttg ctg gtg gaa tcg gga tgg atg cac aat ctc atc gca ccg agg gat 1075  
 Leu Leu Val Glu Ser Gly Trp Met His Asn Leu Ile Ala Pro Arg Asp  
 310 315 320 325

acc att cgc act agg atg ccg cgt att cag gca gtg ggc gat tcc gat 1123  
 Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala Val Gly Asp Ser Asp  
 330 335 340

ttc cag atg gaa cgc gat cca atg gcc cga tca gcg cgg ctg cct ggc 1171  
 Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser Ala Arg Leu Pro Gly  
 345 350 355

att gcg ttt cat gcg gtg cgc agc gcc tta gaa cgt gat caa cca gcg 1219  
 Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu Arg Asp Gln Pro Ala  
 360 365 370

ctt atc cag gta cca agg aaa ggc tac gtg cca acc ttg gcg tgt gga 1267  
 Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro Thr Leu Ala Cys Gly  
 375 380 385

aac tgc cgc acc cca gcg cgg tgc cgg cac tgt aat ggg cct gtg gga 1315  
 Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys Asn Gly Pro Val Gly  
 390 395 400 405

ctt ccc cag gga agc tct gat cta gcg gga gtg ccc act tgc cga tgg 1363  
 Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val Pro Thr Cys Arg Trp  
 410 415 420

tgc gga cgc cct gat tcg cgg ttt aag tgc caa aac tgc ggc tct cca 1411  
 Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln Asn Cys Gly Ser Pro  
 425 430 435

aaa ctg cgt gct gtg gtg ctg gga acg gaa cgc aca gca gaa gaa ctg 1459  
 Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg Thr Ala Glu Glu Leu  
 440 445 450

ggc cgc gcg ttc ccg tct gtg cgg gta att acc tct ggt ggc aac aag 1507  
 Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr Ser Gly Gly Asn Lys  
 455 460 465

gtg gtg gat tcg gtg gaa aac cga gcc agc att gtg gtg tcc acg cca 1555



Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile Val Val Ser Thr Pro  
 470 475 480 485

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 490 495

<210> 158

<211> 499

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

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Ile Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly Val Arg Val Arg  
 35 40 45

Val Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr  
 50 55 60

Ala Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile  
 65 70 75 80

Ser Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln  
 85 90 95

Leu Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala  
 100 105 110

Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser  
 115 120 125

Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser  
 130 135 140

Ala Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr  
 145 150 155 160

Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu  
 165 170 175

Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala  
 180 185 190

Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala  
 195 200 205

Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly  
 210 215 220

Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly  
 225 230 235 240

Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val  
 245 250 255

Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu  
 260 265 270  
 Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr  
 275 280 285  
 Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg  
 290 295 300  
 Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp Met His Asn Leu  
 305 310 315 320  
 Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala  
 325 330 335  
 Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser  
 340 345 350  
 Ala Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu  
 355 360 365  
 Arg Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro  
 370 375 380  
 Thr Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys  
 385 390 395 400  
 Asn Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val  
 405 410 415  
 Pro Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln  
 420 425 430  
 Asn Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg  
 435 440 445  
 Thr Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr  
 450 455 460  
 Ser Gly Gly Asn Lys Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile  
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 Arg Pro Glu

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 <222> (101)..(2128)  
 <223> FRXA02241

<400> 159

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				Val Ala Arg Val Leu	5	
				1		
cct ctt ttg ggg tta cct cac ctg gat cga ctg ttt gat tac cgc atc	163					
Pro Leu Leu Gly Leu Pro His Leu Asp Arg Leu Phe Asp Tyr Arg Ile						
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agc gaa gac caa cac gat gat gtg caa cct gcc gtg cgg gtg cgc gtg	211					
Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly Val Arg Val Arg Val						
	25		30		35	
cgt ttt ggt gga cgt tta gtt gat gcc atc gtg atg tca cgc acc gcg	259					
Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val Met Ser Arg Thr Ala						
	40		45		50	
caa acc tcg cac gag gga aag ctg atg tgg ctg gat cgg gtg att tcg	307					
Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu Asp Arg Val Ile Ser						
	55		60		65	
ccg atc gtg gtg tat cca cct caa aca gca aag cta att gag caa ctc	355					
Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys Leu Ile Glu Gln Leu						
	70		75		80	
agt gat cgc tat ggc ggg gta cgt tcg gat ctc atc cgt tcg gcg cta	403					
Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu Ile Arg Ser Ala Leu						
	90		95		100	
ccg gcg cgg cat gct ggg gca gaa gag gca gat acc tcc acg tcg tgg	451					
Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp Thr Ser Thr Ser Trp						
	105		110		115	
gag tca ttg ggt gag gtt aaa gaa ccc gat tta tcg tcg tgg tct gcg	499					
Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu Ser Ser Trp Ser Ala						
	120		125		130	
tat cag cat ggt caa tca ttt gtt gac gcc gtc ttg gcg gga aca act	547					
Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val Leu Ala Gly Thr Thr						
	135		140		145	
gcg cgg gcg tca tgg cag att gct ccc gga gat gat tgg gcg ctg gct	595					
Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp Asp Trp Ala Leu Ala						
	150		155		160	
ttg gct tct ttg gcg gtc aag gtt gtc aaa gac gcc gcc gga gcg ctt	643					
Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp Gly Gly Gly Ala Leu						
	170		175		180	
ctc gta gtg cct gat cag cgc gat ctc gac cgc ttg gaa gct gcg ctt	691					
Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg Leu Glu Ala Ala Leu						
	185		190		195	
cga ggt ttg gtt gcg gcg aaa caa atc act gtg ctt aat tca ggt ctt	739					
Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val Leu Asn Ser Gly Leu						
	200		205		210	
ggt ccg cag gca cga tat cgg cgt ttc cta tcg gta ctc agt ggg cag	787					
Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser Val Leu Ser Gly Gln						
	215		220		225	

gga cga ctg att att gga acc aga agt gcc gct ttt gca ccc gtg aag 835  
 Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala Phe Ala Pro Val Lys  
 230 235 240 245

gat ctg aaa ctg gcc gtc att tta aat gat ggc gac gac aac ctc gtt 883  
 Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly Asp Asp Asn Leu Val  
 250 255 260

gat cct aga gcg ccc tat gcc cac gcc agg gaa gtg ctg acc acg cgt 931  
 Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu Val Leu Thr Thr Arg  
 265 270 275

tcc agt ttg gaa gca agc tcc ttg att att gcg gga cat gcg cgg acc 979  
 Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala Gly His Ala Arg Thr  
 280 285 290

gcg gaa acc caa ttg ctg gtg gaa tcg gga tgg atg cac aat ctc atc 1027  
 Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp Met His Asn Leu Ile  
 295 300 305

gca ccg agg gat acc att cgc act agg atg ccg cgt att cag gca gtg 1075  
 Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro Arg Ile Gln Ala Val  
 310 315 320 325

ggc gat tcc gat ttc cag atg gaa cgc gat cca atg gcc cga tca gcg 1123  
 Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro Met Ala Arg Ser Ala  
 330 335 340

cgg ctg cct ggc att gcg ttt cat gcg gtg cgc agc gcc tta gaa cgt 1171  
 Arg Leu Pro Gly Ile Ala Phe His Ala Val Arg Ser Ala Leu Glu Arg  
 345 350 355

gat caa cca gcg ctt atc cag gta cca agg aaa ggc tac gtg cca acc 1219  
 Asp Gln Pro Ala Leu Ile Gln Val Pro Arg Lys Gly Tyr Val Pro Thr  
 360 365 370

ttg gcg tgt gga aac tgc cgc acc cca gcg cgg tgc cgg cac tgt aat 1267  
 Leu Ala Cys Gly Asn Cys Arg Thr Pro Ala Arg Cys Arg His Cys Asn  
 375 380 385

ggg cct gtg gga ctt ccc cag gga agc tct gat cta gcg gga gtg ccc 1315  
 Gly Pro Val Gly Leu Pro Gln Gly Ser Ser Asp Leu Ala Gly Val Pro  
 390 395 400 405

act tgc cga tgg tgc gga cgc cct gat tcg cgg ttt aag tgc caa aac 1363  
 Thr Cys Arg Trp Cys Gly Arg Pro Asp Ser Arg Phe Lys Cys Gln Asn  
 410 415 420

tgc ggc tct cca aaa ctg cgt gct gtg gtg ctg gga acg gaa cgc aca 1411  
 Cys Gly Ser Pro Lys Leu Arg Ala Val Val Leu Gly Thr Glu Arg Thr  
 425 430 435

gca gaa gaa ctg ggc cgc gcg ttc ccg tct gtg cgg gta att acc tct 1459  
 Ala Glu Glu Leu Gly Arg Ala Phe Pro Ser Val Arg Val Ile Thr Ser  
 440 445 450

ggt ggc aac aag gtg gtg gat tcg gtg gaa aac cga gcc agc att gtg 1507  
 Gly Gly Asn Lys Val Val Asp Ser Val Glu Asn Arg Ala Ser Ile Val  
 455 460 465

gtg tcc acg cca ggt gca gaa cct ttt gtg gcc aac tcg ccg gag aga 1555  
Val Ser Thr Pro Gly Ala Glu Pro Phe Val Ala Asn Ser Pro Glu Arg  
470 475 480 485

cca gag aaa tcg gag aaa cca gag cac aag ggc gct tac ggt gcc ttg 1603  
Pro Glu Lys Ser Glu Lys Pro Glu His Lys Gly Ala Tyr Gly Ala Leu  
490 495 500

tta ttg ctg gat acc tgg gcg ttg atg ggt cgg caa gat ctg cgc gcc 1651  
Leu Leu Leu Asp Thr Trp Ala Leu Met Gly Arg Gln Asp Leu Arg Ala  
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atg gag gac gcg ctg cac aag tgg gca gcg gcg gcc acg ctg gtg cat 1699  
Met Glu Asp Ala Leu His Lys Trp Ala Ala Ala Thr Leu Val His  
520 525 530

tct cat ctg cac cag ggt caa gtc atc gtg gtt gca gat cca tcg ttt 1747  
Ser His Leu His Gln Gly Gln Val Ile Val Val Ala Asp Pro Ser Phe  
535 540 545

cct gct gtg caa tcg ttg att cgg tgg gat atg gca ggt gct gca gcg 1795  
Pro Ala Val Gln Ser Leu Ile Arg Trp Asp Met Ala Gly Ala Ala  
550 555 560 565

caa gag ttg gct agc cga cgc gag gtt atg ttc ccg cct tct gta cac 1843  
Gln Glu Leu Ala Ser Arg Arg Glu Val Met Phe Pro Pro Ser Val His  
570 575 580

atg gca gca atc gat ggg gct acc gct gca ttg gaa agt ttc ttg gat 1891  
Met Ala Ala Ile Asp Gly Ala Thr Ala Ala Leu Glu Ser Phe Leu Asp  
585 590 595

ttg gcg gag ctt ccc gat cat gct gaa gtc ctc ggc cct gtt gat ctg 1939  
Leu Ala Glu Leu Pro Asp His Ala Glu Val Leu Gly Pro Val Asp Leu  
600 605 610

cca ccg ggt gtg agt ttg cct ggt gaa tat gat gag cag cgc ttt ggt 1987  
Pro Pro Gly Val Ser Leu Pro Gly Glu Tyr Asp Glu Gln Arg Phe Gly  
615 620 625

ccg ccg cag cgc ctt ctc atc aga act cca ttg gga ccg ccg tct gag 2035  
Pro Pro Gln Arg Leu Leu Ile Arg Thr Pro Leu Gly Pro Arg Ser Glu  
630 635 640 645

ttg ggt aga gcg ctg cgc tca gcc cag gtg gcg cgt gcg gtg agg aag 2083  
Leu Gly Arg Ala Leu Arg Ser Ala Gln Val Ala Arg Ala Val Arg Lys  
650 655 660

aat gat ttg ccg ttg cgt att cag atg gat ccg att cac atc gga 2128  
Asn Asp Leu Pro Leu Arg Ile Gln Met Asp Pro Ile His Ile Gly  
665 670 675

taaaactgct ggtgaaaggc cta 2151

&lt;210&gt; 160

&lt;211&gt; 676

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 160

Val Ala Arg Val Leu Pro Leu Leu Gly Leu Pro His Leu Asp Arg Leu  
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 Phe Asp Tyr Arg Ile Ser Glu Asp Gln His Asp Asp Val Gln Pro Gly  
 20 25 30  
 Val Arg Val Arg Val Arg Phe Gly Gly Arg Leu Val Asp Ala Ile Val  
 35 40 45  
 Met Ser Arg Thr Ala Gln Thr Ser His Glu Gly Lys Leu Met Trp Leu  
 50 55 60  
 Asp Arg Val Ile Ser Pro Ile Val Val Tyr Pro Pro Gln Thr Ala Lys  
 65 70 75 80  
 Leu Ile Glu Gln Leu Ser Asp Arg Tyr Gly Gly Val Arg Ser Asp Leu  
 85 90 95  
 Ile Arg Ser Ala Leu Pro Ala Arg His Ala Gly Ala Glu Glu Ala Asp  
 100 105 110  
 Thr Ser Thr Ser Trp Glu Ser Leu Gly Glu Val Lys Glu Pro Asp Leu  
 115 120 125  
 Ser Ser Trp Ser Ala Tyr Gln His Gly Gln Ser Phe Val Asp Ala Val  
 130 135 140  
 Leu Ala Gly Thr Thr Ala Arg Ala Ser Trp Gln Ile Ala Pro Gly Asp  
 145 150 155 160  
 Asp Trp Ala Leu Ala Leu Ala Ser Leu Ala Val Lys Val Val Lys Asp  
 165 170 175  
 Gly Gly Gly Ala Leu Leu Val Val Pro Asp Gln Arg Asp Leu Asp Arg  
 180 185 190  
 Leu Glu Ala Ala Leu Arg Gly Leu Val Ala Ala Lys Gln Ile Thr Val  
 195 200 205  
 Leu Asn Ser Gly Leu Gly Pro Gln Ala Arg Tyr Arg Arg Phe Leu Ser  
 210 215 220  
 Val Leu Ser Gly Gln Gly Arg Leu Ile Ile Gly Thr Arg Ser Ala Ala  
 225 230 235 240  
 Phe Ala Pro Val Lys Asp Leu Lys Leu Ala Val Ile Leu Asn Asp Gly  
 245 250 255  
 Asp Asp Asn Leu Val Asp Pro Arg Ala Pro Tyr Ala His Ala Arg Glu  
 260 265 270  
 Val Leu Thr Thr Arg Ser Ser Leu Glu Ala Ser Ser Leu Ile Ile Ala  
 275 280 285  
 Gly His Ala Arg Thr Ala Glu Thr Gln Leu Leu Val Glu Ser Gly Trp  
 290 295 300  
 Met His Asn Leu Ile Ala Pro Arg Asp Thr Ile Arg Thr Arg Met Pro  
 305 310 315 320  
 Arg Ile Gln Ala Val Gly Asp Ser Asp Phe Gln Met Glu Arg Asp Pro

				325						330							335
Met	Ala	Arg	Ser	Ala	Arg	Leu	Pro	Gly	Ile	Ala	Phe	His	Ala	Val	Arg		
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Ser	Ala	Leu	Glu	Arg	Asp	Gln	Pro	Ala	Leu	Ile	Gln	Val	Pro	Arg	Lys		
	355						360					365					
Gly	Tyr	Val	Pro	Thr	Leu	Ala	Cys	Gly	Asn	Cys	Arg	Thr	Pro	Ala	Arg		
	370					375					380						
Cys	Arg	His	Cys	Asn	Gly	Pro	Val	Gly	Leu	Pro	Gln	Gly	Ser	Ser	Asp		
385					390					395					400		
Leu	Ala	Gly	Val	Pro	Thr	Cys	Arg	Trp	Cys	Gly	Arg	Pro	Asp	Ser	Arg		
				405					410					415			
Phe	Lys	Cys	Gln	Asn	Cys	Gly	Ser	Pro	Lys	Leu	Arg	Ala	Val	Val	Leu		
			420					425					430				
Gly	Thr	Glu	Arg	Thr	Ala	Glu	Glu	Leu	Gly	Arg	Ala	Phe	Pro	Ser	Val		
		435					440					445					
Arg	Val	Ile	Thr	Ser	Gly	Gly	Asn	Lys	Val	Val	Asp	Ser	Val	Glu	Asn		
	450					455					460						
Arg	Ala	Ser	Ile	Val	Val	Ser	Thr	Pro	Gly	Ala	Glu	Pro	Phe	Val	Ala		
465					470					475					480		
Asn	Ser	Pro	Glu	Arg	Pro	Glu	Lys	Ser	Glu	Lys	Pro	Glu	His	Lys	Gly		
				485					490					495			
Ala	Tyr	Gly	Ala	Leu	Leu	Leu	Leu	Asp	Thr	Trp	Ala	Leu	Met	Gly	Arg		
			500					505					510				
Gln	Asp	Leu	Arg	Ala	Met	Glu	Asp	Ala	Leu	His	Lys	Trp	Ala	Ala	Ala		
	515						520					525					
Ala	Thr	Leu	Val	His	Ser	His	Leu	His	Gln	Gly	Gln	Val	Ile	Val	Val		
	530					535					540						
Ala	Asp	Pro	Ser	Phe	Pro	Ala	Val	Gln	Ser	Leu	Ile	Arg	Trp	Asp	Met		
545					550					555					560		
Ala	Gly	Ala	Ala	Ala	Gln	Glu	Leu	Ala	Ser	Arg	Arg	Glu	Val	Met	Phe		
				565					570					575			
Pro	Pro	Ser	Val	His	Met	Ala	Ala	Ile	Asp	Gly	Ala	Thr	Ala	Ala	Leu		
			580					585					590				
Glu	Ser	Phe	Leu	Asp	Leu	Ala	Glu	Leu	Pro	Asp	His	Ala	Glu	Val	Leu		
	595						600					605					
Gly	Pro	Val	Asp	Leu	Pro	Pro	Gly	Val	Ser	Leu	Pro	Gly	Glu	Tyr	Asp		
	610					615					620						
Glu	Gln	Arg	Phe	Gly	Pro	Pro	Gln	Arg	Leu	Leu	Ile	Arg	Thr	Pro	Leu		
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Gly	Pro																

Arg Ala Val Arg Lys Asn Asp Leu Pro Leu Arg Ile Gln Met Asp Pro  
 660 665 670

Ile His Ile Gly  
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<210> 161  
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 <213> Corynebacterium glutamicum

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 <222> (101)..(2767)  
 <223> RXN00061

<400> 161  
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 Val Thr Glu Lys Thr  
 1 5  
 gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163  
 Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala  
 10 15 20  
 ttc ttt gct ttg ccg gct gag aat ttc tcc acg tcg ggc ggg cag gcc 211  
 Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala  
 25 30 35  
 acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259  
 Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys  
 40 45 50  
 gat gag cag cct act cat gtg gcg gtg gct ttc gat gtg ggg cgt aag 307  
 Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys  
 55 60 65  
 acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca 355  
 Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala  
 70 75 80 85  
 acg cca cct gag ttt aag ggc cag gtg gaa atc ctc aag gag gtg ttg 403  
 Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu  
 90 95 100  
 tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat 451  
 Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp  
 105 110 115  
 gat gtg atc gcc acg ttg tct gtg gcg gcg aaa cct tta ggc ttt aag 499  
 Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys  
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 acg ctg att gtt acg ggt gac cgt gat tcc ttc cag ttg gtc aat gac 547  
 Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp  
 135 140 145



acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt 595  
 Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg  
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 Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln  
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tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct 691  
 Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro  
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aat att cct ggc gtg ggc gag aag act gct acc aag tgg att gcc cag 739  
 Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr Lys Trp Ile Ala Gln  
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tat gaa act ttg gat aat ttg ctt gat cac gct gat gag atc aag ggc 787  
 Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala Asp Glu Ile Lys Gly  
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aag gtt ggc gcc agc ctg cgt gag cgc att gag cag gtc cgg atg aac 835  
 Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu Gln Val Arg Met Asn  
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cgc aag ctc acg gag atg gtg aag gat ctg gag ctg ccg ctt ggt ccg 883  
 Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu Leu Pro Leu Gly Pro  
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gac gat ttt gag atg aag cct gtg cag gtt gcg gag gtt gcg gcg aag 931  
 Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala Glu Val Ala Ala Lys  
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ttt gac gat ctg gag ttt ggt acc aat ttg cgt gag cgg gtg ctg gcg 979  
 Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg Glu Arg Val Leu Ala  
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 Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val Glu Glu Val Glu Ala  
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gaa cag gtt gtc gtc gat acg caa tct ttg gcg caa tgg ctg cct gct 1075  
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agg gct ggc cag gcg ctt gct tta gcg ctg gct gga gtg gct aaa cct 1123  
 Arg Ala Gly Gln Ala Leu Ala Leu Ala Gly Val Ala Lys Pro  
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gct gct ggc gac acg tat gcg cta gcg att gcg gat acc aag cgc cat 1171  
 Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala Asp Thr Lys Arg His  
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ctg gcc acg tgg ttg gcg tcg gaa gat cca aag atg ctg cac ggc gct 1267  
 Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys Met Leu His Gly Ala  
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aag gcc gcc tat cat atg ctc gct ggg cgc ggt ttt gag ctg cac ggc 1315

Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly Phe Glu Leu His Gly  
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 gtg gtg cat gac acg gcg atc gcg gca tac ttg ctg cgt ccg ggc caa 1363  
 Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu Leu Arg Pro Gly Gln  
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 cgc acc tat gag ctt gcc gac gtc tac cag cgg cat ctt caa cga cag 1411  
 Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg His Leu Gln Arg Gln  
 425 430 435  
 ttg tct aca aac gac aat ggc ggc cag ctc acg ctg ctc gac gca gct 1459  
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 Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala Ile Leu Glu Leu Ser  
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 His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu Ala Arg Met Glu Ala  
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 Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu Glu Gln Leu Lys Thr  
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 Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val Ala Pro Asp Gly Arg  
 600 605 610  
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 Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser Thr Gly Arg Leu Ser  
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 Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Glu Ala Gly

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Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu	650	655	660	
ctg act gcc gac tat tgc cag att gaa atg cgc gtg atg gct cac ctt				2131
Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu	665	670	675	
tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg				2179
Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu	680	685	690	
cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg				2227
His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val	695	700	705	
acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg				2275
Thr Pro Glu Leu Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val	710	715	720	725
tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct				2323
Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala	730	735	740	
ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga				2371
Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly	745	750	755	
gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc				2419
Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly	760	765	770	
tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc				2467
Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr	775	780	785	
tgc gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac				2515
Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn	790	795	800	805
gcc ccg att cag gga act gcc gca gac atc atc aag gtg gcc atg atc				2563
Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile	810	815	820	
cgg gtg gac cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg				2611
Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu	825	830	835	
ctt cag gtg cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg				2659
Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu	840	845	850	
gaa caa gtc cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag				2707
Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys	855	860	865	
ctg tcc gtt cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat				2755
Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp	870	875	880	885

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Ala Ala Ala His

2790

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<213> Corynebacterium glutamicum

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Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu  
35 40 45  
Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe  
50 55 60  
Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys  
65 70 75 80  
Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile  
85 90 95  
Leu Lys Glu Val Leu Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile  
100 105 110  
Asp Phe Glu Ala Asp Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys  
115 120 125  
Pro Leu Gly Phe Lys Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe  
130 135 140  
Gln Leu Val Asn Asp Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val  
145 150 155 160  
Ser Val Leu His Arg Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly  
165 170 175  
Leu Thr Pro Arg Gln Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr  
195 200 205  
Lys Trp Ile Ala Gln Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala  
210 215 220  
Asp Glu Ile Lys Gly Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu  
225 230 235 240  
Gln Val Arg Met Asn Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu  
245 250 255  
Leu Pro Leu Gly Pro Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala

260	265	270
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Glu Arg Val Leu Ala Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val 290 295 300		
Glu Glu Val Glu Ala Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala 305 310 315 320		
Gln Trp Leu Pro Ala Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala 325 330 335		
Gly Val Ala Lys Pro Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala 340 345 350		
Asp Thr Lys Arg His Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala 355 360 365		
Glu Asp Glu Lys Ala Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys 370 375 380		
Met Leu His Gly Ala Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly 385 390 395 400		
Phe Glu Leu His Gly Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu 405 410 415		
Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg 420 425 430		
His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr 435 440 445		
Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala 450 455 460		
Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln 465 470 475 480		
Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu 485 490 495		
Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu 500 505 510		
Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala 515 520 525		
Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys 530 535 540		
Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys 545 550 555 560		
Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu 565 570 575		
Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg 580 585 590		

Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val  
 595 600 605  
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser  
 610 615 620  
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val  
 625 630 635 640  
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu  
 645 650 655  
 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg  
 660 665 670  
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg  
 675 680 685  
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val  
 690 695 700  
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met  
 705 710 715 720  
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln  
 725 730 735  
 Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe  
 740 745 750  
 Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu  
 755 760 765  
 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr  
 770 775 780  
 Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu  
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 Arg Ala Ala Leu Asn Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile  
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 Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val  
 820 825 830  
 Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val  
 835 840 845  
 Ala Ala Gly Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met  
 850 855 860  
 Asp Asn Ala Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp  
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 Gly Val Asn Trp Asp Ala Ala Ala His  
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<213> *Corynebacterium glutamicum*

&lt;220&gt;

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&lt;222&gt; (101)..(2557)

&lt;223&gt; FRXA00060

&lt;400&gt; 163

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 Val Thr Glu Lys Thr  
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gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163  
 Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala  
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 Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala  
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acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259  
 Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys  
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gat gag cag cct act cat gtg gcg gtg gct ttc gat gtg ggg cgt aag 307  
 Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys  
 55 60 65

acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca 355  
 Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala  
 70 75 80 85

acg cca cct gag ttt aag ggc cag gtg gaa atc ctc aag gag gtg ttg 403  
 Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu  
 90 95 100

tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat 451  
 Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp  
 105 110 115

gat gtg atc gcc acg ttg tct gtg gcg gcg aaa cct tta ggc ttt aag 499  
 Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys  
 120 125 130

acg ctg att gtt acg ggt gac cgt gat tcc ttc cag ttg gtc aat gac 547  
 Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp  
 135 140 145

acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt 595  
 Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg  
 150 155 160 165

ttc acg ccg gaa gca gtg gag gag aag tat gga ctg aca ccg agg cag 643  
 Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln  
 170 175 180

tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct 691  
 Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro

185										190					195					
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Asn	Ile	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Thr	Lys	Trp	Ile	Ala	Gln					
200						205						210								
tat	gaa	act	ttg	gat	aat	ttg	ctt	gat	cac	gct	gat	gag	atc	aag	ggc	787				
Tyr	Glu	Thr	Leu	Asp	Asn	Leu	Leu	Asp	His	Ala	Asp	Glu	Ile	Lys	Gly					
215						220						225								
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Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu	Gln	Val	Arg	Met	Asn					
230						235						245								
cgc	aag	ctc	acg	gag	atg	gtg	aag	gat	ctg	gag	ctg	ccg	ctt	ggt	ccg	883				
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250									255			260								
gac	gat	ttt	gag	atg	aag	cct	gtg	cag	gtt	gcg	gag	gtt	gcg	gcg	aag	931				
Asp	Asp	Phe	Glu	Met	Lys	Pro	Val	Gln	Val	Ala	Glu	Val	Ala	Ala	Lys					
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gcg	gtg	ttg	gtt	gat	gtg	gct	gat	att	tca	gcg	gag	gat	gaa	aag	gcg	1219				
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ctg	gcc	acg	tgg	ttg	gcg	tgc	gaa	gat	cca	aag	atg	ctg	cac	ggc	gct	1267				
Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys	Met	Leu	His	Gly	Ala					
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Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu	Leu	Arg	Pro	Gly	Gln					
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cgc	acc	tat	gag	ctt	gcc	gac	gtc	tac	cag	cgg	cat	ctt	caa	cga	cag	1411				
Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg	His	Leu	Gln	Arg	Gln					
425						430						435								



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atc ggt atc gct gtt gat gtt gcc act ttg gaa gag cag ttg aag act Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu Glu Gln Leu Lys Thr 505 510 515	1651
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cga aag att cgt tcg gga ttc gtc gta ggc gag ggg tat gaa acc ttg Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu 650 655 660	2083
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 Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu  
 680 685 690

cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg 2227  
 His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val  
 695 700 705

acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg 2275  
 Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val  
 710 715 720 725

tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct 2323  
 Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala  
 730 735 740

ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga 2371  
 Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly  
 745 750 755

gta cag gcg tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc 2419  
 Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly  
 760 765 770

tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc 2467  
 Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr  
 775 780 785

tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac 2515  
 Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn  
 790 795 800 805

gcc ccg att agg gaa ctg ccg cag aca tca tca agg tgg cca 2557  
 Ala Pro Ile Arg Glu Leu Pro Gln Thr Ser Ser Arg Trp Pro  
 810 815

tgatccgggt ggaccgttca ctc 2580

&lt;210&gt; 164

&lt;211&gt; 819

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 164

Val Thr Glu Lys Thr Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser  
 1 5 10 15

Met Ala Phe Arg Ala Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr  
 20 25 30

Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu  
 35 40 45

Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe  
 50 55 60

Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys  
 65 70 75 80

Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile

[illegible]

Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg  
 420 425 430  
 His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr  
 435 440 445  
 Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala  
 450 455 460  
 Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln  
 465 470 475 480  
 Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu  
 485 490 495  
 Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu  
 500 505 510  
 Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala  
 515 520 525  
 Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys  
 530 535 540  
 Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys  
 545 550 555 560  
 Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Glu Ile Glu Ala Leu  
 565 570 575  
 Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg  
 580 585 590  
 Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val  
 595 600 605  
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser  
 610 615 620  
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val  
 625 630 635 640  
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu  
 645 650 655  
 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg  
 660 665 670  
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg  
 675 680 685  
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val  
 690 695 700  
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met  
 705 710 715 720  
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln  
 725 730 735

Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe  
           740                          745                          750  
 Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu  
           755                          760                          765  
 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr  
           770                          775                          780  
 Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu  
           785                          790                          795                          800  
 Arg Ala Ala Leu Asn Ala Pro Ile Arg Glu Leu Pro Gln Thr Ser Ser  
                           805                          810                          815  
 Arg Trp Pro

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 <211> 333  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(310)  
 <223> FRXA00061

<400> 165  
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 ccccgattag ggaactgccg cagacatcat caaggtggcc atg atc cgg gtg gac 115  
   Met Ile Arg Val Asp  
   1                          5  
 cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg ctt cag gtg 163  
 Arg Ser Leu Lys Glu Ala Val Lys Ser Arg Val Leu Leu Gln Val  
                           10                          15                          20  
 cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg gaa caa gtc 211  
 His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu Glu Gln Val  
                           25                          30                          35  
 cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag ctg tcc gtt 259  
 Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys Leu Ser Val  
                           40                          45                          50  
 cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat gct gca gcg 307  
 Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp Ala Ala Ala  
                           55                          60                          65  
 cac taagaggtaa ctgccttttc gtc 333  
 His  
           70

<210> 166  
 <211> 70  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 166

Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg  
 1 5 10 15

Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly  
 20 25 30

Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala  
 35 40 45

Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn  
 50 55 60

Trp Asp Ala Ala Ala His  
 65 70

&lt;210&gt; 167

&lt;211&gt; 3705

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3682)

&lt;223&gt; RXA02657

&lt;400&gt; 167

tatgcgagta cgccgaaaat catagctggt accttataacc taggttagaa aagccgagat 60

caatgcggtta atgaaatagg agtttcacgg gtgtaaggag atg gct aga ctg tcc 115  
 Met Ala Arg Leu Ser  
 1 5

cac atg gcc aag caa tcc tca ttt gta cat ctt cac aac cac acc gag 163  
 His Met Ala Lys Gln Ser Ser Phe Val His Leu His Asn His Thr Glu  
 10 15 20

ttt tcc atg ctt gat gga atg gcc aag atc gat atg ttg gcc gat gag 211  
 Phe Ser Met Leu Asp Gly Met Ala Lys Ile Asp Met Leu Ala Asp Glu  
 25 30 35

gtt aaa gcc cag gga atg cct gcg gtc gga atc acc gac cac ggc aat 259  
 Val Lys Ala Gln Gly Met Pro Ala Val Gly Ile Thr Asp His Gly Asn  
 40 45 50

atg tat ggc tcc aac ccc ttt tat cgc aag atg aca gag atg ggc att 307  
 Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met Thr Glu Met Gly Ile  
 55 60 65

aag ccc atc att ggc att gaa acg tat atg gca cct gag tct cgt ttt 355  
 Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala Pro Glu Ser Arg Phe  
 70 75 80 85

aag aaa gag cgt gtg cgt tgg ggc gaa cca cac caa aaa tca gat gat 403  
 Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His Gln Lys Ser Asp Asp  
 90 95 100

gtt tct ggt tcc ggt gcg tat ttg cac cag acg atg ctt gca gaa aac 451  
 Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr Met Leu Ala Glu Asn

105	110	115	
acc aca ggt tta aga aac ctc ttt tat cta tct tcg atg gca tcg tac			499
Thr Thr Gly Leu Arg Asn Leu Phe Tyr Leu Ser Ser Met Ala Ser Tyr			
120	125	130	
gaa ggc cag cta ggc aag tgg ccc cgc atg gac gcc gat atc atc gct			547
Glu Gly Gln Leu Gly Lys Trp Pro Arg Met Asp Ala Asp Ile Ile Ala			
135	140	145	
gag cac gcc gaa ggc atc atc gcc acc acg ggt tgc cct tcc ggc gat			595
Glu His Ala Glu Gly Ile Ile Ala Thr Thr Gly Cys Pro Ser Gly Asp			
150	155	160	165
gtg caa aca cgc ctg cgc ttg ggc cag ttc gac gaa gcc ctt gaa gca			643
Val Gln Thr Arg Leu Arg Leu Gly Gln Phe Asp Glu Ala Leu Glu Ala			
170	175	180	
gcc gcc atg tgg cag gac atc tat ggt cgc gac aac tac ttc ctc gag			691
Ala Ala Met Trp Gln Asp Ile Tyr Gly Arg Asp Asn Tyr Phe Leu Glu			
185	190	195	
ttg atg gac cac ggg ctc gac att gaa acc cgt gtg cgc agt gag ctg			739
Leu Met Asp His Gly Leu Asp Ile Glu Thr Arg Val Arg Ser Glu Leu			
200	205	210	
ctc gaa atc gga cgc aag ctc aat ttg cca ccc ctg gtc acc aac gac			787
Leu Glu Ile Gly Arg Lys Leu Asn Leu Pro Pro Leu Val Thr Asn Asp			
215	220	225	
tgc cac tat gtg ctg gaa tct cag gcg caa gcc cac gag gca atg ctc			835
Cys His Tyr Val Leu Glu Ser Gln Ala Gln Ala His Glu Ala Met Leu			
230	235	240	245
tgc gtg caa aca ggc aag acg ctt cat gat gaa gac cga ttc aaa ttc			883
Cys Val Gln Thr Gly Lys Thr Leu His Asp Glu Asp Arg Phe Lys Phe			
250	255	260	
ggc gga acc ggc tat tac gtt aaa tct gca gaa caa atg cgt gca ctc			931
Gly Gly Thr Gly Tyr Tyr Val Lys Ser Ala Glu Gln Met Arg Ala Leu			
265	270	275	
tgg gac gac atg gtt cca gat ggc tgc gac aac acc ctg tgg atc gct			979
Trp Asp Asp Met Val Pro Asp Gly Cys Asp Asn Thr Leu Trp Ile Ala			
280	285	290	
gaa cgt gtg cag tcc tat gac gaa atc tgg gaa gaa cac tca cac gac			1027
Glu Arg Val Gln Ser Tyr Asp Glu Ile Trp Glu Glu His Ser His Asp			
295	300	305	
cgc atg cct atc gct gat gtt cca gaa ggc tac acc cca acc act tgg			1075
Arg Met Pro Ile Ala Asp Val Pro Glu Gly Tyr Thr Pro Thr Thr Trp			
310	315	320	325
ttg cac cat gaa gtg atg gct ggc ttg gag gat cgt ttc tct gga cag			1123
Leu His His Glu Val Met Ala Gly Leu Glu Asp Arg Phe Ser Gly Gln			
330	335	340	
caa gtt cct gag gat tat att gag cgc gcg gag tat gag atc tcc gtt			1171
Gln Val Pro Glu Asp Tyr Ile Glu Arg Ala Glu Tyr Glu Ile Ser Val			
345	350	355	

att gat atg aag ggc tac cct tcc tac ttc ctc atc gtt gct gaa att 1219  
 Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu Ile Val Ala Glu Ile  
 360 365 370

atc aag cac gct cgt tcc att ggc atc cgt gta gga cct ggc cgt ggt 1267  
 Ile Lys His Ala Arg Ser Ile Gly Ile Arg Val Gly Pro Gly Arg Gly  
 375 380 385

tcg gct gca ggt gca ttg gtt gcc tac gcg ttg acc atc acc aac att 1315  
 Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu Thr Ile Thr Asn Ile  
 390 395 400 405

gac ccc atg gaa cac gga ttg ctg ttc gag aga ttc ctc aac cca gaa 1363  
 Asp Pro Met Glu His Gly Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu  
 410 415 420

cga cca tcc gca ccc gat atc gat att gac ttc gat gat cgc cgc cgc 1411  
 Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe Asp Asp Arg Arg Arg  
 425 430 435

ggt gaa atg atc cgt tac gca gct gac cgt tgg ggc gag gac aag att 1459  
 Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp Gly Glu Asp Lys Ile  
 440 445 450

gct cag gtg atc acc ttc ggt acg gtg aaa aca aag cag gca ctg aaa 1507  
 Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr Lys Gln Ala Leu Lys  
 455 460 465

gac tcc gcc cgt gtg caa atg ggg cag cca ggc tat caa atc gct gac 1555  
 Asp Ser Ala Arg Val Gln Met Gly Gln Pro Gly Tyr Gln Ile Ala Asp  
 470 475 480 485

cgc gtg atc aag gag ctt cca cct gcc att atg gcg aag gat att ccg 1603  
 Arg Val Ile Lys Glu Leu Pro Pro Ala Ile Met Ala Lys Asp Ile Pro  
 490 495 500

ttg tcc ggt atc acc gat ccg gat cac cct cgt ttt aat gaa gca ggt 1651  
 Leu Ser Gly Ile Thr Asp Pro Asp His Pro Arg Phe Asn Glu Ala Gly  
 505 510 515

gcg gtg cgc cag ctg atc gaa acc gac cct gat gtg aag cgc att tac 1699  
 Ala Val Arg Gln Leu Ile Glu Thr Asp Pro Asp Val Lys Arg Ile Tyr  
 520 525 530

gac acc gct cgt ggt ttg gaa ggc gtg gtg cgc caa tct ggc gtg cac 1747  
 Asp Thr Ala Arg Gly Leu Glu Gly Val Val Arg Gln Ser Gly Val His  
 535 540 545

gcg tgt gcc gtg att atg tct tct gta ccg ctg ctg gac tgc att ccg 1795  
 Ala Cys Ala Val Ile Met Ser Ser Val Pro Leu Leu Asp Cys Ile Pro  
 550 555 560 565

atg tgg aag cgg cca gcc gac ggc gca ctg att aca ggc tgg gat tac 1843  
 Met Trp Lys Arg Pro Ala Asp Gly Ala Leu Ile Thr Gly Trp Asp Tyr  
 570 575 580

cca gca tgt gag gcc att ggc ctg ttg aag atg gac ttc ctg gga ctt 1891  
 Pro Ala Cys Glu Ala Ile Gly Leu Leu Lys Met Asp Phe Leu Gly Leu  
 585 590 595



cga aac ctt acc gtt att ggc gat gcg att gaa aac att aag gcc aac 1939  
 Arg Asn Leu Thr Val Ile Gly Asp Ala Ile Glu Asn Ile Lys Ala Asn  
 600 605 610

cgc gat ggg gaa gtg ctt gat cta gaa aac cta gcg atc gag gat gaa 1987  
 Arg Asp Gly Glu Val Leu Asp Leu Glu Asn Leu Ala Ile Glu Asp Glu  
 615 620 625

gaa acc tac aag ctg cta ggc cgt gga gaa acc ctt ggt gtg ttc cag 2035  
 Glu Thr Tyr Lys Leu Leu Gly Arg Gly Glu Thr Leu Gly Val Phe Gln  
 630 635 640 645

ctt gat ggt ggt ggc atg cag gag ctg ctg aag cgt atg cag cca acc 2083  
 Leu Asp Gly Gly Gly Met Gln Glu Leu Leu Lys Arg Met Gln Pro Thr  
 650 655 660

ggc ttc aat gac atc gtc gca gcg ctt gcg ctg tat cgc cca ggc ccc 2131  
 Gly Phe Asn Asp Ile Val Ala Ala Leu Ala Leu Tyr Arg Pro Gly Pro  
 665 670 675

atg ggt gtg aac gcg cac tgg gat tac gcc gac cgt aaa aac gga cgc 2179  
 Met Gly Val Asn Ala His Trp Asp Tyr Ala Asp Arg Lys Asn Gly Arg  
 680 685 690

aag ccc att act cca att cac cca gag ttg gag gaa gct ctg gaa gaa 2227  
 Lys Pro Ile Thr Pro Ile His Pro Glu Leu Glu Glu Ala Leu Glu Glu  
 695 700 705

atc ctt ggt gaa acc tat ggt ctg att gtg tac cag gag cag atc atg 2275  
 Ile Leu Gly Glu Thr Tyr Gly Leu Ile Val Tyr Gln Glu Gln Ile Met  
 710 715 720 725

agg atc tcc cag aag gtc gca aac tac acc gct ggt caa gca gat ggt 2323  
 Arg Ile Ser Gln Lys Val Ala Asn Tyr Thr Ala Gly Gln Ala Asp Gly  
 730 735 740

ttc cgt aaa gcc atg ggt aag aag aag ccc gag gtc ctg gaa aag gag 2371  
 Phe Arg Lys Lys Ala Met Gly Lys Lys Lys Pro Glu Val Leu Glu Lys Glu  
 745 750 755

ttc gca aac ttc gaa ggt gga atg aag gcg aac ggc tat tca gat gcc 2419  
 Phe Ala Asn Phe Glu Gly Gly Met Lys Ala Asn Gly Tyr Ser Asp Ala  
 760 765 770

gcg att aag act ttg tgg gat acc att ctg ccg ttc gcc ggc tac gcg 2467  
 Ala Ile Lys Thr Leu Trp Asp Thr Ile Leu Pro Phe Ala Gly Tyr Ala  
 775 780 785

ttc aac aag tct cac gcc gca ggt tat gga ctt gta tcc ttc tgg act 2515  
 Phe Asn Lys Ser His Ala Ala Gly Tyr Gly Leu Val Ser Phe Trp Thr  
 790 795 800 805

gcc tat ttg aag gcg cac tac gcg ccg gaa tac atg gca gca ctg ctg 2563  
 Ala Tyr Leu Lys Ala His Tyr Ala Pro Glu Tyr Met Ala Ala Leu Leu  
 810 815 820

act tct gtg ggt gat aac aag gac aaa tcg gcg atc tac ctt tct gat 2611  
 Thr Ser Val Gly Asp Asn Lys Asp Lys Ser Ala Ile Tyr Leu Ser Asp  
 825 830 835

tgc cga cac ctt gga att cga gtg ctt tcg ccg gat att aac gag tcc 2659

Cys	Arg	His	Leu	Gly	Ile	Arg	Val	Leu	Ser	Pro	Asp	Ile	Asn	Glu	Ser		
		840					845					850					
tcg	ttg	aac	ttc	ctt	cct	gtt	ggc	acc	gat	att	cgc	tat	ggc	ctg	gga	2707	
Ser	Leu	Asn	Phe	Leu	Pro	Val	Gly	Thr	Asp	Ile	Arg	Tyr	Gly	Leu	Gly		
		855				860					865						
gcc	att	aga	aac	gtg	ggg	gct	gaa	gtt	gtg	gat	tcc	att	ttg	gat	acc	2755	
Ala	Ile	Arg	Asn	Val	Gly	Ala	Glu	Val	Val	Asp	Ser	Ile	Leu	Asp	Thr		
870					875					880					885		
cgc	aag	gaa	aag	ggc	cta	ttt	aag	gac	ttc	tca	gac	tac	ttg	gac	aag	2803	
Arg	Lys	Glu	Lys	Gly	Leu	Phe	Lys	Asp	Phe	Ser	Asp	Tyr	Leu	Asp	Lys		
				890				895							900		
atc	gat	acc	ctg	ccg	tgt	aac	aag	cgc	atc	acc	gag	tct	ttg	atc	aag	2851	
Ile	Asp	Thr	Leu	Pro	Cys	Asn	Lys	Arg	Ile	Thr	Glu	Ser	Leu	Ile	Lys		
			905					910						915			
ggg	ggc	gct	ttt	gac	tcc	ctt	gga	cac	gca	cga	aaa	ggc	ctc	atg	ctg	2899	
Gly	Gly	Ala	Phe	Asp	Ser	Leu	Gly	His	Ala	Arg	Lys	Gly	Leu	Met	Leu		
			920				925						930				
gtc	ttc	gaa	gat	gcc	gtt	gat	tcc	gtc	atc	gct	acc	aaa	aaa	gct	gct	2947	
Val	Phe	Glu	Asp	Ala	Val	Asp	Ser	Val	Ile	Ala	Thr	Lys	Lys	Ala	Ala		
		935				940					945						
gac	aag	gga	caa	ttt	gat	ctc	ttt	gca	gct	ttc	gac	tcg	gat	aac	aac	2995	
Asp	Lys	Gly	Gln	Phe	Asp	Leu	Phe	Ala	Ala	Phe	Asp	Ser	Asp	Asn	Asn		
		950			955					960					965		
gac	gat	gtg	gca	agt	ttc	ttc	cag	atc	acc	gtt	cct	gat	gac	gaa	tgg	3043	
Asp	Asp	Val	Ala	Ser	Phe	Phe	Gln	Ile	Thr	Val	Pro	Asp	Asp	Glu	Trp		
				970					975						980		
gac	cgt	aag	cat	gag	ctc	gca	ctc	gag	cga	gaa	atg	ctg	ggg	ctg	tat	3091	
Asp	Arg	Lys	His	Glu	Leu	Ala	Leu	Glu	Arg	Glu	Met	Leu	Gly	Leu	Tyr		
			985					990						995			
gtt	tct	gga	cac	cca	ctc	gat	ggc	tat	gaa	gat	gcc	att	gct	gcc	cag	3139	
Val	Ser	Gly	His	Pro	Leu	Asp	Gly	Tyr	Glu	Asp	Ala	Ile	Ala	Ala	Gln		
		1000					1005						1010				
gtt	gat	aca	gca	ctg	acc	acc	att	gtt	gcc	ggg	gaa	ctc	aag	cac	ggc	3187	
Val	Asp	Thr	Ala	Leu	Thr	Thr	Ile	Val	Ala	Gly	Glu	Leu	Lys	His	Gly		
		1015					1020					1025					
gca	gaa	gtg	acc	gtg	ggg	ggc	att	atc	tct	ggg	gtg	gat	cga	cgg	ttc	3235	
Ala	Glu	Val	Thr	Val	Gly	Gly	Ile	Ile	Ser	Gly	Val	Asp	Arg	Arg	Phe		
1030					1035					1040					1045		
tcc	aag	aag	gac	ggg	tcc	cct	tgg	gcg	att	gtc	acc	att	gaa	gat	cac	3283	
Ser	Lys	Lys	Asp	Gly	Ser	Pro	Trp	Ala	Ile	Val	Thr	Ile	Glu	Asp	His		
			1050					1055						1060			
aac	ggc	gcg	tcc	gtt	gaa	ttg	ttg	gtc	ttc	aac	aag	gtg	tat	tcc	atc	3331	
Asn	Gly	Ala	Ser	Val	Glu	Leu	Leu	Val	Phe	Asn	Lys	Val	Tyr	Ser	Ile		
			1065					1070					1075				
gtt	gga	tcc	atg	att	gtg	gaa	gac	aac	atc	atc	ttg	gcc	aag	gca	cac	3379	
Val	Gly	Ser	Met	Ile	Val	Glu	Asp	Asn	Ile	Ile	Leu	Ala	Lys	Ala	His		

1080	1085	1090	
atc tcc att cga gat gat cgt atg agc ctt ttc tgt gat gat ctc cgc			3427
Ile Ser Ile Arg Asp Asp Arg Met Ser Leu Phe Cys Asp Asp Leu Arg			
1095	1100	1105	
ggt cca gag ctt ggg cca gga aac ggg caa gga ctt ccg ctt cgt ttg			3475
Val Pro Glu Leu Gly Pro Gly Asn Gly Gln Gly Leu Pro Leu Arg Leu			
1110	1115	1120	1125
tcc atg cgt act gat cag tgc acc atg tcc aac att gcc aag ctc aag			3523
Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn Ile Ala Lys Leu Lys			
1130	1135	1140	
cag gtg ctg gtg gac aac aag ggt gaa tct gat gtg tac ctc aat ttg			3571
Gln Val Leu Val Asp Asn Lys Gly Glu Ser Asp Val Tyr Leu Asn Leu			
1145	1150	1155	
atc gat ggg gat aac tcc acg gtc atg att ttg ggt gat cac tta aga			3619
Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu Gly Asp His Leu Arg			
1160	1165	1170	
gtc aac cga tcc gca agt ttg atg ggc gac ctc aag gca acg atg ggg			3667
Val Asn Arg Ser Ala Ser Leu Met Gly Asp Leu Lys Ala Thr Met Gly			
1175	1180	1185	
cca ggc atc ctc ggt taatcacatc acactgggat tac			3705
Pro Gly Ile Leu Gly			
1190			
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<211> 1194			
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<213> Corynebacterium glutamicum			
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Met Ala Arg Leu Ser His Met Ala Lys Gln Ser Ser Phe Val His Leu			
1	5	10	15
His Asn His Thr Glu Phe Ser Met Leu Asp Gly Met Ala Lys Ile Asp			
20	25	30	
Met Leu Ala Asp Glu Val Lys Ala Gln Gly Met Pro Ala Val Gly Ile			
35	40	45	
Thr Asp His Gly Asn Met Tyr Gly Ser Asn Pro Phe Tyr Arg Lys Met			
50	55	60	
Thr Glu Met Gly Ile Lys Pro Ile Ile Gly Ile Glu Thr Tyr Met Ala			
65	70	75	80
Pro Glu Ser Arg Phe Lys Lys Glu Arg Val Arg Trp Gly Glu Pro His			
85	90	95	
Gln Lys Ser Asp Val Ser Gly Ser Gly Ala Tyr Leu His Gln Thr			
100	105	110	
Met Leu Ala Glu Asn Thr Thr Gly Leu Arg Asn Leu Phe Tyr Leu Ser			
115	120	125	

Ser Met Ala Ser Tyr Glu Gly Gln Leu Gly Lys Trp Pro Arg Met Asp  
 130 135 140  
 Ala Asp Ile Ile Ala Glu His Ala Glu Gly Ile Ile Ala Thr Thr Gly  
 145 150 155 160  
 Cys Pro Ser Gly Asp Val Gln Thr Arg Leu Arg Leu Gly Gln Phe Asp  
 165 170 175  
 Glu Ala Leu Glu Ala Ala Ala Met Trp Gln Asp Ile Tyr Gly Arg Asp  
 180 185 190  
 Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Asp Ile Glu Thr Arg  
 195 200 205  
 Val Arg Ser Glu Leu Leu Glu Ile Gly Arg Lys Leu Asn Leu Pro Pro  
 210 215 220  
 Leu Val Thr Asn Asp Cys His Tyr Val Leu Glu Ser Gln Ala Gln Ala  
 225 230 235 240  
 His Glu Ala Met Leu Cys Val Gln Thr Gly Lys Thr Leu His Asp Glu  
 245 250 255  
 Asp Arg Phe Lys Phe Gly Gly Thr Gly Tyr Tyr Val Lys Ser Ala Glu  
 260 265 270  
 Gln Met Arg Ala Leu Trp Asp Asp Met Val Pro Asp Gly Cys Asp Asn  
 275 280 285  
 Thr Leu Trp Ile Ala Glu Arg Val Gln Ser Tyr Asp Glu Ile Trp Glu  
 290 295 300  
 Glu His Ser His Asp Arg Met Pro Ile Ala Asp Val Pro Glu Gly Tyr  
 305 310 315 320  
 Thr Pro Thr Thr Trp Leu His His Glu Val Met Ala Gly Leu Glu Asp  
 325 330 335  
 Arg Phe Ser Gly Gln Gln Val Pro Glu Asp Tyr Ile Glu Arg Ala Glu  
 340 345 350  
 Tyr Glu Ile Ser Val Ile Asp Met Lys Gly Tyr Pro Ser Tyr Phe Leu  
 355 360 365  
 Ile Val Ala Glu Ile Ile Lys His Ala Arg Ser Ile Gly Ile Arg Val  
 370 375 380  
 Gly Pro Gly Arg Gly Ser Ala Ala Gly Ala Leu Val Ala Tyr Ala Leu  
 385 390 395 400  
 Thr Ile Thr Asn Ile Asp Pro Met Glu His Gly Leu Leu Phe Glu Arg  
 405 410 415  
 Phe Leu Asn Pro Glu Arg Pro Ser Ala Pro Asp Ile Asp Ile Asp Phe  
 420 425 430  
 Asp Asp Arg Arg Arg Gly Glu Met Ile Arg Tyr Ala Ala Asp Arg Trp  
 435 440 445  
 Gly Glu Asp Lys Ile Ala Gln Val Ile Thr Phe Gly Thr Val Lys Thr

450	455	460
Lys Gln Ala Leu Lys Asp Ser Ala Arg Val Gln Met Gly Gln Pro Gly 465	470	475 480
Tyr Gln Ile Ala Asp Arg Val Ile Lys Glu Leu Pro Pro Ala Ile Met 485	490	495
Ala Lys Asp Ile Pro Leu Ser Gly Ile Thr Asp Pro Asp His Pro Arg 500	505	510
Phe Asn Glu Ala Gly Ala Val Arg Gln Leu Ile Glu Thr Asp Pro Asp 515	520	525
Val Lys Arg Ile Tyr Asp Thr Ala Arg Gly Leu Glu Gly Val Val Arg 530	535	540
Gln Ser Gly Val His Ala Cys Ala Val Ile Met Ser Ser Val Pro Leu 545	550	555 560
Leu Asp Cys Ile Pro Met Trp Lys Arg Pro Ala Asp Gly Ala Leu Ile 565	570	575
Thr Gly Trp Asp Tyr Pro Ala Cys Glu Ala Ile Gly Leu Leu Lys Met 580	585	590
Asp Phe Leu Gly Leu Arg Asn Leu Thr Val Ile Gly Asp Ala Ile Glu 595	600	605
Asn Ile Lys Ala Asn Arg Asp Gly Glu Val Leu Asp Leu Glu Asn Leu 610	615	620
Ala Ile Glu Asp Glu Glu Thr Tyr Lys Leu Leu Gly Arg Gly Glu Thr 625	630	635 640
Leu Gly Val Phe Gln Leu Asp Gly Gly Gly Met Gln Glu Leu Leu Lys 645	650	655
Arg Met Gln Pro Thr Gly Phe Asn Asp Ile Val Ala Ala Leu Ala Leu 660	665	670
Tyr Arg Pro Gly Pro Met Gly Val Asn Ala His Trp Asp Tyr Ala Asp 675	680	685
Arg Lys Asn Gly Arg Lys Pro Ile Thr Pro Ile His Pro Glu Leu Glu 690	695	700
Glu Ala Leu Glu Glu Ile Leu Gly Glu Thr Tyr Gly Leu Ile Val Tyr 705	710	715 720
Gln Glu Gln Ile Met Arg Ile Ser Gln Lys Val Ala Asn Tyr Thr Ala 725	730	735
Gly Gln Ala Asp Gly Phe Arg Lys Ala Met Gly Lys Lys Lys Pro Glu 740	745	750
Val Leu Glu Lys Glu Phe Ala Asn Phe Glu Gly Gly Met Lys Ala Asn 755	760	765
Gly Tyr Ser Asp Ala Ala Ile Lys Thr Leu Trp Asp Thr Ile Leu Pro 770	775	780

Phe Ala Gly Tyr Ala Phe Asn Lys Ser His Ala Ala Gly Tyr Gly Leu  
 785 790 795 800  
 Val Ser Phe Trp Thr Ala Tyr Leu Lys Ala His Tyr Ala Pro Glu Tyr  
 805 810 815  
 Met Ala Ala Leu Leu Thr Ser Val Gly Asp Asn Lys Asp Lys Ser Ala  
 820 825 830  
 Ile Tyr Leu Ser Asp Cys Arg His Leu Gly Ile Arg Val Leu Ser Pro  
 835 840 845  
 Asp Ile Asn Glu Ser Ser Leu Asn Phe Leu Pro Val Gly Thr Asp Ile  
 850 855 860  
 Arg Tyr Gly Leu Gly Ala Ile Arg Asn Val Gly Ala Glu Val Val Asp  
 865 870 875 880  
 Ser Ile Leu Asp Thr Arg Lys Glu Lys Gly Leu Phe Lys Asp Phe Ser  
 885 890 895  
 Asp Tyr Leu Asp Lys Ile Asp Thr Leu Pro Cys Asn Lys Arg Ile Thr  
 900 905 910  
 Glu Ser Leu Ile Lys Gly Gly Ala Phe Asp Ser Leu Gly His Ala Arg  
 915 920 925  
 Lys Gly Leu Met Leu Val Phe Glu Asp Ala Val Asp Ser Val Ile Ala  
 930 935 940  
 Thr Lys Lys Ala Ala Asp Lys Gly Gln Phe Asp Leu Phe Ala Ala Phe  
 945 950 955 960  
 Asp Ser Asp Asn Asn Asp Asp Val Ala Ser Phe Phe Gln Ile Thr Val  
 965 970 975  
 Pro Asp Asp Glu Trp Asp Arg Lys His Glu Leu Ala Leu Glu Arg Glu  
 980 985 990  
 Met Leu Gly Leu Tyr Val Ser Gly His Pro Leu Asp Gly Tyr Glu Asp  
 995 1000 1005  
 Ala Ile Ala Ala Gln Val Asp Thr Ala Leu Thr Thr Ile Val Ala Gly  
 1010 1015 1020  
 Glu Leu Lys His Gly Ala Glu Val Thr Val Gly Gly Ile Ile Ser Gly  
 1025 1030 1035 1040  
 Val Asp Arg Arg Phe Ser Lys Lys Asp Gly Ser Pro Trp Ala Ile Val  
 1045 1050 1055  
 Thr Ile Glu Asp His Asn Gly Ala Ser Val Glu Leu Leu Val Phe Asn  
 1060 1065 1070  
 Lys Val Tyr Ser Ile Val Gly Ser Met Ile Val Glu Asp Asn Ile Ile  
 1075 1080 1085  
 Leu Ala Lys Ala His Ile Ser Ile Arg Asp Asp Arg Met Ser Leu Phe  
 1090 1095 1100

Cys Asp Asp Leu Arg Val Pro Glu Leu Gly Pro Gly Asn Gly Gln Gly  
1105 1110 1115 1120

Leu Pro Leu Arg Leu Ser Met Arg Thr Asp Gln Cys Thr Met Ser Asn  
1125 1130 1135

Ile Ala Lys Leu Lys Gln Val Leu Val Asp Asn Lys Gly Glu Ser Asp  
1140 1145 1150

Val Tyr Leu Asn Leu Ile Asp Gly Asp Asn Ser Thr Val Met Ile Leu  
1155 1160 1165

Gly Asp His Leu Arg Val Asn Arg Ser Ala Ser Leu Met Gly Asp Leu  
1170 1175 1180

Lys Ala Thr Met Gly Pro Gly Ile Leu Gly  
1185 1190

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<211> 1524

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1501)

<223> RXA01238

<400> 169

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aggggtggtgt ccattgattc agatcgaaag gaccacacct gtg atc gcg gct tac 115  
Val Ile Ala Ala Tyr  
1 5

ggc gca tcc atc tct ttg gat gat tcc acc ctc acc atc tct tat tcc 163  
Gly Ala Ser Ile Ser Leu Asp Asp Ser Thr Leu Thr Ile Ser Tyr Ser  
10 15 20

cct ctt ctt gct gct ctt tct aag tcc agc gca caa tcg gaa tcg gtt 211  
Pro Leu Leu Ala Ala Leu Ser Lys Ser Ser Ala Gln Ser Glu Ser Val  
25 30 35

gat ctg aca cag gtc tct gga gta tct gtg cag gat ccc act gct ttt 259  
Asp Leu Thr Gln Val Ser Gly Val Ser Val Gln Asp Pro Thr Ala Phe  
40 45 50

act cac ggc ttt tta aac ctg gag ggc gtg gat aaa tcc atc gcc ttt 307  
Thr His Gly Phe Leu Asn Leu Glu Gly Val Asp Lys Ser Ile Ala Phe  
55 60 65

gcc cca aat agt tcg gca gat tta gct gcg ctg gca gct gat att gat 355  
Ala Pro Asn Ser Ser Ala Asp Leu Ala Ala Leu Ala Ala Asp Ile Asp  
70 75 80 85

gct gtg ttg aag ggt gaa aag cca cag cac ctg ggt ggc gga gcc cca 403  
Ala Val Leu Lys Gly Glu Lys Pro Gln His Leu Gly Gly Gly Ala Pro  
90 95 100

gta gtg cct tca gct cca tct act gtt gct ggt ctg aat ttc gtg ggc 451

Val Val Pro Ser Ala Pro Ser Thr Val Ala Gly Leu Asn Phe Val Gly	
105 110 115	
ttt gac gta gag acg gcc aat gat gat tgg ggt tcc atc tgc cag att	499
Phe Asp Val Glu Thr Ala Asn Asp Asp Trp Gly Ser Ile Cys Gln Ile	
120 125 130	
ggt ttg gtc aag tac gtc gat ggt gtg gag gaa tct tgc gag tca tgg	547
Gly Leu Val Lys Tyr Val Asp Gly Val Glu Glu Ser Ser Glu Ser Trp	
135 140 145	
ttg tgt act cct cct gag agc ctg aat ttc ttc aat gag atc aac att	595
Leu Cys Thr Pro Pro Glu Ser Leu Asn Phe Phe Asn Glu Ile Asn Ile	
150 155 160 165	
ggt att cac ggc atc acc cca gag atg gtt gct gat cag cct cgt ttt	643
Gly Ile His Gly Ile Thr Pro Glu Met Val Ala Asp Gln Pro Arg Phe	
170 175 180	
gca gac ctt gtg ccc aag atg gtg gag ttc gtt ggg gat ttg ccg ttg	691
Ala Asp Leu Val Pro Lys Met Val Glu Phe Val Gly Asp Leu Pro Leu	
185 190 195	
gtt gct cac aat gcg cag ttt gat ttc acc gca ttg tgc cgc gcg tgt	739
Val Ala His Asn Ala Gln Phe Asp Phe Thr Ala Leu Ser Arg Ala Cys	
200 205 210	
gct gcc tca ggg atc gat gtc cca gag atg att tat ggc tgc tgc ttg	787
Ala Ala Ser Gly Ile Asp Val Pro Glu Met Ile Tyr Gly Cys Ser Leu	
215 220 225	
acg ttg gca cgc aat gag aag ctg cag gtg gaa aac cat aag ctt cca	835
Thr Leu Ala Arg Asn Glu Lys Leu Gln Val Glu Asn His Lys Leu Pro	
230 235 240 245	
acg gtg gct agt cat tta ggg ttt gag ctg aaa aac cac cac gat gct	883
Thr Val Ala Ser His Leu Gly Phe Glu Leu Lys Asn His His Asp Ala	
250 255 260	
gct gaa gat gct cgc gcg tgt gct gcg att acc att gcg ttg gca aag	931
Ala Glu Asp Ala Arg Ala Cys Ala Ala Ile Thr Ile Ala Leu Ala Lys	
265 270 275	
cgc cac agc ttt gag ggc agc ttt gtg gat ttc gtt cac agc cgt ggt	979
Arg His Ser Phe Glu Gly Ser Phe Val Asp Phe Val His Ser Arg Gly	
280 285 290	
ttc acc atg gga acc gtg gat aac gcc cgg gtg tat ccg gtg ctg aag	1027
Phe Thr Met Gly Thr Val Asp Asn Ala Arg Val Tyr Pro Val Leu Lys	
295 300 305	
gat cgt tct gga gct aac gtt gcg ttg cag cgt cga aac ttt ggt ttg	1075
Asp Arg Ser Gly Ala Asn Val Ala Leu Gln Arg Arg Asn Phe Gly Leu	
310 315 320 325	
gat gca ggc aag acc gaa gtc ccc gtg cag cca gct gtt gat cca gcg	1123
Asp Ala Gly Lys Thr Glu Val Pro Val Gln Pro Ala Val Asp Pro Ala	
330 335 340	
tgg gaa acc ccg aag gcg gag cca aaa aag caa tct ggc cgc cgt gca	1171
Trp Glu Thr Pro Lys Ala Glu Pro Lys Lys Gln Ser Gly Arg Arg Ala	



345	350	355	
ccg tgg gac aag gtg gct acc cct gag gtc att cca gat ccc aat ccc			1219
Pro Trp Asp Lys Val Ala Thr Pro Glu Val Ile Pro Asp Pro Asn Pro			
360	365	370	
gat gct gat ccg tcg agc att ctc tat ggc cag aat gtg acc ttg act			1267
Asp Ala Asp Pro Ser Ser Ile Leu Tyr Gly Gln Asn Val Thr Leu Thr			
375	380	385	
ggg gat ttc gag cca tat gaa aag ggt gcg ctg tgg cag cgg atc gct			1315
Gly Asp Phe Glu Pro Tyr Glu Lys Gly Ala Leu Trp Gln Arg Ile Ala			
390	395	400	405
gat caa ggt gcg ctg atc ggt aag aac gtg act aag aag acc acc att			1363
Asp Gln Gly Ala Leu Ile Gly Lys Asn Val Thr Lys Lys Thr Thr Ile			
410	415		420
ttg gtt gct ggc ccg tgg gca acg att acc agt aag caa aaa cgt gct			1411
Leu Val Ala Gly Pro Trp Ala Thr Ile Thr Ser Lys Gln Lys Arg Ala			
425	430		435
gag gag ttg aaa gaa aaa gga cag gac atc cag atc tgg gat gaa aag			1459
Glu Glu Leu Lys Glu Lys Gly Gln Asp Ile Gln Ile Trp Asp Glu Lys			
440	445		450
cag ctg ttt acg gct ctg ggg tta gat gaa cag ccc ccg ttt			1501
Gln Leu Phe Thr Ala Leu Gly Leu Asp Glu Gln Pro Pro Phe			
455	460	465	
taaaagaatt ttctaaaact cgg			1524
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Thr Ile Ser Tyr Ser Pro Leu Leu Ala Ala Leu Ser Lys Ser Ser Ala			
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Gln Ser Glu Ser Val Asp Leu Thr Gln Val Ser Gly Val Ser Val Gln			
35	40		45
Asp Pro Thr Ala Phe Thr His Gly Phe Leu Asn Leu Glu Gly Val Asp			
50	55		60
Lys Ser Ile Ala Phe Ala Pro Asn Ser Ser Ala Asp Leu Ala Ala Leu			
65	70		75
Ala Ala Asp Ile Asp Ala Val Leu Lys Gly Glu Lys Pro Gln His Leu			
85	90		95
Gly Gly Gly Ala Pro Val Val Pro Ser Ala Pro Ser Thr Val Ala Gly			
100	105		110
Leu Asn Phe Val Gly Phe Asp Val Glu Thr Ala Asn Asp Asp Trp Gly			

115	120	125
Ser Ile Cys Gln Ile Gly 130	Leu Val Lys Tyr Val 135	Asp Gly Val Glu Glu 140
Ser Ser Glu Ser Trp 145	Leu Cys Thr Pro Pro 150	Glu Ser Leu Asn Phe Phe 155 160
Asn Glu Ile Asn Ile Gly 165	Ile His Gly Ile Thr Pro 170	Glu Met Val Ala 175
Asp Gln Pro Arg Phe Ala 180	Asp Leu Val Pro Lys Met 185	Val Glu Phe Val 190
Gly Asp Leu Pro Leu Val 195	Ala His Asn Ala Gln Phe 200	Asp Phe Thr Ala 205
Leu Ser Arg Ala Cys Ala 210	Ala Ser Gly Ile Asp Val 215	Pro Glu Met Ile 220
Tyr Gly Cys Ser Leu Thr 225	Leu Ala Arg Asn Glu Lys 230	Leu Gln Val Glu 235 240
Asn His Lys Leu Pro Thr 245	Val Ala Ser His Leu Gly 250	Phe Glu Leu Lys 255
Asn His His Asp Ala Ala 260	Glu Asp Ala Arg Ala Cys 265	Ala Ala Ile Thr 270
Ile Ala Leu Ala Lys Arg 275	His Ser Phe Glu Gly Ser 280	Phe Val Asp Phe 285
Val His Ser Arg Gly Phe 290	Thr Met Gly Thr Val Asp 295	Asn Ala Arg Val 300
Tyr Pro Val Leu Lys Asp 305	Arg Ser Gly Ala Asn Val 310	Ala Leu Gln Arg 315 320
Arg Asn Phe Gly Leu Asp 325	Ala Gly Lys Thr Glu Val 330	Pro Val Gln Pro 335
Ala Val Asp Pro Ala Trp 340	Glu Thr Pro Lys Ala Glu 345	Pro Lys Lys Gln 350
Ser Gly Arg Arg Ala Pro 355	Trp Asp Lys Val Ala Thr 360	Pro Glu Val Ile 365
Pro Asp Pro Asn Pro Asp 370	Ala Asp Pro Ser Ser Ile 375	Leu Tyr Gly Gln 380
Asn Val Thr Leu Thr Gly 385	Asp Phe Glu Pro Tyr Glu 390	Lys Gly Ala Leu 395 400
Trp Gln Arg Ile Ala Asp 405	Gln Gly Ala Leu Ile Gly 410	Lys Asn Val Thr 415
Lys Lys Thr Thr Ile Leu 420	Val Ala Gly Pro Trp Ala 425	Thr Ile Thr Ser 430
Lys Gln Lys Arg Ala Glu 435	Glu Glu Leu Lys Glu Lys 440	Gly Gln Asp Ile Gln 445

Ile Trp Asp Glu Lys Gln Leu Phe Thr Ala Leu Gly Leu Asp Glu Gln  
 450 455 460

Pro Pro Phe  
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<210> 171  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(2764)  
 <223> RXN00407

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 Met Val Ala Glu His  
 1 5  
 gct gca ggg gat tgg gtg gtc ctt gca ggt ttt cag tgg ttg gac aaa 163  
 Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe Gln Trp Leu Asp Lys  
 10 15 20  
 atc gac tat gtg atc gat tgc ttt aaa ccg gaa aat att gtg ctg gaa 211  
 Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu Asn Ile Val Leu Glu  
 25 30 35  
 ttc ggt tca acc atg aca ccg gaa gac gcc gac cgc aat gaa tac ctc 259  
 Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp Arg Asn Glu Tyr Leu  
 40 45 50  
 aga aga acg caa gcc aaa ttc cag ctt cga ggc atc cta agc acc aac 307  
 Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly Ile Leu Ser Thr Asn  
 55 60 65  
 cca gaa tcc gct gcc cgg ggg agc gtg cgg ctt gcc ggc gcc aag cag 355  
 Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu Ala Gly Ala Lys Gln  
 70 75 80 85  
 gca cta gcc cgc aag atg ccg ctt gcc gac gcc gaa agc gag cta cat 403  
 Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala Glu Ser Glu Leu His  
 90 95 100  
 ccc atg ggc act acc tgg atg cgc agc ggg gat aca ttg tta aaa gca 451  
 Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp Thr Leu Leu Lys Ala  
 105 110 115  
 cac cct gat tac gcg gat ctc att gca acc acg gtg gaa tta gct gct 499  
 His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr Val Glu Leu Ala Ala  
 120 125 130  
 gaa tgt gct ttc acc cta gat ttg gtg gcc ccg aat ctg ccc aag tgg 547  
 Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro Asn Leu Pro Lys Trp  
 135 140 145

gat acc cct ggt gaa cac acg gaa atg tcc tgg ctt gcg cac ctg gtt	595
Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp Leu Ala His Leu Val	
150 155 160 165	
tcc act cgg att gat acc cgc tat gtg ggg cgc tcc gca gac atc aaa	643
Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg Ser Ala Asp Ile Lys	
170 175 180	
gca cga gct gcc aca caa att gac tat gaa tta ggc gtt att gaa aag	691
Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu Gly Val Ile Glu Lys	
185 190 195	
ctg ggt ttt cca ggc tat ttc ctc gtc gtt aat gat ctg gtg gag ttt	739
Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn Asp Leu Val Glu Phe	
200 205 210	
tgt cgc gat tcc aat att ttg tgc caa ggc aga ggt tcc gcg gcg aac	787
Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg Gly Ser Ala Ala Asn	
215 220 225	
tcg gcg gtg tgc ttt gtc cta ggc atc acc aac gcg gag ccg atc tct	835
Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn Ala Glu Pro Ile Ser	
230 235 240 245	
gct gga ttg ttg ttt gaa cgg ttt tta tct cct gac cgg gat ggt cca	883
Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro Asp Arg Asp Gly Pro	
250 255 260	
cca gat att gac att gat att gaa tcc ggc agg cgc gaa gaa gta atc	931
Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg Arg Glu Glu Val Ile	
265 270 275	
caa tac gtg tat gaa aaa tac gga agg gat aac gca gct caa gta gcc	979
Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn Ala Ala Gln Val Ala	
280 285 290	
aat gtc att acc tac cga aca aaa ggc gcg atg cgt gat gct gcc cgt	1027
Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met Arg Asp Ala Ala Arg	
295 300 305	
gca ctg ggt tac ccg caa ggt gct gcc gat gcc tgg gct aaa gga acc	1075
Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala Trp Ala Lys Gly Thr	
310 315 320 325	
tcg gaa cca ccc gat gat gtg ctg gaa tta gct gcg caa ttt aaa ggg	1123
Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala Ala Gln Phe Lys Gly	
330 335 340	
caa cca cgg cat ttg ggt att cac tcc ggt ggc atg gtc att tgc gat	1171
Gln Pro Arg His Leu Gly Ile His Ser Gly Gly Met Val Ile Cys Asp	
345 350 355	
cgc ccc atc gcc gat gtg gtg cca gtg gaa tgg gct cgg atg gat aac	1219
Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp Ala Arg Met Asp Asn	
360 365 370	
cgc tcg gtt gtg caa tgg gat aaa gat gac tgt gcc acg gca ggc ttg	1267
Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys Ala Thr Ala Gly Leu	
375 380 385	
gtc aaa ttc gac ctt ttg gga ttg ggc atg ttg gaa gcc atc cat cac	1315

Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu Glu Ala Ile His His	
390	405
atg ctg gat ctg gtg gca gaa cac cga ggt aaa aag atc aat ttg tgg	1363
Met Leu Asp Leu Val Ala Glu His Arg Gly Lys Lys Ile Asn Leu Trp	
410	420
gaa cta gat ctg gcg gaa ccg gag gtc tat gac atg ttg tgc aag gca	1411
Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp Met Leu Cys Lys Ala	
425	435
gat gcc gtg ggt gtg ttc cag gtg gaa tca cgt gcg cag tta tcc acg	1459
Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg Ala Gln Leu Ser Thr	
440	450
ctg cct cga ctc aag ccc cgc acc ttc ttt gac ctg gtc gtg gag gta	1507
Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp Leu Val Val Glu Val	
455	465
gct ctg att cgt cca ggt ccc atc caa ggc gga tcg gtg cac ccg tat	1555
Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly Ser Val His Pro Tyr	
470	485
ttg cgg cgc cgt gct ggt gaa gag gcc atc act tat gac cac ccc gtg	1603
Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr Tyr Asp His Pro Val	
490	500
ttg gaa aag tct ttg ggt aaa acc tta gga atc cca ctg ttt cag gaa	1651
Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile Pro Leu Phe Gln Glu	
505	515
cag ctc atg cag gta gct gtt gat gct gca ggt ttt agt ggt ggg gaa	1699
Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly Phe Ser Gly Gly Glu	
520	530
gcg gat tcc ttg cgc aga gcg atg ggg tcg aaa cgc tca cct gaa cgc	1747
Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys Arg Ser Pro Glu Arg	
535	545
atg gct gcg ttg cgc tcg cgg ttt ttc caa ggg ctg aaa gat acc aat	1795
Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly Leu Lys Asp Thr Asn	
550	560
ggg att gtg ggg gag acc gcc gag aaa ctg tgg aac aaa att gtg gcc	1843
Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp Asn Lys Ile Val Ala	
570	580
ttt gct gcc tac ggt ttt ccg gaa tcg cat tcg cag tcg ttt gcg tcc	1891
Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser Gln Ser Phe Ala Ser	
585	595
ttg gtg tat ttc tcc gcg tgg ttt aaa tac cac tac ccg gct gaa ttc	1939
Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His Tyr Pro Ala Glu Phe	
600	610
tgc gtg gga tta ttg cgg gca caa ccc atg ggt ttc tat tca cca cag	1987
Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly Phe Tyr Ser Pro Gln	
615	625
tct ttg atc agt gat gcc aga cgc cac ggc gtg agt atc ctg ccg atc	2035
Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val Ser Ile Leu Pro Ile	

630	635	640	645	
acg gtc aat gat tcc ggt gtg gag gcc gat gct ccg aat ggt gcg att				2083
Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala Pro Asn Gly Ala Ile	650	655	660	
cga ttg ggg ctc aac ctg gtg aaa ggc ctt ggc cac gat gcc gcg caa				2131
Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly His Asp Ala Ala Gln	665	670	675	
aga ata gag gac aac gcc ccg ttt gat tcc att ccg gat tta tcg cgc				2179
Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile Pro Asp Leu Ser Arg	680	685	690	
cgg gct gat ctt aat gtt gct caa gtt gag gca ttg gcg cga gcg gga				2227
Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly	695	700	705	
gcg gtg gac tgc ttg ggg gtc gga cgt cga caa gca tta tgg caa gcg				2275
Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala	710	715	720	725
ggc gtc gca gcg acc gaa aaa cct gga atg ctg cct ggc ctt tcg gtg				2323
Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val	730	735	740	
att gaa gct ccg gcg ttg ccg ggg atg agc gcc ttt gag ctg atg gcg				2371
Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala	745	750	755	
acc aat att tcc gcc acg gga gtc acc gcg gat tat cag ccg atg gcg				2419
Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala	760	765	770	
ttg att cgg gag cgg atg gag gag ctg ggg atc gtg ccg gcg gat cgg				2467
Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg	775	780	785	
cta ttg gag gtg gaa gat ggc acg cgg ctg cgg atc gct ggc att gtc				2515
Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val	790	795	800	805
acg cac cgg cag cgc ccg caa act gcg tcg ggg ctg aca ttt tta ggg				2563
Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly	810	815	820	
atg gag gat gag acc ggg ctg atg aat gtg atg gtg tcc gtt ggg ttg				2611
Met Glu Asp Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu	825	830	835	
tgg cag cgg cag cgc gtg ctg gcc aga aat gcc aag gcg ttg att att				2659
Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile	840	845	850	
cga ggg att gtg cag aat gcg caa ggg gtg gcg aca gtt gtc gct gac				2707
Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp	855	860	865	
cgg ttg gaa ccg ttg gac atg ggg gag ttt ctc agc cgt ggc tca cga				2755
Arg Leu Glu Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg	870	875	880	885

gat ttt cga taatttggca aagtggacat tat  
 Asp Phe Arg

2787

&lt;210&gt; 172

&lt;211&gt; 888

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 172

Met Val Ala Glu His Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe  
 1 5 10 15

Gln Trp Leu Asp Lys Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu  
 20 25 30

Asn Ile Val Leu Glu Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp  
 35 40 45

Arg Asn Glu Tyr Leu Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly  
 50 55 60

Ile Leu Ser Thr Asn Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu  
 65 70 75 80

Ala Gly Ala Lys Gln Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala  
 85 90 95

Glu Ser Glu Leu His Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp  
 100 105 110

Thr Leu Leu Lys Ala His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr  
 115 120 125

Val Glu Leu Ala Ala Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro  
 130 135 140

Asn Leu Pro Lys Trp Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp  
 145 150 155 160

Leu Ala His Leu Val Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg  
 165 170 175

Ser Ala Asp Ile Lys Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu  
 180 185 190

Gly Val Ile Glu Lys Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn  
 195 200 205

Asp Leu Val Glu Phe Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg  
 210 215 220

Gly Ser Ala Ala Asn Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn  
 225 230 235 240

Ala Glu Pro Ile Ser Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro  
 245 250 255

Asp Arg Asp Gly Pro Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg

260	265	270
Arg Glu Glu Val Ile Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn 275	280	285
Ala Ala Gln Val Ala Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met 290	295	300
Arg Asp Ala Ala Arg Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala 305	310	315 320
Trp Ala Lys Gly Thr Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala 325	330	335
Ala Gln Phe Lys Gly Gln Pro Arg His Leu Gly Ile His Ser Gly Gly 340	345	350
Met Val Ile Cys Asp Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp 355	360	365
Ala Arg Met Asp Asn Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys 370	375	380
Ala Thr Ala Gly Leu Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu 385	390	395 400
Glu Ala Ile His His Met Leu Asp Leu Val Ala Glu His Arg Gly Lys 405	410	415
Lys Ile Asn Leu Trp Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp 420	425	430
Met Leu Cys Lys Ala Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg 435	440	445
Ala Gln Leu Ser Thr Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp 450	455	460
Leu Val Val Glu Val Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly 465	470	475 480
Ser Val His Pro Tyr Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr 485	490	495
Tyr Asp His Pro Val Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile 500	505	510
Pro Leu Phe Gln Glu Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly 515	520	525
Phe Ser Gly Gly Glu Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys 530	535	540
Arg Ser Pro Glu Arg Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly 545	550	555 560
Leu Lys Asp Thr Asn Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp 565	570	575
Asn Lys Ile Val Ala Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser 580	585	590



Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His  
 595 600 605  
 Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly  
 610 615 620  
 Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val  
 625 630 635 640  
 Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala Asp Ala  
 645 650 655  
 Pro Asn Gly Ala Ile Arg Leu Gly Leu Asn Leu Val Lys Gly Leu Gly  
 660 665 670  
 His Asp Ala Ala Gln Arg Ile Glu Asp Asn Ala Pro Phe Asp Ser Ile  
 675 680 685  
 Pro Asp Leu Ser Arg Arg Ala Asp Leu Asn Val Ala Gln Val Glu Ala  
 690 695 700  
 Leu Ala Arg Ala Gly Ala Val Asp Cys Leu Gly Val Gly Arg Arg Gln  
 705 710 715 720  
 Ala Leu Trp Gln Ala Gly Val Ala Ala Thr Glu Lys Pro Gly Met Leu  
 725 730 735  
 Pro Gly Leu Ser Val Ile Glu Ala Pro Ala Leu Pro Gly Met Ser Ala  
 740 745 750  
 Phe Glu Leu Met Ala Thr Asn Ile Ser Ala Thr Gly Val Thr Ala Asp  
 755 760 765  
 Tyr Gln Pro Met Ala Leu Ile Arg Glu Arg Met Glu Glu Leu Gly Ile  
 770 775 780  
 Val Pro Ala Asp Arg Leu Leu Glu Val Glu Asp Gly Thr Arg Leu Arg  
 785 790 795 800  
 Ile Ala Gly Ile Val Thr His Arg Gln Arg Pro Gln Thr Ala Ser Gly  
 805 810 815  
 Leu Thr Phe Leu Gly Met Glu Asp Glu Thr Gly Leu Met Asn Val Met  
 820 825 830  
 Val Ser Val Gly Leu Trp Gln Arg Gln Arg Val Leu Ala Arg Asn Ala  
 835 840 845  
 Lys Ala Leu Ile Ile Arg Gly Ile Val Gln Asn Ala Gln Gly Val Ala  
 850 855 860  
 Thr Val Val Ala Asp Arg Leu Glu Pro Leu Asp Met Gly Glu Phe Leu  
 865 870 875 880  
 Ser Arg Gly Ser Arg Asp Phe Arg  
 885

&lt;210&gt; 173

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(576)

&lt;223&gt; FRXA00407

&lt;400&gt; 173

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ctt aat gtt gct caa gtt gag gca ttg gcg cga gcg gga gcg gtg gac      48
Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly Ala Val Asp
   1             5             10             15

tgc ttg ggg gtc gga cgt cga caa gca tta tgg caa gcg ggc gtc gca      96
Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala Gly Val Ala
          20             25             30

gcg acc gaa aaa cct gga atg ctg cct ggc ctt tcg gtg att gaa gct      144
Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val Ile Glu Ala
          35             40             45

ccg gcg ttg ccg ggg atg agc gcc ttt gag ctg atg gcg acc aat att      192
Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala Thr Asn Ile
          50             55             60

tcc gcc acg gga gtc acc gcg gat tat cag ccg atg gcg ttg att cgg      240
Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala Leu Ile Arg
          65             70             75             80

gag cgg atg gag gag ctg ggg atc gtg ccg gcg gat cgg cta ttg gag      288
Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg Leu Leu Glu
          85             90             95

gtg gaa gat ggc acg cgg ctg cgg atc gct ggc att gtc acg cac cgg      336
Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val Thr His Arg
          100             105             110

cag cgc ccg caa act gcg tcg ggg ctg aca ttt tta ggg atg gag gat      384
Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly Met Glu Asp
          115             120             125

gag acc ggg ctg atg aat gtg atg gtg tcc gtt ggg ttg tgg cag cgg      432
Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu Trp Gln Arg
          130             135             140

cag cgc gtg ctg gcc aga aat gcc aag gcg ttg att att cga ggg att      480
Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile Arg Gly Ile
          145             150             155             160

gtg cag aat gcg caa ggg gtg gcg aca gtt gtc gct gac cgg ttg gaa      528
Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp Arg Leu Glu
          165             170             175

ccg ttg gac atg ggg gag ttt ctc agc cgt ggc tca cga gat ttt cga      576
Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg Asp Phe Arg
          180             185             190

taatttggca aagtggacat tat      599

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&lt;210&gt; 174

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<400> 174
Leu Asn Val Ala Gln Val Glu Ala Leu Ala Arg Ala Gly Ala Val Asp
 1              5              10              15

Cys Leu Gly Val Gly Arg Arg Gln Ala Leu Trp Gln Ala Gly Val Ala
      20              25              30

Ala Thr Glu Lys Pro Gly Met Leu Pro Gly Leu Ser Val Ile Glu Ala
      35              40              45

Pro Ala Leu Pro Gly Met Ser Ala Phe Glu Leu Met Ala Thr Asn Ile
 50              55              60

Ser Ala Thr Gly Val Thr Ala Asp Tyr Gln Pro Met Ala Leu Ile Arg
 65              70              75              80

Glu Arg Met Glu Glu Leu Gly Ile Val Pro Ala Asp Arg Leu Leu Glu
      85              90              95

Val Glu Asp Gly Thr Arg Leu Arg Ile Ala Gly Ile Val Thr His Arg
      100              105              110

Gln Arg Pro Gln Thr Ala Ser Gly Leu Thr Phe Leu Gly Met Glu Asp
      115              120              125

Glu Thr Gly Leu Met Asn Val Met Val Ser Val Gly Leu Trp Gln Arg
      130              135              140

Gln Arg Val Leu Ala Arg Asn Ala Lys Ala Leu Ile Ile Arg Gly Ile
      145              150              155              160

Val Gln Asn Ala Gln Gly Val Ala Thr Val Val Ala Asp Arg Leu Glu
      165              170              175

Pro Leu Asp Met Gly Glu Phe Leu Ser Arg Gly Ser Arg Asp Phe Arg
      180              185              190

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<220>  
<221> CDS  
<222> (101)..(2062)  
<223> FRXA00415
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<400> 175
tgtgtaaaaa tccggaaggc tacaaaaagc tcagtcacct gatcagtgac gcgaaaatgg 60

cacgggggaga aaagggggaag ttcgctatcc gccgctgcc a  atg gtt gct gaa cat 115
               Met Val Ala Glu His
                1             5

```

gct gca ggg gat tgg gtg gtc ctt gca ggt ttt cag tgg ttg gac aaa 163  
 Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe Gln Trp Leu Asp Lys  
 10 15 20

atc gac tat gtg atc gat tgc ttt aaa ccg gaa aat att gtg ctg gaa 211  
 Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu Asn Ile Val Leu Glu  
 25 30 35

ttc ggt tca acc atg aca ccg gaa gac gcc gac cgc aat gaa tac ctc 259  
 Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp Arg Asn Glu Tyr Leu  
 40 45 50

aga aga acg caa gcc aaa ttc cag ctt cga ggc atc cta agc acc aac 307  
 Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly Ile Leu Ser Thr Asn  
 55 60 65

cca gaa tcc gct gcc ccg ggg agc gtg ccg ctt gcc ggc gcc aag cag 355  
 Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu Ala Gly Ala Lys Gln  
 70 75 80 85

gca cta gcc cgc aag atg ccg ctt gcc gac gcc gaa agc gag cta cat 403  
 Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala Glu Ser Glu Leu His  
 90 95 100

ccc atg ggc act acc tgg atg cgc agc ggg gat aca ttg tta aaa gca 451  
 Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp Thr Leu Leu Lys Ala  
 105 110 115

cac cct gat tac gcg gat ctc att gca acc acg gtg gaa tta gct gct 499  
 His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr Val Glu Leu Ala Ala  
 120 125 130

gaa tgt gct ttc acc cta gat ttg gtg gcc ccg aat ctg ccc aag tgg 547  
 Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro Asn Leu Pro Lys Trp  
 135 140 145

gat acc cct ggt gaa cac acg gaa atg tcc tgg ctt gcg cac ctg gtt 595  
 Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp Leu Ala His Leu Val  
 150 155 160 165

tcc act ccg att gat acc cgc tat gtg ggg cgc tcc gca gac atc aaa 643  
 Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg Ser Ala Asp Ile Lys  
 170 175 180

gca cga gct gcc aca caa att gac tat gaa tta ggc gtt att gaa aag 691  
 Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu Gly Val Ile Glu Lys  
 185 190 195

ctg ggt ttt cca ggc tat ttc ctc gtc gtt aat gat ctg gtg gag ttt 739  
 Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn Asp Leu Val Glu Phe  
 200 205 210

tgt cgc gat tcc aat att ttg tgc caa ggc aga ggt tcc gcg gcg aac 787  
 Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg Gly Ser Ala Ala Asn  
 215 220 225

tcg gcg gtg tgc ttt gtc cta ggc atc acc aac gcg gag ccg atc tct 835  
 Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn Ala Glu Pro Ile Ser  
 230 235 240 245

gct gga ttg ttg ttt gaa cgg ttt tta tct cct gac cgg gat ggt cca 883  
 Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro Asp Arg Asp Gly Pro  
 250 255 260

cca gat att gac att gat att gaa tcc ggc agg cgc gaa gaa gta atc 931  
 Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg Arg Glu Glu Val Ile  
 265 270 275

caa tac gtg tat gaa aaa tac gga agg gat aac gca gct caa gta gcc 979  
 Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn Ala Ala Gln Val Ala  
 280 285 290

aat gtc att acc tac cga aca aaa ggc gcg atg cgt gat gct gcc cgt 1027  
 Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met Arg Asp Ala Ala Arg  
 295 300 305

gca ctg ggt tac ccg caa ggt gct gcc gat gcc tgg gct aaa gga acc 1075  
 Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala Trp Ala Lys Gly Thr  
 310 315 320 325

tcg gaa cca ccc gat gat gtg ctg gaa tta gct gcg caa ttt aaa ggg 1123  
 Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala Ala Gln Phe Lys Gly  
 330 335 340

caa cca cgg cat ttg ggt att cac tcc ggt ggc atg gtc att tgc gat 1171  
 Gln Pro Arg His Leu Gly Ile His Ser Gly Gly Met Val Ile Cys Asp  
 345 350 355

cgc ccc atc gcc gat gtg gtg cca gtg gaa tgg gct cgg atg gat aac 1219  
 Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp Ala Arg Met Asp Asn  
 360 365 370

cgc tcg gtt gtg caa tgg gat aaa gat gac tgt gcc acg gca ggc ttg 1267  
 Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys Ala Thr Ala Gly Leu  
 375 380 385

gtc aaa ttc gac ctt ttg gga ttg ggc atg ttg gaa gcc atc cat cac 1315  
 Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu Glu Ala Ile His His  
 390 395 400 405

atg ctg gat ctg gtg gca gaa cac cga ggt aaa aag atc aat ttg tgg 1363  
 Met Leu Asp Leu Val Ala Glu His Arg Gly Lys Lys Ile Asn Leu Trp  
 410 415 420

gaa cta gat ctg gcg gaa ccg gag gtc tat gac atg ttg tgc aag gca 1411  
 Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp Met Leu Cys Lys Ala  
 425 430 435

gat gcc gtg ggt gtg ttc cag gtg gaa tca cgt gcg cag tta tcc acg 1459  
 Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg Ala Gln Leu Ser Thr  
 440 445 450

ctg cct cga ctc aag ccc cgc acc ttc ttt gac ctg gtc gtg gag gta 1507  
 Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp Leu Val Val Glu Val  
 455 460 465

gct ctg att cgt cca ggt ccc atc caa ggc gga tcg gtg cac ccg tat 1555  
 Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly Ser Val His Pro Tyr  
 470 475 480 485

ttg cgg cgc cgt gct ggt gaa gag gcc atc act tat gac cac ccc gtg 1603

Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr Tyr Asp His Pro Val  
 490 495 500

ttg gaa aag tct ttg ggt aaa acc tta gga atc cca ctg ttt cag gaa 1651  
 Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile Pro Leu Phe Gln Glu  
 505 510 515

cag ctc atg cag gta gct gtt gat gct gca ggt ttt agt ggt ggg gaa 1699  
 Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly Phe Ser Gly Gly Glu  
 520 525 530

gcg gat tcc ttg cgc aga gcg atg ggg tcg aaa cgc tca cct gaa cgc 1747  
 Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys Arg Ser Pro Glu Arg  
 535 540 545

atg gct gcg ttg cgc tcg cgg ttt ttc caa ggg ctg aaa gat acc aat 1795  
 Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly Leu Lys Asp Thr Asn  
 550 555 560 565

ggg att gtg ggg gag acc gcc gag aaa ctg tgg aac aaa att gtg gcc 1843  
 Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp Asn Lys Ile Val Ala  
 570 575 580

ttt gct gcc tac ggt ttt ccg gaa tcg cat tcg cag tcg ttt gcg tcc 1891  
 Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser Gln Ser Phe Ala Ser  
 585 590 595

ttg gtg tat ttc tcc gcg tgg ttt aaa tac cac tac ccg gct gaa ttc 1939  
 Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His Tyr Pro Ala Glu Phe  
 600 605 610

tgc gtg gga tta ttg cgg gca caa ccc atg ggt ttc tat tca cca cag 1987  
 Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly Phe Tyr Ser Pro Gln  
 615 620 625

tct ttg atc agt gat gcc aga cgc cac ggc gtg agt atc ctg ccg atc 2035  
 Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val Ser Ile Leu Pro Ile  
 630 635 640 645

acg gtc aat gat tcc ggt gtg gag gcc 2062  
 Thr Val Asn Asp Ser Gly Val Glu Ala  
 650

<210> 176

<211> 654

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Val Ala Glu His Ala Ala Gly Asp Trp Val Val Leu Ala Gly Phe  
 1 5 10 15

Gln Trp Leu Asp Lys Ile Asp Tyr Val Ile Asp Cys Phe Lys Pro Glu  
 20 25 30

Asn Ile Val Leu Glu Phe Gly Ser Thr Met Thr Pro Glu Asp Ala Asp  
 35 40 45

Arg Asn Glu Tyr Leu Arg Arg Thr Gln Ala Lys Phe Gln Leu Arg Gly  
 50 55 60

Ile Leu Ser Thr Asn Pro Glu Ser Ala Ala Arg Gly Ser Val Arg Leu  
 65 70 75 80  
 Ala Gly Ala Lys Gln Ala Leu Ala Arg Lys Met Pro Leu Ala Asp Ala  
 85 90 95  
 Glu Ser Glu Leu His Pro Met Gly Thr Thr Trp Met Arg Ser Gly Asp  
 100 105 110  
 Thr Leu Leu Lys Ala His Pro Asp Tyr Ala Asp Leu Ile Ala Thr Thr  
 115 120 125  
 Val Glu Leu Ala Ala Glu Cys Ala Phe Thr Leu Asp Leu Val Ala Pro  
 130 135 140  
 Asn Leu Pro Lys Trp Asp Thr Pro Gly Glu His Thr Glu Met Ser Trp  
 145 150 155 160  
 Leu Ala His Leu Val Ser Thr Arg Ile Asp Thr Arg Tyr Val Gly Arg  
 165 170 175  
 Ser Ala Asp Ile Lys Ala Arg Ala Ala Thr Gln Ile Asp Tyr Glu Leu  
 180 185 190  
 Gly Val Ile Glu Lys Leu Gly Phe Pro Gly Tyr Phe Leu Val Val Asn  
 195 200 205  
 Asp Leu Val Glu Phe Cys Arg Asp Ser Asn Ile Leu Cys Gln Gly Arg  
 210 215 220  
 Gly Ser Ala Ala Asn Ser Ala Val Cys Phe Val Leu Gly Ile Thr Asn  
 225 230 235 240  
 Ala Glu Pro Ile Ser Ala Gly Leu Leu Phe Glu Arg Phe Leu Ser Pro  
 245 250 255  
 Asp Arg Asp Gly Pro Pro Asp Ile Asp Ile Asp Ile Glu Ser Gly Arg  
 260 265 270  
 Arg Glu Glu Val Ile Gln Tyr Val Tyr Glu Lys Tyr Gly Arg Asp Asn  
 275 280 285  
 Ala Ala Gln Val Ala Asn Val Ile Thr Tyr Arg Thr Lys Gly Ala Met  
 290 295 300  
 Arg Asp Ala Ala Arg Ala Leu Gly Tyr Pro Gln Gly Ala Ala Asp Ala  
 305 310 315 320  
 Trp Ala Lys Gly Thr Ser Glu Pro Pro Asp Asp Val Leu Glu Leu Ala  
 325 330 335  
 Ala Gln Phe Lys Gly Gln Pro Arg His Leu Gly Ile His Ser Gly Gly  
 340 345 350  
 Met Val Ile Cys Asp Arg Pro Ile Ala Asp Val Val Pro Val Glu Trp  
 355 360 365  
 Ala Arg Met Asp Asn Arg Ser Val Val Gln Trp Asp Lys Asp Asp Cys  
 370 375 380

Ala Thr Ala Gly Leu Val Lys Phe Asp Leu Leu Gly Leu Gly Met Leu  
 385 390 395 400  
 Glu Ala Ile His His Met Leu Asp Leu Val Ala Glu His Arg Gly Lys  
 405 410 415  
 Lys Ile Asn Leu Trp Glu Leu Asp Leu Ala Glu Pro Glu Val Tyr Asp  
 420 425 430  
 Met Leu Cys Lys Ala Asp Ala Val Gly Val Phe Gln Val Glu Ser Arg  
 435 440 445  
 Ala Gln Leu Ser Thr Leu Pro Arg Leu Lys Pro Arg Thr Phe Phe Asp  
 450 455 460  
 Leu Val Val Glu Val Ala Leu Ile Arg Pro Gly Pro Ile Gln Gly Gly  
 465 470 475 480  
 Ser Val His Pro Tyr Leu Arg Arg Arg Ala Gly Glu Glu Ala Ile Thr  
 485 490 495  
 Tyr Asp His Pro Val Leu Glu Lys Ser Leu Gly Lys Thr Leu Gly Ile  
 500 505 510  
 Pro Leu Phe Gln Glu Gln Leu Met Gln Val Ala Val Asp Ala Ala Gly  
 515 520 525  
 Phe Ser Gly Gly Glu Ala Asp Ser Leu Arg Arg Ala Met Gly Ser Lys  
 530 535 540  
 Arg Ser Pro Glu Arg Met Ala Ala Leu Arg Ser Arg Phe Phe Gln Gly  
 545 550 555 560  
 Leu Lys Asp Thr Asn Gly Ile Val Gly Glu Thr Ala Glu Lys Leu Trp  
 565 570 575  
 Asn Lys Ile Val Ala Phe Ala Ala Tyr Gly Phe Pro Glu Ser His Ser  
 580 585 590  
 Gln Ser Phe Ala Ser Leu Val Tyr Phe Ser Ala Trp Phe Lys Tyr His  
 595 600 605  
 Tyr Pro Ala Glu Phe Cys Val Gly Leu Leu Arg Ala Gln Pro Met Gly  
 610 615 620  
 Phe Tyr Ser Pro Gln Ser Leu Ile Ser Asp Ala Arg Arg His Gly Val  
 625 630 635 640  
 Ser Ile Leu Pro Ile Thr Val Asn Asp Ser Gly Val Glu Ala  
 645 650

&lt;210&gt; 177

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(454)

&lt;223&gt; RXN00414



&lt;400&gt; 177

attatcgtgg tccaaattgg aaagaatcct ctcaggtaaa aaggtcgaat ctctgcgtcc 60

ggtgctgcat gagccggatg cgcaggcgcc ttcattctgcc atg cag ggg gaa gcg 115  
 Met Gln Gly Glu Ala  
 1 5

tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc 163  
 Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu  
 10 15 20

act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta 211  
 Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu  
 25 30 35

gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca 259  
 Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala  
 40 45 50

gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat 307  
 Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly Met His Thr Val Tyr  
 55 60 65

ggt gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa 355  
 Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys  
 70 75 80 85

aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa 403  
 Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys  
 90 95 100

atg gca cgg gag aaa agg gga agt tcg cta tcc gcc gct gcc aat ggt 451  
 Met Ala Arg Glu Lys Arg Gly Ser Ser Leu Ser Ala Ala Ala Asn Gly  
 105 110 115

tgc tgaacatgct gcaggggatt ggg 477  
 Cys

&lt;210&gt; 178

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 178

Met Gln Gly Glu Ala Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser  
 1 5 10 15

Ser Tyr Asn Phe Leu Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val  
 20 25 30

Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp  
 35 40 45

Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly  
 50 55 60

Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu  
 65 70 75 80

Thr Val Leu Cys Lys Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu  
85 90 95

Ile Ser Asp Ala Lys Met Ala Arg Glu Lys Arg Gly Ser Ser Leu Ser  
100 105 110

Ala Ala Ala Asn Gly Cys  
115

<210> 179

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> FRXA00414

<400> 179

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ggtgctgcat gagccggatg cgcaggcgcc ttcattctgcc atg cag ggg gaa gcg 115  
Met Gln Gly Glu Ala  
1 5

tcg gtt cct ttt gcc gag ctg cat gcc acc agc agt tat aac ttt ctc 163  
Ser Val Pro Phe Ala Glu Leu His Ala Thr Ser Ser Tyr Asn Phe Leu  
10 15 20

act ggc gca tcg gat ccg tct gat gtg gtt gtg cag gcc aaa aag tta 211  
Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val Gln Ala Lys Lys Leu  
25 30 35

gga ctt gct gct cta tca gtc atg gat agg gat ggt ttt tat ggt gca 259  
Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp Gly Phe Tyr Gly Ala  
40 45 50

gtg aga ttt gcg gaa gct gcc gcg gaa gct gga atg cat acc gtt tat 307  
Val Arg Phe Ala Glu Ala Ala Glu Ala Gly Met His Thr Val Tyr  
55 60 65

ggt gcg gag ctg agt ctg caa gaa ggc gtg ttg aca gtc ttg tgt aaa 355  
Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu Thr Val Leu Cys Lys  
70 75 80 85

aat ccg gaa ggc tac aaa aag ctc agt cac ctg atc agt gac gcg aaa 403  
Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu Ile Ser Asp Ala Lys  
90 95 100

atg gca cgg gga gaa aag ggg aag ttc gct atc cgc cgc tgc caa tgg 451  
Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile Arg Arg Cys Gln Trp  
105 110 115

ttg ctg aac atg ctg cag ggg att ggg tgg tcc ttg cag gtt ttc agt 499  
Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser Leu Gln Val Phe Ser  
120 125 130

ggt tgg aca aaa tcg act atg tgatcgattg ctttaaaccg gaa 543

Gly Trp Thr Lys Ser Thr Met  
135 140

<210> 180  
<211> 140  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 180  
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Ser Tyr Asn Phe Leu Thr Gly Ala Ser Asp Pro Ser Asp Val Val Val  
20 25 30  
Gln Ala Lys Lys Leu Gly Leu Ala Ala Leu Ser Val Met Asp Arg Asp  
35 40 45  
Gly Phe Tyr Gly Ala Val Arg Phe Ala Glu Ala Ala Ala Glu Ala Gly  
50 55 60  
Met His Thr Val Tyr Gly Ala Glu Leu Ser Leu Gln Glu Gly Val Leu  
65 70 75 80  
Thr Val Leu Cys Lys Asn Pro Glu Gly Tyr Lys Lys Leu Ser His Leu  
85 90 95  
Ile Ser Asp Ala Lys Met Ala Arg Gly Glu Lys Gly Lys Phe Ala Ile  
100 105 110  
Arg Arg Cys Gln Trp Leu Leu Asn Met Leu Gln Gly Ile Gly Trp Ser  
115 120 125  
Leu Gln Val Phe Ser Gly Trp Thr Lys Ser Thr Met  
130 135 140

<210> 181  
<211> 1365  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(1342)  
<223> RXN00807

<400> 181  
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gtagtgagga agtagtgtag agatcgtgac taattcgagt gtg ttt gac agt ctc 115  
Val Phe Asp Ser Leu  
1 5  
gcc ggc tcc aaa aca gtg tcc aag acg ctt ttc gac gcg gcc tcc agc 163  
Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe Asp Ala Ala Ser Ser  
10 15 20  
gcg cgt gcc ctt gtc cgc gcc cga acc aca gaa cgt gcc cgc gcc cgg 211  
Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu Arg Ala Arg Ala Arg

25	30	35	
gca gaa cac caa aac cct gca atg atc cac gac tcc ggc ttt gcc cag			259
Ala Glu His Gln Asn Pro Ala Met Ile His Asp Ser Gly Phe Ala Gln			
40	45	50	
tca tgg ctg ttt aca ggc cct ccc gga tcg gga cgt tct gtg gca gcc			307
Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly Arg Ser Val Ala Ala			
55	60	65	
aag gtt ttc gcc gct acg ctc gta tgt tcg aat ccg gat gtt gtg ggc			355
Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn Pro Asp Val Val Gly			
70	75	80	85
tgt gga caa tgc gag gat tgc cgc gcc gcc atg gga ggc agc cac ccc			403
Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met Gly Gly Ser His Pro			
90	95	100	
gat att gaa cac atc gtc ccg cag caa ttg tct atc ggt gtt gat gca			451
Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser Ile Gly Val Asp Ala			
105	110	115	
gct aga gag gtc atc aaa gcc gca gcg gtc agt cct gtt gca gga aac			499
Ala Arg Glu Val Ile Lys Ala Ala Ala Val Ser Pro Val Ala Gly Asn			
120	125	130	
tgg cga gtc gtc atc ttc gaa aac gcc gac cga ctc acc atg caa gcc			547
Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg Leu Thr Met Gln Ala			
135	140	145	
gcc aac gcc ttg ctg aaa acc gtg gag gaa cca acc gaa agc acc gtg			595
Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro Thr Glu Ser Thr Val			
150	155	160	165
atg att ctg tgc gca ccc acc aca gac ccc cgc gac att gcg atc acc			643
Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg Asp Ile Ala Ile Thr			
170	175	180	
ctc cgc tcc cgc tgc agg cac ctc tac att ccc acc ccc tcc atc gcg			691
Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro Thr Pro Ser Ile Ala			
185	190	195	
gaa gtc gca cga atc ctc gta gct gaa ggc aac gtc agc caa gcg gat			739
Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn Val Ser Gln Ala Asp			
200	205	210	
gca gaa tta gcg gcg gct gcc tca ggc gct cac atc ggc agg gct cga			787
Ala Glu Leu Ala Ala Ala Ala Ser Gly Ala His Ile Gly Arg Ala Arg			
215	220	225	
tac tta gcg cac aac aac gcc gcc caa cgc aga cgc gcc agc atc ctc			835
Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg Arg Ala Ser Ile Leu			
230	235	240	245
aac ctg gcc gaa tta atc ttc cac ggt gat gtc gcc ttc cgc tcc gta			883
Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val Ala Phe Arg Ser Val			
250	255	260	
aac acc ttg gtc aaa atg gtg gaa acc gaa gcc aaa gac agc aac aaa			931
Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala Lys Asp Ser Asn Lys			
265	270	275	

gaa aaa gaa gaa ggc gat ctc gaa gcc gta aga atc tca ctc ggc atg 979  
 Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg Ile Ser Leu Gly Met  
 280 285 290

ggg gcc aaa ggc aaa ggt gtc cac aaa gca gta cgt gga gga gcg gga 1027  
 Gly Ala Lys Gly Lys Gly Val His Lys Ala Val Arg Gly Gly Ala Gly  
 295 300 305

gat ttc aaa gca ctc gaa gac caa caa aaa ctc cga cgc acc cga ttc 1075  
 Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu Arg Arg Thr Arg Phe  
 310 315 320 325

ctc cgc gac agc ctc gac ctc gca ctc gtc gac cta gcc ggc atc tac 1123  
 Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp Leu Ala Gly Ile Tyr  
 330 335 340

cgc gat gcc atc atc att tcc tcc caa gcc caa gtc gga ctc aca cac 1171  
 Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln Val Gly Leu Thr His  
 345 350 355

ccc gat atg gaa ggc ctc tcc caa gaa ctc gca aca aaa gta agc caa 1219  
 Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala Thr Lys Val Ser Gln  
 360 365 370

gaa gga ctc ctg gca tgc ctc gac gcg atc tcc aaa tgc cgc gaa tcc 1267  
 Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser Lys Cys Arg Glu Ser  
 375 380 385

ttc ggc ttc aat gta cga ccc atc gtg gcc atg gac gcc ctg gta gga 1315  
 Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met Asp Ala Leu Val Gly  
 390 395 400 405

cgc ctg cgc aaa gcc tac aaa gtg tcc taaacacccc aaattattga 1362  
 Arg Leu Arg Lys Ala Tyr Lys Val Ser  
 410

agt 1365

&lt;210&gt; 182

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 182

Val Phe Asp Ser Leu Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe  
 1 5 10 15

Asp Ala Ala Ser Ser Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu  
 20 25 30

Arg Ala Arg Ala Arg Ala Glu His Gln Asn Pro Ala Met Ile His Asp  
 35 40 45

Ser Gly Phe Ala Gln Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly  
 50 55 60

Arg Ser Val Ala Ala Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn  
 65 70 75 80

Pro Asp Val Val Gly Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met  
                             85                            90                            95

Gly Gly Ser His Pro Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser  
                             100                            105                            110

Ile Gly Val Asp Ala Ala Arg Glu Val Ile Lys Ala Ala Ala Val Ser  
                             115                            120                            125

Pro Val Ala Gly Asn Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg  
                             130                            135                            140

Leu Thr Met Gln Ala Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro  
 145                            150                            155                            160

Thr Glu Ser Thr Val Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg  
                             165                            170                            175

Asp Ile Ala Ile Thr Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro  
                             180                            185                            190

Thr Pro Ser Ile Ala Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn  
                             195                            200                            205

Val Ser Gln Ala Asp Ala Glu Leu Ala Ala Ala Ala Ser Gly Ala His  
                             210                            215                            220

Ile Gly Arg Ala Arg Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg  
 225                            230                            235                            240

Arg Ala Ser Ile Leu Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val  
                             245                            250                            255

Ala Phe Arg Ser Val Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala  
                             260                            265                            270

Lys Asp Ser Asn Lys Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg  
                             275                            280                            285

Ile Ser Leu Gly Met Gly Ala Lys Gly Lys Gly Val His Lys Ala Val  
                             290                            295                            300

Arg Gly Gly Ala Gly Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu  
 305                            310                            315                            320

Arg Arg Thr Arg Phe Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp  
                             325                            330                            335

Leu Ala Gly Ile Tyr Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln  
                             340                            345                            350

Val Gly Leu Thr His Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala  
                             355                            360                            365

Thr Lys Val Ser Gln Glu Gly Leu Leu Ala Cys Leu Asp Ala Ile Ser  
                             370                            375                            380

Lys Cys Arg Glu Ser Phe Gly Phe Asn Val Arg Pro Ile Val Ala Met  
 385                            390                            395                            400

Asp Ala Leu Val Gly Arg Leu Arg Lys Ala Tyr Lys Val Ser

410

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<222> (101)..(1219)  
<223> FRXA00807
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<400> 183																														
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																	Val	Phe	Asp	Ser	Leu									
																	1						5							
gcc	ggc	tcc	aaa	aca	gtg	tcc	aag	acg	ctt	ttc	gac	gcg	gcc	tcc	agc			163												
Ala	Gly	Ser	Lys	Thr	Val	Ser	Lys	Thr	Leu	Phe	Asp	Ala	Ala	Ser	Ser															
																	10						15						20	
gcg	cgt	gcc	ctt	gtc	cgc	gcc	cga	acc	aca	gaa	cgt	gcc	cgc	gcc	cgg			211												
Ala	Arg	Ala	Leu	Val	Arg	Ala	Arg	Thr	Thr	Glu	Arg	Ala	Arg	Ala	Arg															
																	25						30						35	
gca	gaa	cac	caa	aac	cct	gca	atg	atc	cac	gac	tcc	ggc	ttt	gcc	cag			259												
Ala	Glu	His	Gln	Asn	Pro	Ala	Met	Ile	His	Asp	Ser	Gly	Phe	Ala	Gln															
																	40						45						50	
tca	tgg	ctg	ttt	aca	ggc	cct	ccc	gga	tcg	gga	cgt	tct	gtg	gca	gcc			307												
Ser	Trp	Leu	Phe	Thr	Gly	Pro	Pro	Gly	Ser	Gly	Arg	Ser	Val	Ala	Ala															
																	55						60						65	
aag	gtt	ttc	gcc	gct	acg	ctc	gta	tgt	tcg	aat	ccg	gat	gtt	gtg	ggc			355												
Lys	Val	Phe	Ala	Ala	Thr	Leu	Val	Cys	Ser	Asn	Pro	Asp	Val	Val	Gly															
																	70						75						80	85
tgt	gga	caa	tgc	gag	gat	tgc	cgc	gcc	gcc	atg	gga	ggc	agc	cac	ccc			403												
Cys	Gly	Gln	Cys	Glu	Asp	Cys	Arg	Ala	Ala	Met	Gly	Gly	Ser	His	Pro															
																	90						95						100	
gat	att	gaa	cac	atc	gtc	ccg	cag	caa	ttg	tct	atc	ggg	gtt	gat	gca			451												
Asp	Ile	Glu	His	Ile	Val	Pro	Gln	Gln	Leu	Ser	Ile	Gly	Val	Asp	Ala															
																	105						110						115	
gct	aga	gag	gtc	atc	aaa	gcc	gca	gcg	gtc	agt	cct	gtt	gca	gga	aac			499												
Ala	Arg	Glu	Val	Ile	Lys	Ala	Ala	Ala	Val	Ser	Pro	Val	Ala	Gly	Asn															
																	120						125						130	
tgg	cga	gtc	gtc	atc	ttc	gaa	aac	gcc	gac	cga	ctc	acc	atg	caa	gcc			547												
Trp	Arg	Val	Val	Ile	Phe	Glu	Asn	Ala	Asp	Arg	Leu	Thr	Met	Gln	Ala															
																	135						140						145	
gcc	aac	gcc	ttg	ctg	aaa	acc	gtg	gag	gaa	cca	acc	gaa	agc	acc	gtg			595												
Ala	Asn	Ala	Leu	Leu	Lys	Thr	Val	Glu	Glu	Pro	Thr	Glu	Ser	Thr	Val															
																	150						155						160	165
atg att ctg tgc gca ccc acc aca gac ccc cgc gac att gcg atc acc																						643								

Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg Asp Ile Ala Ile Thr  
 170 175 180

ctc cgc tcc cgc tgc agg cac ctc tac att ccc acc ccc tcc atc gcg 691  
 Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro Thr Pro Ser Ile Ala  
 185 190 195

gaa gtc gca cga atc ctc gta gct gaa ggc aac gtc agc caa gcg gat 739  
 Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn Val Ser Gln Ala Asp  
 200 205 210

gca gaa tta gcg gcg gct gcc tca ggc gct cac atc ggc agg gct cga 787  
 Ala Glu Leu Ala Ala Ala Ala Ser Gly Ala His Ile Gly Arg Ala Arg  
 215 220 225

tac tta gcg cac aac aac gcc gcc caa cgc aga cgc gcc agc atc ctc 835  
 Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg Arg Ala Ser Ile Leu  
 230 235 240 245

aac ctg gcc gaa tta atc ttc cac ggt gat gtc gcc ttc cgc tcc gta 883  
 Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val Ala Phe Arg Ser Val  
 250 255 260

aac acc ttg gtc aaa atg gtg gaa acc gaa gcc aaa gac agc aac aaa 931  
 Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala Lys Asp Ser Asn Lys  
 265 270 275

gaa aaa gaa gaa ggc gat ctc gaa gcc gta aga atc tca ctc ggc atg 979  
 Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg Ile Ser Leu Gly Met  
 280 285 290

gcg gcc aaa ggc aaa ggt gtc cac aaa gca gta cgt gga gga gcg gga 1027  
 Ala Ala Lys Gly Lys Gly Val His Lys Ala Val Arg Gly Gly Ala Gly  
 295 300 305

gat ttc aaa gca ctc gaa gac caa caa aaa ctc cga cgc acc cga ttc 1075  
 Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu Arg Arg Thr Arg Phe  
 310 315 320 325

ctc cgc gac agc ctc gac ctc gca ctc gtc gac cta gcc ggc atc tac 1123  
 Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp Leu Ala Gly Ile Tyr  
 330 335 340

cgc gat gcc atc atc att tcc tcc caa gcc caa gtc gga ctc aca cac 1171  
 Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln Val Gly Leu Thr His  
 345 350 355

ccc gat atg gaa ggc ctc tcc caa gaa ctc gca aca aaa gta agc caa 1219  
 Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala Thr Lys Val Ser Gln  
 360 365 370

taagcactcc tggcatgcct cca 1242

&lt;210&gt; 184

&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 184

Val Phe Asp Ser Leu Ala Gly Ser Lys Thr Val Ser Lys Thr Leu Phe



1	5	10	15
Asp Ala Ala Ser Ser Ala Arg Ala Leu Val Arg Ala Arg Thr Thr Glu	20	25	30
Arg Ala Arg Ala Arg Ala Glu His Gln Asn Pro Ala Met Ile His Asp	35	40	45
Ser Gly Phe Ala Gln Ser Trp Leu Phe Thr Gly Pro Pro Gly Ser Gly	50	55	60
Arg Ser Val Ala Ala Lys Val Phe Ala Ala Thr Leu Val Cys Ser Asn	65	70	75
Pro Asp Val Val Gly Cys Gly Gln Cys Glu Asp Cys Arg Ala Ala Met	85	90	95
Gly Gly Ser His Pro Asp Ile Glu His Ile Val Pro Gln Gln Leu Ser	100	105	110
Ile Gly Val Asp Ala Ala Arg Glu Val Ile Lys Ala Ala Val Ser	115	120	125
Pro Val Ala Gly Asn Trp Arg Val Val Ile Phe Glu Asn Ala Asp Arg	130	135	140
Leu Thr Met Gln Ala Ala Asn Ala Leu Leu Lys Thr Val Glu Glu Pro	145	150	155
Thr Glu Ser Thr Val Met Ile Leu Cys Ala Pro Thr Thr Asp Pro Arg	165	170	175
Asp Ile Ala Ile Thr Leu Arg Ser Arg Cys Arg His Leu Tyr Ile Pro	180	185	190
Thr Pro Ser Ile Ala Glu Val Ala Arg Ile Leu Val Ala Glu Gly Asn	195	200	205
Val Ser Gln Ala Asp Ala Glu Leu Ala Ala Ala Ser Gly Ala His	210	215	220
Ile Gly Arg Ala Arg Tyr Leu Ala His Asn Asn Ala Ala Gln Arg Arg	225	230	235
Arg Ala Ser Ile Leu Asn Leu Ala Glu Leu Ile Phe His Gly Asp Val	245	250	255
Ala Phe Arg Ser Val Asn Thr Leu Val Lys Met Val Glu Thr Glu Ala	260	265	270
Lys Asp Ser Asn Lys Glu Lys Glu Glu Gly Asp Leu Glu Ala Val Arg	275	280	285
Ile Ser Leu Gly Met Ala Ala Lys Gly Lys Gly Val His Lys Ala Val	290	295	300
Arg Gly Gly Ala Gly Asp Phe Lys Ala Leu Glu Asp Gln Gln Lys Leu	305	310	315
Arg Arg Thr Arg Phe Leu Arg Asp Ser Leu Asp Leu Ala Leu Val Asp	325	330	335

Leu Ala Gly Ile Tyr Arg Asp Ala Ile Ile Ile Ser Ser Gln Ala Gln  
 340 345 350

Val Gly Leu Thr His Pro Asp Met Glu Gly Leu Ser Gln Glu Leu Ala  
 355 360 365

Thr Lys Val Ser Gln  
 370

<210> 185

<211> 834

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(811)

<223> RXA00214

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gggcacccgg tgtcccatgc gactattagg gtttaggaacc atg aac tca cca agc 115  
 Met Asn Ser Pro Ser  
 1 5

aat cca tct ccc acc gtc cca agc ttg gac acc acc aag atg ctc tcc 163  
 Asn Pro Ser Pro Thr Val Pro Ser Leu Asp Thr Thr Lys Met Leu Ser  
 10 15 20

ttc gac ctg gaa aca acg ggc gtc aat ccc ttt gac acc cgc atc gtc 211  
 Phe Asp Leu Glu Thr Thr Gly Val Asn Pro Phe Asp Thr Arg Ile Val  
 25 30 35

acc tcc gca atg gtt acg atc acc agc aaa ggc gct gag cct att gag 259  
 Thr Ser Ala Met Val Thr Ile Thr Ser Lys Gly Ala Glu Pro Ile Glu  
 40 45 50

cta ttg gct gac ccc ggc atc gaa atc ccc gag gcc gcc act gca gtc 307  
 Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu Ala Ala Thr Ala Val  
 55 60 65

cac ggc atc acc acc gaa cat gcc cgc gcc aac ggc cgt ccg cac gat 355  
 His Gly Ile Thr Thr Glu His Ala Arg Ala Asn Gly Arg Pro His Asp  
 70 75 80 85

gag gtg tta gcc gaa acc atc tcc agg ctg cgc gcc ggc tgg cag gca 403  
 Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg Ala Gly Trp Gln Ala  
 90 95 100

gga ctg tcg gtc att gtc ttc aac gca tcc tat gac ctg acc gta tta 451  
 Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr Asp Leu Thr Val Leu  
 105 110 115

aga aac cat gat cca agc ttc acc atc gac ggc cta gtt tat gac ccc 499  
 Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly Leu Val Tyr Asp Pro  
 120 125 130

ttc gtt atc gac aaa gtc aaa gac cgt tac cgc aaa ggc aag cgc aca 547

Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg Lys Gly Lys Arg Thr  
 135 140 145  
 ctc act gat atg tgt gct cac tac gac gtt caa tta ggc aac gcc cac 595  
 Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln Leu Gly Asn Ala His  
 150 155 160 165  
 gaa gcc acc tca gat gcg ctc gca gcc gca cgc atc gcc tgg aag cag 643  
 Glu Ala Thr Ser Asp Ala Leu Ala Ala Ala Arg Ile Ala Trp Lys Gln  
 170 175 180  
 gtc cgc ctg tgg cca gaa ctc acc aag atg aca ggc gaa gaa ctc atg 691  
 Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr Gly Glu Glu Leu Met  
 185 190 195  
 gag ttc caa gca gtc aac tat tac gag caa caa aag agc ttc cgt agc 739  
 Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln Lys Ser Phe Arg Ser  
 200 205 210  
 tat ctc atc ggg caa ggc cgc gat gcc agc gat gtg aac act tca tgg 787  
 Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp Val Asn Thr Ser Trp  
 215 220 225  
 cca gtg caa act gac ccc gca tcc taaaccgcgc cagatttcta cct 834  
 Pro Val Gln Thr Asp Pro Ala Ser  
 230 235

&lt;210&gt; 186

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 186

Met Asn Ser Pro Ser Asn Pro Ser Pro Thr Val Pro Ser Leu Asp Thr  
 1 5 10 15  
 Thr Lys Met Leu Ser Phe Asp Leu Glu Thr Thr Gly Val Asn Pro Phe  
 20 25 30  
 Asp Thr Arg Ile Val Thr Ser Ala Met Val Thr Ile Thr Ser Lys Gly  
 35 40 45  
 Ala Glu Pro Ile Glu Leu Leu Ala Asp Pro Gly Ile Glu Ile Pro Glu  
 50 55 60  
 Ala Ala Thr Ala Val His Gly Ile Thr Thr Glu His Ala Arg Ala Asn  
 65 70 75 80  
 Gly Arg Pro His Asp Glu Val Leu Ala Glu Thr Ile Ser Arg Leu Arg  
 85 90 95  
 Ala Gly Trp Gln Ala Gly Leu Ser Val Ile Val Phe Asn Ala Ser Tyr  
 100 105 110  
 Asp Leu Thr Val Leu Arg Asn His Asp Pro Ser Phe Thr Ile Asp Gly  
 115 120 125  
 Leu Val Tyr Asp Pro Phe Val Ile Asp Lys Val Lys Asp Arg Tyr Arg  
 130 135 140

Lys Gly Lys Arg Thr Leu Thr Asp Met Cys Ala His Tyr Asp Val Gln  
 145 150 155 160  
 Leu Gly Asn Ala His Glu Ala Thr Ser Asp Ala Leu Ala Ala Arg  
 165 170 175  
 Ile Ala Trp Lys Gln Val Arg Leu Trp Pro Glu Leu Thr Lys Met Thr  
 180 185 190  
 Gly Glu Glu Leu Met Glu Phe Gln Ala Val Asn Tyr Tyr Glu Gln Gln  
 195 200 205  
 Lys Ser Phe Arg Ser Tyr Leu Ile Gly Gln Gly Arg Asp Ala Ser Asp  
 210 215 220  
 Val Asn Thr Ser Trp Pro Val Gln Thr Asp Pro Ala Ser  
 225 230 235

<210> 187  
 <211> 1203  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1180)  
 <223> RXA01255

<400> 187  
 tgcccggtgta tcctatggat ttggtcatct acaaccatca acgaccattt gcatgccttg 60  
 aaatgctgtg aaacctctct aagcaactag agttgtaaaa atg agc acc act tcg 115  
 Met Ser Thr Thr Ser  
 1 5  
 gaa tca caa gat cac gcc gca aga atc gaa gct gag cgc caa gaa gct 163  
 Glu Ser Gln Asp His Ala Ala Arg Ile Glu Ala Glu Arg Gln Glu Ala  
 10 15 20  
 att gag gcg gct cct ttt gtt tcc gtc agc att caa tca agt gga atc 211  
 Ile Glu Ala Ala Pro Phe Val Ser Val Ser Ile Gln Ser Ser Gly Ile  
 25 30 35  
 cac cca tcg act tca cgc atg gtc acc att gat ttg gta acg ctg tcc 259  
 His Pro Ser Thr Ser Arg Met Val Thr Ile Asp Leu Val Thr Leu Ser  
 40 45 50  
 cct aat ttg gag ccg gtg gaa act ttt cat gcc gtg ttg gat tcc aaa 307  
 Pro Asn Leu Glu Pro Val Glu Thr Phe His Ala Val Leu Asp Ser Lys  
 55 60 65  
 act gat cct ggc ccc ttc cac ctt cat ggc gtg aca gag gaa gaa ttt 355  
 Thr Asp Pro Gly Pro Phe His Leu His Gly Val Thr Glu Glu Glu Phe  
 70 75 80 85  
 gcc agc gct aag cgt ttc ggc cag att ttg aaa agc ttg gac cgc ctc 403  
 Ala Ser Ala Lys Arg Phe Gly Gln Ile Leu Lys Ser Leu Asp Arg Leu  
 90 95 100  
 atc gat ggt cgt acc ctg ttg atc cac aat gct gcg cga agt tgg ggc 451

Ile Asp Gly Arg Thr Leu Leu Ile His Asn Ala Ala Arg Ser Trp Gly  
 105 110 115

ttt att gtt tcc gaa gcc aag cgc gct atg aat gat gct gcg cgc gcc 499  
 Phe Ile Val Ser Glu Ala Lys Arg Ala Met Asn Asp Ala Ala Arg Ala  
 120 125 130

aat cgc aac agc aat cgt gga aat cgc cgt ggt ggt cgc gga cgc cgc 547  
 Asn Arg Asn Ser Asn Arg Gly Asn Arg Arg Gly Gly Arg Gly Arg Arg  
 135 140 145

agg cag cgc gtg ggg cac atc cca aag ccg ctg gtg atc gtc gat acg 595  
 Arg Gln Arg Val Gly His Ile Pro Lys Pro Leu Val Ile Val Asp Thr  
 150 155 160 165

ctt gca tcg gcg cgt cga caa gca atc gct tta gac gac gtg cgc atc 643  
 Leu Ala Ser Ala Arg Arg Gln Ala Ile Ala Leu Asp Asp Val Arg Ile  
 170 175 180

cgg ggt gtc gca cac acc ctc ggc ctt gac gcg cct gca gcg gag gcg 691  
 Arg Gly Val Ala His Thr Leu Gly Leu Asp Ala Pro Ala Ala Glu Ala  
 185 190 195

tcg gtg gaa cgc gcg cag gtg tcg cac cgc cag ttg tgc cgc gaa gaa 739  
 Ser Val Glu Arg Ala Gln Val Ser His Arg Gln Leu Cys Arg Glu Glu  
 200 205 210

act ttg ctt gtg gca cgg ctt tat ggt gcg ttg aag cag tca gga ccg 787  
 Thr Leu Leu Val Ala Arg Leu Tyr Gly Ala Leu Lys Gln Ser Gly Pro  
 215 220 225

ctg gcg gaa atc gat ccc cag tcc ttg cgc gcc gat aag ttt ggt ttg 835  
 Leu Ala Glu Ile Asp Pro Gln Ser Leu Arg Ala Asp Lys Phe Gly Leu  
 230 235 240 245

caa cgc tcg atc atc cgg gtg cag gcg cag gaa gct tcg cca acg ctg 883  
 Gln Arg Ser Ile Ile Arg Val Gln Ala Gln Glu Ala Ser Pro Thr Leu  
 250 255 260

gtc aac cct ggt acg tat gag ccg gga aag acg ctg atc gct ggg atg 931  
 Val Asn Pro Gly Thr Tyr Glu Pro Gly Lys Thr Leu Ile Ala Gly Met  
 265 270 275

gaa gtt gtg gtc gcg ccg gaa att gag atg gat ccg gac atc att atc 979  
 Glu Val Val Val Ala Pro Glu Ile Glu Met Asp Pro Asp Ile Ile Ile  
 280 285 290

caa gcg tgc gtc gat gca gat ttg tcc tat tct gag aag ctc acc cgg 1027  
 Gln Ala Cys Val Asp Ala Asp Leu Ser Tyr Ser Glu Lys Leu Thr Arg  
 295 300 305

caa acc tca gtg gtg gtg tgc aat caa acc cgc gac att gac ggc aaa 1075  
 Gln Thr Ser Val Val Val Cys Asn Gln Thr Arg Asp Ile Asp Gly Lys  
 310 315 320 325

gcg atg cat gcc cag cgt aaa gga att ccg ctg ctg tcc gat gtt gcc 1123  
 Ala Met His Ala Gln Arg Lys Gly Ile Pro Leu Leu Ser Asp Val Ala  
 330 335 340

ttc tta gca gct gtt aaa agg gta aaa gaa ggg aag aaa gtg gac gtc 1171  
 Phe Leu Ala Ala Val Lys Arg Val Lys Glu Gly Lys Lys Val Asp Val

345 350 355 1203

gaa aag cgc tagtgccact tgcttaacta gac  
 Glu Lys Arg  
 360

<210> 188  
 <211> 360  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 188  
 Met Ser Thr Thr Ser Glu Ser Gln Asp His Ala Ala Arg Ile Glu Ala  
 1 5 10 15  
 Glu Arg Gln Glu Ala Ile Glu Ala Ala Pro Phe Val Ser Val Ser Ile  
 20 25 30  
 Gln Ser Ser Gly Ile His Pro Ser Thr Ser Arg Met Val Thr Ile Asp  
 35 40 45  
 Leu Val Thr Leu Ser Pro Asn Leu Glu Pro Val Glu Thr Phe His Ala  
 50 55 60  
 Val Leu Asp Ser Lys Thr Asp Pro Gly Pro Phe His Leu His Gly Val  
 65 70 75 80  
 Thr Glu Glu Glu Phe Ala Ser Ala Lys Arg Phe Gly Gln Ile Leu Lys  
 85 90 95  
 Ser Leu Asp Arg Leu Ile Asp Gly Arg Thr Leu Leu Ile His Asn Ala  
 100 105 110  
 Ala Arg Ser Trp Gly Phe Ile Val Ser Glu Ala Lys Arg Ala Met Asn  
 115 120 125  
 Asp Ala Ala Arg Ala Asn Arg Asn Ser Asn Arg Gly Asn Arg Arg Gly  
 130 135 140  
 Gly Arg Gly Arg Arg Arg Gln Arg Val Gly His Ile Pro Lys Pro Leu  
 145 150 155 160  
 Val Ile Val Asp Thr Leu Ala Ser Ala Arg Arg Gln Ala Ile Ala Leu  
 165 170 175  
 Asp Asp Val Arg Ile Arg Gly Val Ala His Thr Leu Gly Leu Asp Ala  
 180 185 190  
 Pro Ala Ala Glu Ala Ser Val Glu Arg Ala Gln Val Ser His Arg Gln  
 195 200 205  
 Leu Cys Arg Glu Glu Thr Leu Leu Val Ala Arg Leu Tyr Gly Ala Leu  
 210 215 220  
 Lys Gln Ser Gly Pro Leu Ala Glu Ile Asp Pro Gln Ser Leu Arg Ala  
 225 230 235 240  
 Asp Lys Phe Gly Leu Gln Arg Ser Ile Ile Arg Val Gln Ala Gln Glu  
 245 250 255

Ala Ser Pro Thr Leu Val Asn Pro Gly Thr Tyr Glu Pro Gly Lys Thr  
260 265 270

Leu Ile Ala Gly Met Glu Val Val Val Ala Pro Glu Ile Glu Met Asp  
275 280 285

Pro Asp Ile Ile Ile Gln Ala Cys Val Asp Ala Asp Leu Ser Tyr Ser  
290 295 300

Glu Lys Leu Thr Arg Gln Thr Ser Val Val Val Cys Asn Gln Thr Arg  
305 310 315 320

Asp Ile Asp Gly Lys Ala Met His Ala Gln Arg Lys Gly Ile Pro Leu  
325 330 335

Leu Ser Asp Val Ala Phe Leu Ala Ala Val Lys Arg Val Lys Glu Gly  
340 345 350

Lys Lys Val Asp Val Glu Lys Arg  
355 360

<210> 189

<211> 913

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXN00066

<400> 189

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tcgaccggca agttttggtg aactagttgg gcagtcgcaa gtg act gac cct ctg 115  
Val Thr Asp Pro Leu  
1 5

tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg 163  
Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser  
10 15 20

ggt ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg 211  
Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg  
25 30 35

tcc ctc aac tgc gtg gaa ggc cca act tcc acg ccg tgt ggg gtg tgt 259  
Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr Pro Cys Gly Val Cys  
40 45 50

aat tct tgc gta gcg ctg gcc ccg ggt ggc cct gga acc ctt gat gta 307  
Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro Gly Thr Leu Asp Val  
55 60 65

aca gag ctc gac gcc gcg agt aac aat ggt gtc gat gac atg cgt gaa 355  
Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val Asp Asp Met Arg Glu  
70 75 80 85

ctg cgc gaa cgc gcg aac tac gcc ccg gcg gaa tct cgc tac cgc gtg 403  
Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu Ser Arg Tyr Arg Val

90	95	100	
ttc atc att gac gaa gcc cac atg atc agt acc caa ggc ttc aac gcc			451
Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr Gln Gly Phe Asn Ala			
105	110	115	
ttg ctg aaa atc gtt gaa gag cca cca gcg cac ctg att ttc atc ttc			499
Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His Leu Ile Phe Ile Phe			
120	125	130	
gcc acc acc gag ccg gac aaa atg atc ggt acg atc cgt tcc cgc acg			547
Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr Ile Arg Ser Arg Thr			
135	140	145	
cac aat tac cca ttc cgc ctg ctc acc cca ggg gat atg cgc aaa gtg			595
His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly Asp Met Arg Lys Val			
150	155	160	165
ctg aaa aat gcg gtc gat ggc gaa ggc gtc cac gtc gac gat tcc gtt			643
Leu Lys Asn Ala Val Asp Gly Glu Gly Val His Val Asp Asp Ser Val			
170	175	180	
tac cca ctg gtc atc cgc gcc ggc ggc ggc agc ccc cgc gac agc ctc			691
Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser Pro Arg Asp Ser Leu			
185	190	195	
tcc atc ctc gac cag ctc atc gcc ggc tcg ggc ccg gag ggc ttg aca			739
Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly Pro Glu Gly Leu Thr			
200	205	210	
tat gag cgc gcc ttg ccg ctg ctc ggt gtc aca agc ttc acg ctt atc			787
Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr Ser Phe Thr Leu Ile			
215	220	225	
gac gat tcg atc cat gcc ctt gca tct aaa gac aac gca agc atg ttc			835
Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp Asn Ala Ser Met Phe			
230	235	240	245
acc acg atc gat aac gtc atc gaa gaa ggc ctc gaa ccg cga cgc ttc			883
Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu Glu Pro Arg Arg Phe			
250	255	260	
acg atc gac ttt ctt tcg acc cgc tcc ggg			913
Thr Ile Asp Phe Leu Ser Thr Arg Ser Gly			
265	270		

&lt;210&gt; 190

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 190

Val Thr Asp Pro Leu Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His
1 5 10 15

Ala Tyr Leu Phe Ser Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala
20 25 30

Arg Ile Leu Ala Arg Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr
35 40 45



Pro Cys Gly Val Cys Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro  
 50 55 60

Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val  
 65 70 75 80

Asp Asp Met Arg Glu Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu  
 85 90 95

Ser Arg Tyr Arg Val Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr  
 100 105 110

Gln Gly Phe Asn Ala Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His  
 115 120 125

Leu Ile Phe Ile Phe Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr  
 130 135 140

Ile Arg Ser Arg Thr His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly  
 145 150 155 160

Asp Met Arg Lys Val Leu Lys Asn Ala Val Asp Gly Glu Gly Val His  
 165 170 175

Val Asp Asp Ser Val Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser  
 180 185 190

Pro Arg Asp Ser Leu Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly  
 195 200 205

Pro Glu Gly Leu Thr Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr  
 210 215 220

Ser Phe Thr Leu Ile Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp  
 225 230 235 240

Asn Ala Ser Met Phe Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu  
 245 250 255

Glu Pro Arg Arg Phe Thr Ile Asp Phe Leu Ser Thr Arg Ser Gly  
 260 265 270

<210> 191

<211> 913

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> FRXA00066

<400> 191

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tcgaccggca agttttggtg aactagttgg gcagtcgcaa gtg act gac cct ctg 115  
 Val Thr Asp Pro Leu  
 1 5

tcc gca gct ttg gat agc ggg cgc atc aac cat gcg tac ctt ttt tcg 163  
 Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His Ala Tyr Leu Phe Ser  
 10 15 20

ggt ccg cgt ggt tgt ggc aag acg tcg tcg gca cgc atc ctt gcc cgg 211  
 Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala Arg Ile Leu Ala Arg  
 25 30 35

tcc ctc aac tgc gtg gaa ggc cca act tcc acg ccg tgt ggg gtg tgt 259  
 Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr Pro Cys Gly Val Cys  
 40 45 50

aat tct tgc gta gcg ctg gcc ccg ggt ggc cct gga acc ctt gat gta 307  
 Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro Gly Thr Leu Asp Val  
 55 60 65

aca gag ctc gac gcc gcg agt aac aat ggt gtc gat gac atg cgt gaa 355  
 Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val Asp Asp Met Arg Glu  
 70 75 80 85

ctg cgc gaa cgc gcg aac tac gcc ccg gcg gaa tct cgc tac cgc gtg 403  
 Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu Ser Arg Tyr Arg Val  
 90 95 100

ttc atc att gac gaa gcc cac atg atc agt acc caa ggc ttc aac gcc 451  
 Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr Gln Gly Phe Asn Ala  
 105 110 115

ttg ctg aaa atc gtt gaa gag cca cca gcg cac ctg att ttc atc ttc 499  
 Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His Leu Ile Phe Ile Phe  
 120 125 130

gcc acc acc gag ccg gac aaa atg atc ggt acg atc cgt tcc cgc acg 547  
 Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr Ile Arg Ser Arg Thr  
 135 140 145

cac aat tac cca ttc cgc ctg ctc acc cca ggg gat atg cgc aaa gtg 595  
 His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly Asp Met Arg Lys Val  
 150 155 160 165

ctg aaa aat gcg gtc gat ggc gaa ggc gtc cac gtc gac gat tcc gtt 643  
 Leu Lys Asn Ala Val Asp Gly Glu Gly Val His Val Asp Asp Ser Val  
 170 175 180

tac cca ctg gtc atc cgc gcc ggc ggc ggc agc ccc cgc gac agc ctc 691  
 Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser Pro Arg Asp Ser Leu  
 185 190 195

tcc atc ctc gac cag ctc atc gcc ggc tcg ggc ccg gag ggc ttg aca 739  
 Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly Pro Glu Gly Leu Thr  
 200 205 210

tat gag cgc gcc ttg ccg ctg ctc ggt gtc aca agc ttc acg ctt atc 787  
 Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr Ser Phe Thr Leu Ile  
 215 220 225

gac gat tcg atc cat gcc ctt gca tct aaa gac aac gca agc atg ttc 835  
 Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp Asn Ala Ser Met Phe  
 230 235 240 245

acc acg atc gat aac gtc atc gaa gaa ggc ctc gaa ccg cga cgc ttc 883

Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu Glu Pro Arg Arg Phe  
 250 255 260

acg atc gac ctt cct tcg gac ccg ctc cgg  
 Thr Ile Asp Leu Pro Ser Asp Pro Leu Arg  
 265 270

913

<210> 192  
 <211> 271  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 192  
 Val Thr Asp Pro Leu Ser Ala Ala Leu Asp Ser Gly Arg Ile Asn His  
 1 5 10 15

Ala Tyr Leu Phe Ser Gly Pro Arg Gly Cys Gly Lys Thr Ser Ser Ala  
 20 25 30

Arg Ile Leu Ala Arg Ser Leu Asn Cys Val Glu Gly Pro Thr Ser Thr  
 35 40 45

Pro Cys Gly Val Cys Asn Ser Cys Val Ala Leu Ala Pro Gly Gly Pro  
 50 55 60

Gly Thr Leu Asp Val Thr Glu Leu Asp Ala Ala Ser Asn Asn Gly Val  
 65 70 75 80

Asp Asp Met Arg Glu Leu Arg Glu Arg Ala Asn Tyr Ala Pro Ala Glu  
 85 90 95

Ser Arg Tyr Arg Val Phe Ile Ile Asp Glu Ala His Met Ile Ser Thr  
 100 105 110

Gln Gly Phe Asn Ala Leu Leu Lys Ile Val Glu Glu Pro Pro Ala His  
 115 120 125

Leu Ile Phe Ile Phe Ala Thr Thr Glu Pro Asp Lys Met Ile Gly Thr  
 130 135 140

Ile Arg Ser Arg Thr His Asn Tyr Pro Phe Arg Leu Leu Thr Pro Gly  
 145 150 155 160

Asp Met Arg Lys Val Leu Lys Asn Ala Val Asp Gly Glu Gly Val His  
 165 170 175

Val Asp Asp Ser Val Tyr Pro Leu Val Ile Arg Ala Gly Gly Gly Ser  
 180 185 190

Pro Arg Asp Ser Leu Ser Ile Leu Asp Gln Leu Ile Ala Gly Ser Gly  
 195 200 205

Pro Glu Gly Leu Thr Tyr Glu Arg Ala Leu Pro Leu Leu Gly Val Thr  
 210 215 220

Ser Phe Thr Leu Ile Asp Asp Ser Ile His Ala Leu Ala Ser Lys Asp  
 225 230 235 240

Asn Ala Ser Met Phe Thr Thr Ile Asp Asn Val Ile Glu Glu Gly Leu  
 245 250 255

Glu Pro Arg Arg Phe Thr Ile Asp Leu Pro Ser Asp Pro Leu Arg  
 260 265 270

<210> 193

<211> 751

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (89)..(751)

<223> RXN01637

<400> 193

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gcaaacgagc tcgccaaacc tagcctccatg gtg aac tcc gga ctc gac gac atg 115  
 Met Val Asn Ser Gly Leu Asp Asp Met  
 1 5

cgt ggt gcc acc tca ccg cgc ctc ctt ctg gaa atc ctc tgc gcc cga 163  
 Arg Gly Ala Thr Ser Pro Arg Leu Leu Leu Ile Leu Cys Ala Arg  
 10 15 20 25

ctg ctc ctg gca agc aat acc gtg gca ggt cca gcg gtc agt agt tcg 211  
 Leu Leu Leu Ala Ser Asn Thr Val Ala Gly Pro Ala Val Ser Ser Ser  
 30 35 40

act gac gct gcg cct gca gct act ccg ggt ggt ctc act ggt att gct 259  
 Thr Asp Ala Ala Pro Ala Ala Thr Pro Gly Gly Leu Thr Gly Ile Ala  
 45 50 55

gct gcc cgc gcg aaa gca cgg gag tat gga cag aag aag gca gct cca 307  
 Ala Ala Arg Ala Lys Ala Arg Glu Tyr Gly Gln Lys Lys Ala Ala Pro  
 60 65 70

gct cct gca cca act cct gcg ccc gag cca gtg cgc gaa cag tct ctt 355  
 Ala Pro Ala Pro Thr Pro Ala Pro Glu Pro Val Arg Glu Gln Ser Leu  
 75 80 85

gca cca acg cct gaa cca acg cca gcg gct gaa cct aca tct cag ccc 403  
 Ala Pro Thr Pro Glu Pro Thr Pro Ala Ala Glu Pro Thr Ser Gln Pro  
 90 95 100 105

gcg ccg gaa ccg gaa ccc gcc agg gaa cca gtg gtg gaa gtg cgg gag 451  
 Ala Pro Glu Pro Glu Pro Ala Arg Glu Pro Val Val Glu Val Arg Glu  
 110 115 120

gcg agc gtc gaa aag cag cct gca agc agt gat ccc ctc gaa acc att 499  
 Ala Ser Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu Glu Thr Ile  
 125 130 135

cga agc cgc tgg tca gag ctg cgc aac atc gtg gaa aaa caa agt gtg 547  
 Arg Ser Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys Gln Ser Val  
 140 145 150

cgc acc tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga gcc 595  
 Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg Gly  
 155 160 165

gat acc ctc gtg ctc ggt cac agc acc ggg gcg ttg gct gcg cgt ttg 643  
 Asp Thr Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala Ala Arg Leu  
 170 175 180 185  
  
 aac gct gct gat cac aac gga att ttg gtc aag gtg ttg gct gag gaa 691  
 Asn Ala Ala Asp His Asn Gly Ile Leu Val Lys Val Leu Ala Glu Glu  
 190 195 200  
  
 act ggt ctg cag ctc aag gtc gaa tgc att gtg ggc acg aac cca gcc 739  
 Thr Gly Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr Asn Pro Ala  
 205 210 215  
  
 gaa gct gga ttt 751  
 Glu Ala Gly Phe  
 220

&lt;210&gt; 194

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 194

Met Val Asn Ser Gly Leu Asp Asp Met Arg Gly Ala Thr Ser Pro Arg  
 1 5 10 15

Leu Leu Leu Glu Ile Leu Cys Ala Arg Leu Leu Leu Ala Ser Asn Thr  
 20 25 30

Val Ala Gly Pro Ala Val Ser Ser Ser Thr Asp Ala Ala Pro Ala Ala  
 35 40 45

Thr Pro Gly Gly Leu Thr Gly Ile Ala Ala Ala Arg Ala Lys Ala Arg  
 50 55 60

Glu Tyr Gly Gln Lys Lys Ala Ala Pro Ala Pro Ala Pro Thr Pro Ala  
 65 70 75 80

Pro Glu Pro Val Arg Glu Gln Ser Leu Ala Pro Thr Pro Glu Pro Thr  
 85 90 95

Pro Ala Ala Glu Pro Thr Ser Gln Pro Ala Pro Glu Pro Glu Pro Ala  
 100 105 110

Arg Glu Pro Val Val Glu Val Arg Glu Ala Ser Val Glu Lys Gln Pro  
 115 120 125

Ala Ser Ser Asp Pro Leu Glu Thr Ile Arg Ser Arg Trp Ser Glu Leu  
 130 135 140

Arg Asn Ile Val Glu Lys Gln Ser Val Arg Thr Ser Ile Met Leu Thr  
 145 150 155 160

Glu Ala Arg Val Leu Gly Leu Arg Gly Asp Thr Leu Val Leu Gly His  
 165 170 175

Ser Thr Gly Ala Leu Ala Ala Arg Leu Asn Ala Ala Asp His Asn Gly  
 180 185 190

Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly Leu Gln Leu Lys Val

195 200 205

Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala Gly Phe  
 210 215 220

<210> 195  
 <211> 409  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(409)  
 <223> FRXA01637

<400> 195  
 cagtctcttg caccaacgcc tgaaccaacg ccagcgggct gaacctacat tctcagcccg 60  
 cgccgggaac ccggaamccg scaggraamc agtgggtggaa gtg cgg gag gcg agc 115  
 Val Arg Glu Ala Ser  
 1 5

gtc gaa aag cag cct gca agc agt gat ccc ctc gaa acc att cga agc 163  
 Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu Glu Thr Ile Arg Ser  
 10 15 20

cgc tgg tca gag ctg cgc aac atc gtg gaa aaa caa agt gtg cgc acc 211  
 Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys Gln Ser Val Arg Thr  
 25 30 35

tca atc atg ctg acc gaa gcg cga gtt ttg gga ctg cga ggc gat acc 259  
 Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly Leu Arg Gly Asp Thr  
 40 45 50

ctc gtg ctc ggt cac agc acc ggg gcg ttg gct gcg cgt ttg aac gct 307  
 Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala Ala Arg Leu Asn Ala  
 55 60 65

gct gat cac aac gga att ttg gtc aag gtg ttg gct gag gaa act ggt 355  
 Ala Asp His Asn Gly Ile Leu Val Lys Val Leu Ala Glu Glu Thr Gly  
 70 75 80 85

ctg cag ctc aag gtc gaa tgc att gtg ggc acg aac cca gcc gaa gct 403  
 Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr Asn Pro Ala Glu Ala  
 90 95 100

gga ttt 409  
 Gly Phe

<210> 196  
 <211> 103  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 196  
 Val Arg Glu Ala Ser Val Glu Lys Gln Pro Ala Ser Ser Asp Pro Leu  
 1 5 10 15

Glu Thr Ile Arg Ser Arg Trp Ser Glu Leu Arg Asn Ile Val Glu Lys  
                   20                                  25                                  30  
 Gln Ser Val Arg Thr Ser Ile Met Leu Thr Glu Ala Arg Val Leu Gly  
                   35                                  40                                  45  
 Leu Arg Gly Asp Thr Leu Val Leu Gly His Ser Thr Gly Ala Leu Ala  
                   50                                  55                                  60  
 Ala Arg Leu Asn Ala Ala Asp His Asn Gly Ile Leu Val Lys Val Leu  
                   65                                  70                                  75                                  80  
 Ala Glu Glu Thr Gly Leu Gln Leu Lys Val Glu Cys Ile Val Gly Thr  
                                   85                                  90                                  95  
 Asn Pro Ala Glu Ala Gly Phe  
                                   100

&lt;210&gt; 197

&lt;211&gt; 1683

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1660)

&lt;223&gt; RXA00212

&lt;400&gt; 197

ttagagcgtg ccgctactcg tggatgatggc cgcggtgggcg aggacatcac ggccaatgct 60  
 cgcgatgatcg aagatatccc gcaccagctt cagggcactg atg aat atc ctg tgc 115  
   Met Asn Ile Leu Cys  
   1                                  5  
 ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att 163  
 Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile  
                                   10                                  15                                  20  
 tcc cag gag gtc aac gcg cag cgc att gct gat ggt ggc aag ccg ttt 211  
 Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe  
                                   25                                  30                                  35  
 gcc aac ccg cgt aat gct gcg gct ggt tct ctg cgt cag aaa aat att 259  
 Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asn Ile  
                                   40                                  45                                  50  
 gag gac gtg aag aag cgc cgc ctg cgg atg atc agc cat ggc atc ggt 307  
 Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile Ser His Gly Ile Gly  
                                   55                                  60                                  65  
 ttc act gaa ggc ttt agc cct gcg tct cag cat gat gcg tat ctg gca 355  
 Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His Asp Ala Tyr Leu Ala  
                                   70                                  75                                  80                                  85  
 ttg gct gcc tgg ggt ttg ccc acc tcg ccg tac aca gag gct gtg act 403  
 Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr Thr Glu Ala Val Thr  
                                   90                                  95                                  100  
 gat cca gaa gat gtg gtg aaa aag gtc agc tac tgg gct gat cac cgc 451

Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr Trp Ala Asp His Arg	
105 110 115	
cac gac gca ctc cat gag atg gat ggc ctg gtg att aag gtc gat gac	499
His Asp Ala Leu His Glu Met Asp Gly Leu Val Ile Lys Val Asp Asp	
120 125 130	
atc gca tct cag cgt gct ttg ggt tcc acc agc cgc gcg cct cgc tgg	547
Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser Arg Ala Pro Arg Trp	
135 140 145	
gcc att gcg tac aag tac cct ccg gag gag gtc acc acc aag ctg ctt	595
Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val Thr Thr Lys Leu Leu	
150 155 160 165	
gat att cag gtt ggc gtt ggt cgc acc ggc cgt gtc acc cca ttc gcg	643
Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg Val Thr Pro Phe Ala	
170 175 180	
gtc atg gag ccg gtt ctt gtt gca gga tca acg gtg tct atg gcg acg	691
Val Met Glu Pro Val Leu Val Ala Gly Ser Thr Val Ser Met Ala Thr	
185 190 195	
ctg cat aac cag agc gaa gtc aag cgt aaa ggc gtg ctc atc ggt gac	739
Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly Val Leu Ile Gly Asp	
200 205 210	
acc gtg gtt atc cgc aag gcg ggc gag gtt atc cca gag gtg ctt ggc	787
Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile Pro Glu Val Leu Gly	
215 220 225	
cct gtc gta gag ctt cgt gac ggc aca gag cgc gag tac atc ttc cca	835
Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg Glu Tyr Ile Phe Pro	
230 235 240 245	
acg ctg tgc cct gaa tgc ggt acc cgt ctg gcg ccc gcg aag gcc gat	883
Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala Pro Ala Lys Ala Asp	
250 255 260	
gac gtg gat tgg cgt tgc ccc aac atg caa agc tgt cca ggt cag ctg	931
Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser Cys Pro Gly Gln Leu	
265 270 275	
tcc acg cgt ttg acc tac ctt gct ggt cgt ggc gct ttt gat att gaa	979
Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly Ala Phe Asp Ile Glu	
280 285 290	
gca ttg ggc gaa aag ggc gct gaa gac ctc att cgc acc ggc att ttg	1027
Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile Arg Thr Gly Ile Leu	
295 300 305	
ctt gac gag tct ggc ctg ttc gac ctc aca gag gac gat ctg ctg agc	1075
Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu Asp Asp Leu Leu Ser	
310 315 320 325	
tcc aat gtc tac acc acc aac gcc ggc aaa gta aat gcc agc ggc aag	1123
Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val Asn Ala Ser Gly Lys	
330 335 340	
aaa ctg ctg gac aac ctg caa aaa tcc aag cag acc gac ctc tgg cga	1171
Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln Thr Asp Leu Trp Arg	



345	350	355	
gtc ctc gtg gca tta tct atc agg cac gta ggc ccc acc gca gcg cgc			1219
Val Leu Val Ala Leu Ser Ile Arg His Val Gly Pro Thr Ala Ala Arg			
360	365	370	
gcc ctt gca ggt cgc tac cac tcc atc cag gcg ctt atc gac gcc ccc			1267
Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala Leu Ile Asp Ala Pro			
375	380	385	
ctc gag gaa ctc tcc gaa acc gat gga gta ggt acc atc att gcc caa			1315
Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly Thr Ile Ile Ala Gln			
390	395	400	405
tcc ttc aag gac tgg ttc gag gtt gat tgg cac aag gcc atc gtg gac			1363
Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His Lys Ala Ile Val Asp			
410	415	420	
aag tgg gca gcc gct ggt gtg act atg gag gaa gaa gta ggg gag gtc			1411
Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu Glu Val Gly Glu Val			
425	430	435	
gct gaa caa acc ctt gaa ggc cta acc atc gtg gtc acc gga ggg ttg			1459
Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val Val Thr Gly Gly Leu			
440	445	450	
gaa ggc ttc acc aga gat tgc gtg aag gaa gcc atc atc tcc cgt ggc			1507
Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala Ile Ile Ser Arg Gly			
455	460	465	
gga aaa gcc tct gga tct gtc tgc aag aaa act gac tac gtg gtg att			1555
Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr Asp Tyr Val Val Ile			
470	475	480	485
ggt gaa aac gca ggt tcc aag gcc acc aag gca gaa gaa cta ggg ctg			1603
Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala Glu Glu Leu Gly Leu			
490	495	500	
cgc att ctg gat gag gca gga ttc gtc cgt ttg ctc aat acc ggc tca			1651
Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu Leu Asn Thr Gly Ser			
505	510	515	
gct gac gaa tagtcgcaca tgaaaatgcc cca			1683
Ala Asp Glu			
520			

&lt;210&gt; 198

&lt;211&gt; 520

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 198

Met	Asn	Ile	Leu	Cys	Leu	Leu	Cys	Trp	Lys	Phe	Ala	Val	Arg	Cys	Ser
1				5					10					15	

Ser	Leu	Trp	Arg	Ile	Ser	Gln	Glu	Val	Asn	Ala	Gln	Arg	Ile	Ala	Asp
	20							25					30		

Gly	Gly	Lys	Pro	Phe	Ala	Asn	Pro	Arg	Asn	Ala	Ala	Ala	Gly	Ser	Leu
		35					40					45			

Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile  
 50 55 60  
 Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His  
 65 70 75 80  
 Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr  
 85 90 95  
 Thr Glu Ala Val Thr Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr  
 100 105 110  
 Trp Ala Asp His Arg His Asp Ala Leu His Glu Met Asp Gly Leu Val  
 115 120 125  
 Ile Lys Val Asp Asp Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser  
 130 135 140  
 Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val  
 145 150 155 160  
 Thr Thr Lys Leu Leu Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg  
 165 170 175  
 Val Thr Pro Phe Ala Val Met Glu Pro Val Leu Val Ala Gly Ser Thr  
 180 185 190  
 Val Ser Met Ala Thr Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly  
 195 200 205  
 Val Leu Ile Gly Asp Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile  
 210 215 220  
 Pro Glu Val Leu Gly Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg  
 225 230 235 240  
 Glu Tyr Ile Phe Pro Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala  
 245 250 255  
 Pro Ala Lys Ala Asp Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser  
 260 265 270  
 Cys Pro Gly Gln Leu Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly  
 275 280 285  
 Ala Phe Asp Ile Glu Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile  
 290 295 300  
 Arg Thr Gly Ile Leu Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu  
 305 310 315 320  
 Asp Asp Leu Leu Ser Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val  
 325 330 335  
 Asn Ala Ser Gly Lys Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln  
 340 345 350  
 Thr Asp Leu Trp Arg Val Leu Val Ala Leu Ser Ile Arg His Val Gly  
 355 360 365

Pro Thr Ala Ala Arg Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala  
 370 375 380  
 Leu Ile Asp Ala Pro Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly  
 385 390 395 400  
 Thr Ile Ile Ala Gln Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His  
 405 410 415  
 Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu  
 420 425 430  
 Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val  
 435 440 445  
 Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala  
 450 455 460  
 Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr  
 465 470 475 480  
 Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala  
 485 490 495  
 Glu Glu Leu Gly Leu Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu  
 500 505 510  
 Leu Asn Thr Gly Ser Ala Asp Glu  
 515 520

<210> 199  
 <211> 696  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(673)  
 <223> RXA00213

<400> 199  
 aggtctgcac ccattcatat gcgaattttg acgtgagttt tagctttccg agcacctgtg 60  
 cgaatggccg tgtccaccct tagggttaga atcgggaacc gtg act gaa gat aat 115  
 Val Thr Glu Asp Asn  
 1 5  
 gct caa ctg cgt aga acg tgg aac gac tta gcc gag aag gtt cgt tat 163  
 Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala Glu Lys Val Arg Tyr  
 10 15 20  
 cac cga gat cgt tat tac aac gaa cag cca gag atc cct gat gct gat 211  
 His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu Ile Pro Asp Ala Asp  
 25 30 35  
 ttt gat gcg ctt ttt aag cag ctt cag cag ttg gaa gaa gac cac ccg 259  
 Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu Glu Glu Asp His Pro  
 40 45 50  
 gag ctc gcc gtc cct gat agc ccc acc atg gtt gtg ggc gct ccg gtg 307

Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val Val Gly Ala Pro Val  
 55 60 65

gca gag caa tca agc ttt gac aat gtt gag cac ttg gag cga atg ctc 355  
 Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His Leu Glu Arg Met Leu  
 70 75 80 85

agc ttg gac aat gtt ttt gat gag cag gag ttg cgt gat tgg ttg ggc 403  
 Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu Arg Asp Trp Leu Gly  
 90 95 100

agg acg cca gcc aag cag tat ttg acg gag ttg aaa att gat ggc ttg 451  
 Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu Lys Ile Asp Gly Leu  
 105 110 115

tcc atc gac ttg gtg tat cgc aat ggc cag tta gag cgt gcc gct act 499  
 Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu Glu Arg Ala Ala Thr  
 120 125 130

cgt ggt gat ggt cgc gtg ggc gag gac atc acg gcc aat gct cgc gtg 547  
 Arg Gly Asp Gly Arg Val Glu Glu Asp Ile Thr Ala Asn Ala Arg Val  
 135 140 145

atc gaa gat atc ccg cac cag ctt cag ggc act gat gaa tat cct gtg 595  
 Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr Asp Glu Tyr Pro Val  
 150 155 160 165

cct gct gtg ctg gaa att cgc ggt gag gtg ttc atc act gtg gag gat 643  
 Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe Ile Thr Val Glu Asp  
 170 175 180

ttc cca gga ggt caa cgc gca gcg cat tgc tgatgggtggc aagccgtttg 693  
 Phe Pro Gly Gly Gln Arg Ala Ala His Cys  
 185 190

cca 696

<210> 200  
 <211> 191  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 200  
 Val Thr Glu Asp Asn Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala  
 1 5 10 15

Glu Lys Val Arg Tyr His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu  
 20 25 30

Ile Pro Asp Ala Asp Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu  
 35 40 45

Glu Glu Asp His Pro Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val  
 50 55 60

Val Gly Ala Pro Val Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His  
 65 70 75 80

Leu Glu Arg Met Leu Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu  
 85 90 95

Arg Asp Trp Leu Gly Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu  
100 105 110

Lys Ile Asp Gly Leu Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu  
115 120 125

Glu Arg Ala Ala Thr Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr  
130 135 140

Ala Asn Ala Arg Val Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr  
145 150 155 160

Asp Glu Tyr Pro Val Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe  
165 170 175

Ile Thr Val Glu Asp Phe Pro Gly Gly Gln Arg Ala Ala His Cys  
180 185 190

<210> 201

<211> 366

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(343)

<223> RXA00789

<400> 201

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gcacccagca agcaaaactaa aaacttagga gaatgaagaa atg acc aat cca gat 115  
Met Thr Asn Pro Asp  
1 5

atc gtc ggt tcc ggc caa ggc aac gat tcc ttc gag cca gtc gcc caa 163  
Ile Val Gly Ser Gly Gln Gly Asn Asp Ser Phe Glu Pro Val Ala Gln  
10 15 20

tta tcc tac gag cgt gca cgc gat gaa ctc gtt gaa att gta aaa att 211  
Leu Ser Tyr Glu Arg Ala Arg Asp Glu Leu Val Glu Ile Val Lys Ile  
25 30 35

ttg gag ctc ggc caa atg ggc ctc gac gaa tcc ctc aaa tac tgg gag 259  
Leu Glu Leu Gly Gln Met Gly Leu Asp Glu Ser Leu Lys Tyr Trp Glu  
40 45 50

cgc ggc gaa gcc cta gca aag cgc tgc gaa gag cac ctg gcc ggc gcc 307  
Arg Gly Glu Ala Leu Ala Lys Arg Cys Glu Glu His Leu Ala Gly Ala  
55 60 65

tca gcg cgc gtc gag caa gca tta aac cag gca gaa taatgctttt 353  
Ser Ala Arg Val Glu Gln Ala Leu Asn Gln Ala Glu  
70 75 80

cgacgcatcc ctc 366

<210> 202

<211> 81  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 202

Met Thr Asn Pro Asp Ile Val Gly Ser Gly Gln Gly Asn Asp Ser Phe  
 1 5 10 15

Glu Pro Val Ala Gln Leu Ser Tyr Glu Arg Ala Arg Asp Glu Leu Val  
 20 25 30

Glu Ile Val Lys Ile Leu Glu Leu Gly Gln Met Gly Leu Asp Glu Ser  
 35 40 45

Leu Lys Tyr Trp Glu Arg Gly Glu Ala Leu Ala Lys Arg Cys Glu Glu  
 50 55 60

His Leu Ala Gly Ala Ser Ala Arg Val Glu Gln Ala Leu Asn Gln Ala  
 65 70 75 80

Glu

<210> 203  
 <211> 1185  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1162)

<223> RXN00790

<400> 203

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aaagctgtcg aatttgacgc ttcgtgatgt ggagcaagaa atg tct gtg cag ctg 115  
 Met Ser Val Gln Leu  
 1 5

acc tgc ccg acg gac att atc cgc aat cgc ccc aca ccg ctc aag gat 163  
 Thr Cys Pro Thr Asp Ile Ile Arg Asn Arg Pro Thr Pro Leu Lys Asp  
 10 15 20

ggc gac cgc gtg att gtg tac ggc aag ccc gcg ttt tat gca ggc cgc 211  
 Gly Asp Arg Val Ile Val Tyr Gly Lys Pro Ala Phe Tyr Ala Gly Arg  
 25 30 35

ggc act ttt tgc ctg tgg gtg act gat atc cgt ccc gtg ggt att ggt 259  
 Gly Thr Phe Ser Leu Trp Val Thr Asp Ile Arg Pro Val Gly Ile Gly  
 40 45 50

gag ttg ctg gcg cgc att gag gag ctg cgt aaa agg ctt gcc gcg gag 307  
 Glu Leu Leu Ala Arg Ile Glu Glu Leu Arg Lys Arg Leu Ala Ala Glu  
 55 60 65

ggt ctt ttt gat cca gct cgg aag aag cga ctg cca ttt ctg ccc aac 355  
 Gly Leu Phe Asp Pro Ala Arg Lys Lys Arg Leu Pro Phe Leu Pro Asn  
 70 75 80 85

cgc gtt ggt ttg atc acg gga cgt ggt tca gcg gct gag cgc gat gtg 403  
 Arg Val Gly Leu Ile Thr Gly Arg Gly Ser Ala Ala Glu Arg Asp Val  
 90 95 100

ctg agc gtg gct aag gat cgc tgg ccg gaa gtg cag ttt gag gtg atc 451  
 Leu Ser Val Ala Lys Asp Arg Trp Pro Glu Val Gln Phe Glu Val Ile  
 105 110 115

aac acg gca gtt cag ggc gct tca gct gtt cct gaa atc atc gaa gcg 499  
 Asn Thr Ala Val Gln Gly Ala Ser Ala Val Pro Glu Ile Ile Glu Ala  
 120 125 130

ttg cgg gtt tta gat cag gac cct cgc gtg gat gtc atc atc att gcc 547  
 Leu Arg Val Leu Asp Gln Asp Pro Arg Val Asp Val Ile Ile Ile Ala  
 135 140 145

cgc ggc ggc ggt tct gtg gag gat ctg ctc ccc ttc tct gag gag gcc 595  
 Arg Gly Gly Gly Ser Val Glu Asp Leu Leu Pro Phe Ser Glu Glu Ala  
 150 155 160 165

ttg cag cgc gca gtc gcg gca gcg cag acg ccc gtg gtg tcc gcg att 643  
 Leu Gln Arg Ala Val Ala Ala Ala Gln Thr Pro Val Val Ser Ala Ile  
 170 175 180

ggc cac gaa cca gat acg ccg gtg ttg gac aat gtc gcc gac ctt cgc 691  
 Gly His Glu Pro Asp Thr Pro Val Leu Asp Asn Val Ala Asp Leu Arg  
 185 190 195

gcg gcg acc ccg acc gat gca gca aag cgc gtg gtg cct gat gtg gca 739  
 Ala Ala Thr Pro Thr Asp Ala Ala Lys Arg Val Val Pro Asp Val Ala  
 200 205 210

gaa gaa cgc atg ttg atc aat cag ctt cgc agt cgt agt gcc gcg gcg 787  
 Glu Glu Arg Met Leu Ile Asn Gln Leu Arg Ser Arg Ser Ala Ala Ala  
 215 220 225

ttg cgc ggt tgg gtg cag cgc gag cag cag gcg ttg gca gcg att cgc 835  
 Leu Arg Gly Trp Val Gln Arg Glu Gln Gln Ala Leu Ala Ala Ile Arg  
 230 235 240 245

acc agg ccg gtg ctg gct gat ccg atg acc ccg att aac cgc cga cgt 883  
 Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro Ile Asn Arg Arg Arg  
 250 255 260

gat gag att gcc cag gct gtg ggc ttg att agg cgc gat gtc acc cat 931  
 Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg Arg Asp Val Thr His  
 265 270 275

ctc gtc cgc acc gag caa gca ctg gtg gcg tgc ttg cgc gca cag gtt 979  
 Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser Leu Arg Ala Gln Val  
 280 285 290

tcc gcg ctc ggc ccg tcc gca acc ttg gcg cgc ggt tat tcc gtg gtg 1027  
 Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg Gly Tyr Ser Val Val  
 295 300 305

cag gtt att cct cgc gac ggc agc gcc ccg gaa gtg gtc acc acc atc 1075  
 Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu Val Val Thr Thr Ile  
 310 315 320 325

gag caa tca ccg ccc ggc agc cag ctg cgc atc cgc gtt gcc gac ggc 1123

Arg Ser Ala Ala Ala Leu Arg Gly Trp Val Gln Arg Glu Gln Gln Ala  
225 230 235 240



Leu Ala Ala Ile Arg Thr Arg Pro Val Leu Ala Asp Pro Met Thr Pro  
                   245                                  250                                  255  
 Ile Asn Arg Arg Arg Asp Glu Ile Ala Gln Ala Val Gly Leu Ile Arg  
                   260                                  265                                  270  
 Arg Asp Val Thr His Leu Val Arg Thr Glu Gln Ala Leu Val Ala Ser  
                   275                                  280                                  285  
 Leu Arg Ala Gln Val Ser Ala Leu Gly Pro Ser Ala Thr Leu Ala Arg  
                   290                                  295                                  300  
 Gly Tyr Ser Val Val Gln Val Ile Pro Arg Asp Gly Ser Ala Pro Glu  
 305                                  310                                  315                                  320  
 Val Val Thr Thr Ile Glu Gln Ser Pro Pro Gly Ser Gln Leu Arg Ile  
                   325                                  330                                  335  
 Arg Val Ala Asp Gly Ser Ile Thr Ala Ala Ser Met Gly Thr Gln Gln  
                   340                                  345                                  350

Ala Asn

<210> 205

<211> 1049

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1026)

<223> FRXA00790

<400> 205

cgc aat cgc ccc aca ccg ctc aag gat ggc gac cgc gtg att gtg tac	48
Arg Asn Arg Pro Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr	
1                                  5                                  10                                  15	
ggc aag ccc gcg ttt tat gca ggc cgc ggc act ttt tcg ctg tgg gtg	96
Gly Lys Pro Ala Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val	
20                                  25                                  30	
act gat atc cgt ccc gtg ggt att ggt gag ttg ctg gcg cgc att gag	144
Thr Asp Ile Arg Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu	
35                                  40                                  45	
gag ctg cgt aaa agg ctt gcc gcg gag ggt ctt ttt gat cca gct cgg	192
Glu Leu Arg Lys Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg	
50                                  55                                  60	
aag aag cga ctg cca ttt ctg ccc aac cgc gtt ggt ttg atc acg gga	240
Lys Lys Arg Leu Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly	
65                                  70                                  75                                  80	
cgt ggt tca gcg gct gag cgc gat gtg ctg agc gtg gct aag gat cgc	288
Arg Gly Ser Ala Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg	
85                                  90                                  95	
tgg ccg gaa gtg cag ttt gag gtg atc aac acg gca gtt cag ggc gct	336

Trp	Pro	Glu	Val	Gln	Phe	Glu	Val	Ile	Asn	Thr	Ala	Val	Gln	Gly	Ala	
			100					105					110			
tca	gct	gtt	cct	gaa	atc	atc	gaa	gcg	ttg	cgg	gtt	tta	gat	cag	gac	384
Ser	Ala	Val	Pro	Glu	Ile	Ile	Glu	Ala	Leu	Arg	Val	Leu	Asp	Gln	Asp	
		115					120					125				
cct	cgc	gtg	gat	gtc	atc	atc	att	gcc	cgc	ggc	ggc	ggg	tct	gtg	gag	432
Pro	Arg	Val	Asp	Val	Ile	Ile	Ile	Ala	Arg	Gly	Gly	Gly	Ser	Val	Glu	
		130					135					140				
gat	ctg	ctc	ccc	ttc	tct	gag	gag	gcc	ttg	cag	cgc	gca	gtc	gcg	gca	480
Asp	Leu	Leu	Pro	Phe	Ser	Glu	Glu	Ala	Leu	Gln	Arg	Ala	Val	Ala	Ala	
					150					155					160	
gcg	cag	acg	ccc	gtg	gtg	tcc	gcg	att	ggc	cac	gaa	cca	gat	acg	ccg	528
Ala	Gln	Thr	Pro	Val	Val	Ser	Ala	Ile	Gly	His	Glu	Pro	Asp	Thr	Pro	
				165					170					175		
gtg	ttg	gac	aat	gtc	gcc	gac	ctt	cgc	gcg	gcg	acc	ccg	acc	gat	gca	576
Val	Leu	Asp	Asn	Val	Ala	Asp	Leu	Arg	Ala	Ala	Thr	Pro	Thr	Asp	Ala	
			180					185					190			
gca	aag	cgc	gtg	gtg	cct	gat	gtg	gca	gaa	gaa	cgc	atg	ttg	atc	aat	624
Ala	Lys	Arg	Val	Val	Pro	Asp	Val	Ala	Glu	Glu	Arg	Met	Leu	Ile	Asn	
		195					200					205				
cag	ctt	cgc	agt	cgt	agt	gcc	gcg	gcg	ttg	cgc	ggg	tgg	gtg	cag	cgc	672
Gln	Leu	Arg	Ser	Arg	Ser	Ala	Ala	Ala	Leu	Arg	Gly	Trp	Val	Gln	Arg	
	210					215					220					
gag	cag	cag	gcg	ttg	gca	gcg	att	cgc	acc	agg	ccg	gtg	ctg	gct	gat	720
Glu	Gln	Gln	Ala	Leu	Ala	Ala	Ile	Arg	Thr	Arg	Pro	Val	Leu	Ala	Asp	
	225				230				235						240	
ccg	atg	acc	ccg	att	aac	cgc	cga	cgt	gat	gag	att	gcc	cag	gct	gtg	768
Pro	Met	Thr	Pro	Ile	Asn	Arg	Arg	Arg	Asp	Glu	Ile	Ala	Gln	Ala	Val	
				245					250					255		
ggc	ttg	att	agg	cgc	gat	gtc	acc	cat	ctc	gtc	cgc	acc	gag	caa	gca	816
Gly	Leu	Ile	Arg	Arg	Asp	Val	Thr	His	Leu	Val	Arg	Thr	Glu	Gln	Ala	
			260					265					270			
ctg	gtg	gcg	tcg	ttg	cgc	gca	cag	gtt	tcc	gcg	ctc	ggc	ccg	tcc	gca	864
Leu	Val	Ala	Ser	Leu	Arg	Ala	Gln	Val	Ser	Ala	Leu	Gly	Pro	Ser	Ala	
		275					280					285				
acc	ttg	gcg	cgc	ggg	tat	tcc	gtg	gtg	cag	gtt	att	cct	cgc	gac	ggc	912
Thr	Leu	Ala	Arg	Gly	Tyr	Ser	Val	Val	Gln	Val	Ile	Pro	Arg	Asp	Gly	
		290				295					300					
agc	gcc	ccg														

340

&lt;210&gt; 206

&lt;211&gt; 342

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 206

Arg Asn Arg Pro Thr Pro Leu Lys Asp Gly Asp Arg Val Ile Val Tyr  
 1 5 10 15

Gly Lys Pro Ala Phe Tyr Ala Gly Arg Gly Thr Phe Ser Leu Trp Val  
 20 25 30

Thr Asp Ile Arg Pro Val Gly Ile Gly Glu Leu Leu Ala Arg Ile Glu  
 35 40 45

Glu Leu Arg Lys Arg Leu Ala Ala Glu Gly Leu Phe Asp Pro Ala Arg  
 50 55 60

Lys Lys Arg Leu Pro Phe Leu Pro Asn Arg Val Gly Leu Ile Thr Gly  
 65 70 75 80

Arg Gly Ser Ala Ala Glu Arg Asp Val Leu Ser Val Ala Lys Asp Arg  
 85 90 95

Trp Pro Glu Val Gln Phe Glu Val Ile Asn Thr Ala Val Gln Gly Ala  
 100 105 110

Ser Ala Val Pro Glu Ile Ile Glu Ala Leu Arg Val Leu Asp Gln Asp  
 115 120 125

Pro Arg Val Asp Val Ile Ile Ile Ala Arg Gly Gly Gly Ser Val Glu  
 130 135 140

Asp Leu Leu Pro Phe Ser Glu Glu Ala Leu Gln Arg Ala Val Ala Ala  
 145 150 155 160

Ala Gln Thr Pro Val Val Ser Ala Ile Gly His Glu Pro Asp Thr Pro  
 165 170 175

Val Leu Asp Asn Val Ala Asp Leu Arg Ala Ala Thr Pro Thr Asp Ala  
 180 185 190

Ala Lys Arg Val Val Pro Asp Val Ala Glu Glu Arg Met Leu Ile Asn  
 195 200 205

Gln Leu Arg Ser Arg Ser Ala Ala Ala Leu Arg Gly Trp Val Gln Arg  
 210 215 220

Glu Gln Gln Ala Leu Ala Ala Ile Arg Thr Arg Pro Val Leu Ala Asp  
 225 230 235 240

Pro Met Thr Pro Ile Asn Arg Arg Arg Asp Glu Ile Ala Gln Ala Val  
 245 250 255

Gly Leu Ile Arg Arg Asp Val Thr His Leu Val Arg Thr Glu Gln Ala  
 260 265 270

Leu Val Ala Ser Leu Arg Ala Gln Val Ser Ala Leu Gly Pro Ser Ala

ggc cgc gaa atc gca gat cct cac tac gac tac aaa ctg cgc tgg cta 499

Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr Lys Leu Arg Trp Leu  
 120 125 130

ttc tcc ctg cgc aac tac gtg atc gac acc ttg gaa tac cgc ccc gag 547  
 Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu Glu Tyr Arg Pro Glu  
 135 140 145

gaa aaa ctg gtg ttg ctc ggc gac ttc aac atc gcg ccc aca gac atc 595  
 Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile Ala Pro Thr Asp Ile  
 150 155 160 165

gac gtc tgg gac atc gca gcc ttc gaa gga aaa acc cac gtc acc gaa 643  
 Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys Thr His Val Thr Glu  
 170 175 180

cca gaa cgt gca gct ttc gac ggc ctc atc gaa gcc gga ctc aaa gaa 691  
 Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu Ala Gly Leu Lys Glu  
 185 190 195

acc acc ccc gga cct ggt acc tac acc tac tgg gat tac aaa ggc gca 739  
 Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp Asp Tyr Lys Gly Ala  
 200 205 210

cgc ttc ctc aaa ggc gaa ggc atg cgc atc gat ttc cag ctc gca tcc 787  
 Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp Phe Gln Leu Ala Ser  
 215 220 225

ccg gcc ctt gct gca acc gcg ggt gaa acc ttt gtg gac gtt gaa gaa 835  
 Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe Val Asp Val Glu Glu  
 230 235 240 245

cgc agc gga acc ggc gcc tct gac cac gca cca gtc atc gtt gat tac 883  
 Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro Val Ile Val Asp Tyr  
 250 255 260

aag gtg taactgcgta tgatctttca gat 912  
 Lys Val

&lt;210&gt; 208

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 208

Met Arg Ile Val Asn Trp Asn Val Asn Ser Ala Arg Thr Arg Val Asp  
 1 5 10 15

Arg Met Val Asp Phe Leu Leu Arg His Asp Val Asp Val Leu Ala Val  
 20 25 30

Gln Glu Thr Lys Cys Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr  
 35 40 45

Glu Ile Gly Tyr Glu Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly  
 50 55 60

Val Ala Ile Ile Ser Arg Val Gly Ile Glu Asn Val Glu Thr His Phe  
 65 70 75 80

Pro Ala Gln Pro Gly Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile  
                     85                    90                    95

Glu Ala Arg Ala Ile Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser  
                     100                    105                    110

Leu Tyr Val Pro Asn Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr  
                     115                    120                    125

Lys Leu Arg Trp Leu Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu  
                     130                    135                    140

Glu Tyr Arg Pro Glu Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile  
                     145                    150                    155                    160

Ala Pro Thr Asp Ile Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys  
                     165                    170                    175

Thr His Val Thr Glu Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu  
                     180                    185                    190

Ala Gly Leu Lys Glu Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp  
                     195                    200                    205

Asp Tyr Lys Gly Ala Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp  
                     210                    215                    220

Phe Gln Leu Ala Ser Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe  
                     225                    230                    235                    240

Val Asp Val Glu Glu Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro  
                     245                    250                    255

Val Ile Val Asp Tyr Lys Val  
                     260

<210> 209  
 <211> 806  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(783)  
 <223> RXN03175

<400> 209  
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 Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu  
           1                    5                    10                    15

gat aac gga tgg cac tac att ggt gcc cca gca gct gcc aag gga cgt 96  
 Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Lys Gly Arg  
                     20                    25                    30

gcc ggt gtc ggc att ttg tct agg cat gaa ctt gaa gat gtg aac atc 144  
 Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile  
                     35                    40                    45

ggt ttt gga tct ttc ctt gac tcc ggc cgc tac att gaa gca acc atc 192

Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile  
 50 55 60

aaa gac acc acc ctg gat gtg cca gta acc gtg gca tct ctt tac ctc 240  
 Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu  
 65 70 75 80

ccc tca ggt tca gcg ggc acc gac aag cag gat gaa aag tac cgc ttc 288  
 Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe  
 85 90 95

ctc gat gaa ttc gaa ggg ttc ctg gac cag cgc gct aaa gaa cgc tcc 336  
 Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser  
 100 105 110

cac atg gtc atc ggt ggc gac tgg aac atc tgc cac cgc cgc gaa gac 384  
 His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp  
 115 120 125

ctg aaa aac tgg aaa acc aac caa aag aaa tcc ggt ttc ctt ccc gac 432  
 Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp  
 130 135 140

gaa cgc gca ttc atg gat tca gtc ttt ggc acc ttc cca gat gag gca 480  
 Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala  
 145 150 155 160

acc cag gtt gca ggg gcc ggc gac ttc ttc ggt gcc gtg gac tat gaa 528  
 Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu  
 165 170 175

gga acg agg cgt cga gaa gca act acg gac cct gcg tgg ttc gac gtt 576  
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val  
 180 185 190

gca cgt cgc ctg caa cct gaa ggc gac ggc ccc tac act tgg tgg acc 624  
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr  
 195 200 205

tac cgc gga aaa gcc ttc gac acc ggc gcc gga tgg cgc atc gac tac 672  
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr  
 210 215 220

caa gca gca acc gca gcg atg ctc gaa cgc gca gaa cgc tcc tgg gta 720  
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val  
 225 230 235 240

gac aaa gcc gct gca tac gat ttg cgc tgg tca gat cac tca cca ctg 768  
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu  
 245 250 255

aac gtg atc tac tcc taaaatgctg ctgacaattc tat 806  
 Asn Val Ile Tyr Ser  
 260

&lt;210&gt; 210

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 210

Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu  
 1 5 10 15

Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg  
 20 25 30

Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile  
 35 40 45

Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile  
 50 55 60

Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu  
 65 70 75 80

Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe  
 85 90 95

Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser  
 100 105 110

His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp  
 115 120 125

Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp  
 130 135 140

Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala  
 145 150 155 160

Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu  
 165 170 175

Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val  
 180 185 190

Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr  
 195 200 205

Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr  
 210 215 220

Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val  
 225 230 235 240

Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu  
 245 250 255

Asn Val Ile Tyr Ser  
 260

&lt;210&gt; 211

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1012)



<400> 211

ggatggagga tttccccaag caccactag tgtgacaagc atg agt ttt cac atc 115  
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aca tcc gtc aat gtc aac ggc att agg gca gcg gtc aaa cag cga agc 163  
Thr Ser Val Asn Val Asn Gly Ile Arg Ala Ala Val Lys Gln Arg Ser  
10 15 20

gaa aca aac cta ggt ttc ctt ccg tgg ctt gaa gaa act cgc ccg gac 211  
Glu Thr Asn Leu Gly Phe Leu Pro Trp Leu Glu Glu Thr Arg Pro Asp  
25 30 35

ggt gtc ctc ctc caa gaa gtc cgc gca agc gaa aaa gac acc gcc acc 259  
Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu Lys Asp Thr Ala Thr  
40 45 50

gca ctg caa ccc gcc tta gat aac gga tgg cac tac att ggt gcc cca 307  
Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His Tyr Ile Gly Ala Pro  
55 60 65

gca gct gcc aag gga cgt gcc ggt gtc ggc att ttg tct agg cat gaa 355  
Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile Leu Ser Arg His Glu  
70 75 80 85

cct gaa gat gtg aac atc ggt ttt gga tct ttc ctt gac tcc gcc cgc      403  
Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg  
                90                       95                       100

tac att gaa gca acc atc aaa gac acc acc ctg gat gtg cca gta acc 451  
Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu Asp Val Pro Val Thr  
105 110 115

gtg gca tct ctt tac ctc ccc tca ggt tca gcg ggc acc gac aag cag 499  
Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln  
120 125 130

gat gaa aag tac cgc ttc ctc gat gaa ttc gaa ggg ttc ctg gac cag 547  
Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln  
135 140 145

cgc gct aaa gaa cgc tcc cac atg gtc atc ggt ggc gac tgg aac atc 595  
 Arg Ala Lys Glu Arg Ser His Met Val Ile Gly Gly Asp Trp Asn Ile  
 150 155 160 165

tgc cac cgc cgc gaa gac ctg aaa aac tgg aaa acc aac caa aag aaa 643  
Cys His Arg Arg Glu Asp Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys  
170 175 180

tcc ggt ttc ctt ccc gac gaa cgc gca ttc atg gat tca gtc ttt ggc 691  
Ser Gly Phe Leu Pro Asp Glu Arg Ala Phe Met Asp Ser Val Phe Gly  
185 190 195

acc ttc cca gat gag gca acc cag gtt gca ggg gcc ggc gac ttc ttc 739  
Thr Phe Pro Asp Glu Ala Thr Gln Val Ala Gly Ala Gly Asp Phe Phe  
200 205 210

ggt gcc gtg gac tat gaa gga acg agg cgt cga gaa gca act acg gac 787  
 Gly Ala Val Asp Tyr Glu Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp  
 215 220 225

cct gcg tgg ttc gac gtt gca cgt cgc ctg caa cct gaa ggc gac ggc 835  
 Pro Ala Trp Phe Asp Val Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly  
 230 235 240 245

ccc tac act tgg tgg acc tac cgc gga aaa gcc ttc gac acc ggc gcc 883  
 Pro Tyr Thr Trp Trp Thr Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala  
 250 255 260

gga tgg cgc atc gac tac caa gca gca acc gca gcg atg ctc gaa cgc 931  
 Gly Trp Arg Ile Asp Tyr Gln Ala Ala Thr Ala Ala Met Leu Glu Arg  
 265 270 275

gca gaa cgc tcc tgg gta gac aaa gcc gct gca tac gat ttg cgc tgg 979  
 Ala Glu Arg Ser Trp Val Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp  
 280 285 290

tca gat cac tca cca ctg aac gtg atc tac tcc taaaatgctg ctgacaattc 1032  
 Ser Asp His Ser Pro Leu Asn Val Ile Tyr Ser  
 295 300

tat 1035

<210> 212  
 <211> 304  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 212  
 Met Ser Phe His Ile Thr Ser Val Asn Val Asn Gly Ile Arg Ala Ala  
 1 5 10 15  
 Val Lys Gln Arg Ser Glu Thr Asn Leu Gly Phe Leu Pro Trp Leu Glu  
 20 25 30  
 Glu Thr Arg Pro Asp Val Val Leu Leu Gln Glu Val Arg Ala Ser Glu  
 35 40 45  
 Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu Asp Asn Gly Trp His  
 50 55 60  
 Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg Ala Gly Val Gly Ile  
 65 70 75 80  
 Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile Gly Phe Gly Ser Phe  
 85 90 95  
 Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile Lys Asp Thr Thr Leu  
 100 105 110  
 Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu Pro Ser Gly Ser Ala  
 115 120 125  
 Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe Leu Asp Glu Phe Glu  
 130 135 140  
 Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser His Met Val Ile Gly

[illegible]

2000  
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<400> 213
gacccataacc aagacctatc tggggaacct cgacccttct gtgcccaagg aaactcaaca 60

cccctgcata tactttttccg ctgtggaaca atggggagcgc atg aag ctc tat gca 115
Met Lys Leu Tyr Ala
1 5

gca gtc ctc gac ttt gaa cca gtg gca caa gag ttc ggt gtg gag cga 163
Ala Val Leu Asp Phe Glu Pro Val Ala Gln Glu Phe Gly Val Glu Arg
10 15 20

ggt ttt gac cct cat atc cac gac gaa gcc gcg tca agt gtc gat agg 211
Gly Phe Asp Pro His Ile His Asp Glu Ala Ala Ser Ser Val Asp Arg
25 30 35

tat gcg caa gag cgg gaa gat ctc ctg cac atg ccc ttt gtc acc atc 259
Tyr Ala Gln Glu Arg Glu Asp Leu Leu His Met Pro Phe Val Thr Ile
40 45 50
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gat ccc gta ggt tcc aga gac ctc gat caa gct gtg ctg att gag gag Asp Pro Val Gly Ser Arg Asp Leu Asp Gln Ala Val Leu Ile Glu Glu 55 60 65	307
atc gac agc gga ttt cgg gtg cat tac gcg att gca gat gtc gca gcc Ile Asp Ser Gly Phe Arg Val His Tyr Ala Ile Ala Asp Val Ala Ala 70 75 80 85	355
ttc gtg gag ccg ggc agt gaa ttg gaa aag att tcc ctt cac cgc ggg Phe Val Glu Pro Gly Ser Glu Leu Glu Lys Ile Ser Leu His Arg Gly 90 95 100	403
cag act att tat ctg ccg gat tcc cca gcg cga ctg cac cct gag gaa Gln Thr Ile Tyr Leu Pro Asp Ser Pro Ala Arg Leu His Pro Glu Glu 105 110 115	451
tta tcc gaa gat gcg gca agc ctg ctg gag gga caa acg aga cca gcg Leu Ser Glu Asp Ala Ala Ser Leu Leu Glu Gly Gln Thr Arg Pro Ala 120 125 130	499
gtt gtg tgg tgc att gat cta gat gaa cgt ggc gaa gtc aca gcc acc Val Val Trp Ser Ile Asp Leu Asp Glu Arg Gly Glu Val Thr Ala Thr 135 140 145	547
aag gtg cgt cgc ggg ttg gtg aaa tcc ccg gcg cgt ttg gat tat gat Lys Val Arg Arg Gly Leu Val Lys Ser Arg Ala Arg Leu Asp Tyr Asp 150 155 160 165	595
cag gct caa ata gat gcc gag aat ggt ccg ttg cat ccg tcg ata agc Gln Ala Gln Ile Asp Ala Glu Asn Gly Arg Leu His Pro Ser Ile Ser 170 175 180	643
tta ttg ccc aag gtc ggg cag ctg agg cag gaa agc gcg cta ccg cgc Leu Leu Pro Lys Val Gly Gln Leu Arg Gln Glu Ser Ala Leu Arg Arg 185 190 195	691
gaa gcc gtg aat ctt tct att ccc agc cag cga gtg gtg aaa gtg ccc Glu Ala Val Asn Leu Ser Ile Pro Ser Gln Arg Val Val Lys Val Pro 200 205 210	739
aat gat gac gcc ggt gaa cac tat gaa att gtc atc gag cca cgc ccg Asn Asp Asp Ala Gly Glu His Tyr Glu Ile Val Ile Glu Pro Arg Pro 215 220 225	787
cac atc atg gat tac aat tcc gag att tcc ctg ctc aca ggc atg gta His Ile Met Asp Tyr Asn Ser Glu Ile Ser Leu Leu Thr Gly Met Val 230 235 240 245	835
gcg ggg gag atg atg gtg aaa gcg ggg cac ggt ttg ctg cgt aca ctc Ala Gly Glu Met Met Val Lys Ala Gly His Gly Leu Leu Arg Thr Leu 250 255 260	883
gcc ccg gcg acc aaa gaa tcc gaa gct act ttc aga tca gag gcg caa Ala Pro Ala Thr Lys Glu Ser Glu Ala Thr Phe Arg Ser Glu Ala Gln 265 270 275	931
gcc ctt ggt ttt gag atc gcg ccc gaa caa ccc atc ggt gag ttt ctt Ala Leu Gly Phe Glu Ile Ala Pro Glu Gln Pro Ile Gly Glu Phe Leu 280 285 290	979

caa agt gtg gat ccc aat acg ccc aaa ggg atg gcc att cag agg gaa 1027  
 Gln Ser Val Asp Pro Asn Thr Pro Lys Gly Met Ala Ile Gln Arg Glu  
 295 300 305

gca cag aaa ctc ttg cgg ggc tcc ggc tac gcc agc gtg aaa aat ggg 1075  
 Ala Gln Lys Leu Leu Arg Gly Ser Gly Tyr Ala Ser Val Lys Asn Gly  
 310 315 320 325

gac tcg gaa gtg cat tcc ggt gtt ggt ggt tac tat gct cac gtc acc 1123  
 Asp Ser Glu Val His Ser Gly Val Gly Tyr Tyr Ala His Val Thr  
 330 335 340

gca ccg ctg cgc cga ctt atc gac cgt ttc gcc acc gaa cat tgc ctt 1171  
 Ala Pro Leu Arg Arg Leu Ile Asp Arg Phe Ala Thr Glu His Cys Leu  
 345 350 355

gcg att gcc tcc gga acg gac gtt cct gaa tgg gtg acc agg gtg gaa 1219  
 Ala Ile Ala Ser Gly Thr Asp Val Pro Glu Trp Val Thr Arg Val Glu  
 360 365 370

gag caa gtt ctc gac acc atg aaa tac tcc tcc att ttg gcc agc caa 1267  
 Glu Gln Val Leu Asp Thr Met Lys Tyr Ser Ser Ile Leu Ala Ser Gln  
 375 380 385

gtg gat aat gcc tgc ctc gac ctc aca gaa gcc acc gtg ttg aaa tac 1315  
 Val Asp Asn Ala Cys Leu Asp Leu Thr Glu Ala Thr Val Leu Lys Tyr  
 390 395 400 405

tgg gag ggc caa aac ttc aac gcg gtg gtt gta gcg agc gaa cct gaa 1363  
 Trp Glu Gly Gln Asn Phe Asn Ala Val Val Val Ala Ser Glu Pro Glu  
 410 415 420

aag aac tct gct cga ctt ttt gtg tac aaa ccg cca gtg ttg gca aag 1411  
 Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro Pro Val Leu Ala Lys  
 425 430 435

tgt att ggc gcc cca gaa cag gga aca aac caa gat gtc aca ctg gtg 1459  
 Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln Asp Val Thr Leu Val  
 440 445 450

act gcg aac ttg aag aag cgt gaa gtt ttg ttt gcg tgg ccg gct gac 1507  
 Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe Ala Trp Pro Ala Asp  
 455 460 465

taagcatgca ggctgggttaa gta 1530

&lt;210&gt; 214

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 214

Met Lys Leu Tyr Ala Ala Val Leu Asp Phe Glu Pro Val Ala Gln Glu  
 1 5 10 15

Phe Gly Val Glu Arg Gly Phe Asp Pro His Ile His Asp Glu Ala Ala  
 20 25 30

Ser Ser Val Asp Arg Tyr Ala Gln Glu Arg Glu Asp Leu Leu His Met  
 35 40 45

Pro Phe Val Thr Ile Asp Pro Val Gly Ser Arg Asp Leu Asp Gln Ala  
 50 55 60  
 Val Leu Ile Glu Glu Ile Asp Ser Gly Phe Arg Val His Tyr Ala Ile  
 65 70 75 80  
 Ala Asp Val Ala Ala Phe Val Glu Pro Gly Ser Glu Leu Glu Lys Ile  
 85 90 95  
 Ser Leu His Arg Gly Gln Thr Ile Tyr Leu Pro Asp Ser Pro Ala Arg  
 100 105 110  
 Leu His Pro Glu Glu Leu Ser Glu Asp Ala Ala Ser Leu Leu Glu Gly  
 115 120 125  
 Gln Thr Arg Pro Ala Val Val Trp Ser Ile Asp Leu Asp Glu Arg Gly  
 130 135 140  
 Glu Val Thr Ala Thr Lys Val Arg Arg Gly Leu Val Lys Ser Arg Ala  
 145 150 155 160  
 Arg Leu Asp Tyr Asp Gln Ala Gln Ile Asp Ala Glu Asn Gly Arg Leu  
 165 170 175  
 His Pro Ser Ile Ser Leu Leu Pro Lys Val Gly Gln Leu Arg Gln Glu  
 180 185 190  
 Ser Ala Leu Arg Arg Glu Ala Val Asn Leu Ser Ile Pro Ser Gln Arg  
 195 200 205  
 Val Val Lys Val Pro Asn Asp Asp Ala Gly Glu His Tyr Glu Ile Val  
 210 215 220  
 Ile Glu Pro Arg Pro His Ile Met Asp Tyr Asn Ser Glu Ile Ser Leu  
 225 230 235 240  
 Leu Thr Gly Met Val Ala Gly Glu Met Met Val Lys Ala Gly His Gly  
 245 250 255  
 Leu Leu Arg Thr Leu Ala Pro Ala Thr Lys Glu Ser Glu Ala Thr Phe  
 260 265 270  
 Arg Ser Glu Ala Gln Ala Leu Gly Phe Glu Ile Ala Pro Glu Gln Pro  
 275 280 285  
 Ile Gly Glu Phe Leu Gln Ser Val Asp Pro Asn Thr Pro Lys Gly Met  
 290 295 300  
 Ala Ile Gln Arg Glu Ala Gln Lys Leu Leu Arg Gly Ser Gly Tyr Ala  
 305 310 315 320  
 Ser Val Lys Asn Gly Asp Ser Glu Val His Ser Gly Val Gly Gly Tyr  
 325 330 335  
 Tyr Ala His Val Thr Ala Pro Leu Arg Arg Leu Ile Asp Arg Phe Ala  
 340 345 350  
 Thr Glu His Cys Leu Ala Ile Ala Ser Gly Thr Asp Val Pro Glu Trp  
 355 360 365

Val Thr Arg Val Glu Glu Gln Val Leu Asp Thr Met Lys Tyr Ser Ser  
 370 375 380

Ile Leu Ala Ser Gln Val Asp Asn Ala Cys Leu Asp Leu Thr Glu Ala  
 385 390 395 400

Thr Val Leu Lys Tyr Trp Glu Gly Gln Asn Phe Asn Ala Val Val Val  
 405 410 415

Ala Ser Glu Pro Glu Lys Asn Ser Ala Arg Leu Phe Val Tyr Lys Pro  
 420 425 430

Pro Val Leu Ala Lys Cys Ile Gly Ala Pro Glu Gln Gly Thr Asn Gln  
 435 440 445

Asp Val Thr Leu Val Thr Ala Asn Leu Lys Lys Arg Glu Val Leu Phe  
 450 455 460

Ala Trp Pro Ala Asp  
 465

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(496)  
 <223> RXA02077

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tggcagatat cgctcgcgaa attgatcttg gcaaccacat atg ctg ggc aaa ggc 115  
 Met Leu Gly Lys Gly  
 1 5

gaa ttg ctc acc gaa ggt cgc agt aag gat tcc att ctt gcg gac acc 163  
 Glu Leu Leu Thr Glu Gly Arg Ser Lys Asp Ser Ile Leu Ala Asp Thr  
 10 15 20

aca gag gcg ttg ttc ggc gcg att ttc cgc cag cac ggt ttt gaa acc 211  
 Thr Glu Ala Leu Phe Gly Ala Ile Phe Arg Gln His Gly Phe Glu Thr  
 25 30 35

gcc cgc gac gta att ttg cgc ctg ttt gcc tac aag atc gat aac gca 259  
 Ala Arg Asp Val Ile Leu Arg Leu Phe Ala Tyr Lys Ile Asp Asn Ala  
 40 45 50

tcg gcc agg ggc att cac cag gac tgg aag acc acg ctg cag gag gaa 307  
 Ser Ala Arg Gly Ile His Gln Asp Trp Lys Thr Thr Leu Gln Glu Glu  
 55 60 65

ctt gct cag cgc aag cgc ccc atg gct gaa tat tcc gcc acc tca gtc 355  
 Leu Ala Gln Arg Lys Arg Pro Met Ala Glu Tyr Ser Ala Thr Ser Val  
 70 75 80 85

ggc ccg gat cac gat cta gtg ttc acc gcc atc gtg acg ctg gaa ggt 403  
 Gly Pro Asp His Asp Leu Val Phe Thr Ala Ile Val Thr Leu Glu Gly

90	95	100	
gaa gaa atg ggt cgg gga gaa ggc cgg aac aag aag ctg gcc gag cag			451
Glu Glu Met Gly Arg Gly Glu Gly Pro Asn Lys Lys Leu Ala Glu Gln			
105	110	115	
gaa gca gcg cac cag gca ttc cga aag ctt cgg gag tcc cgt gcc			496
Glu Ala Ala His Gln Ala Phe Arg Lys Leu Arg Glu Ser Arg Ala			
120	125	130	
tgaactgcct gaagttgagg tgg			519

<210> 216  
 <211> 132  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 216  
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 1 5 10 15  
 Ile Leu Ala Asp Thr Thr Glu Ala Leu Phe Gly Ala Ile Phe Arg Gln  
 20 25 30  
 His Gly Phe Glu Thr Ala Arg Asp Val Ile Leu Arg Leu Phe Ala Tyr  
 35 40 45  
 Lys Ile Asp Asn Ala Ser Ala Arg Gly Ile His Gln Asp Trp Lys Thr  
 50 55 60  
 Thr Leu Gln Glu Glu Leu Ala Gln Arg Lys Arg Pro Met Ala Glu Tyr  
 65 70 75 80  
 Ser Ala Thr Ser Val Gly Pro Asp His Asp Leu Val Phe Thr Ala Ile  
 85 90 95  
 Val Thr Leu Glu Gly Glu Glu Met Gly Arg Gly Glu Gly Pro Asn Lys  
 100 105 110  
 Lys Leu Ala Glu Gln Glu Ala Ala His Gln Ala Phe Arg Lys Leu Arg  
 115 120 125  
 Glu Ser Arg Ala  
 130

<210> 217  
 <211> 1332  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1309)  
 <223> RXN01563

<400> 217  
 gacctcaccg cgcattgtga agcgttcgca gcagtgttg cctctgttgc tggacttccc 60  
 ccagagggcg tcaccgaact acgaaggtag attggacacc atg gtt tcc gat etc 115



	Met	Val	Ser	Asp	Leu	
	1				5	
ctt caa ccc cgc gac ggc att ccg cct ttg cta tct acc cct ggt gag						163
Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu Ser Thr Pro Gly Glu						
	10				20	
ttc act gct gcg gca gat ctc ttg gct agc gga act ggg ccc ttc gcc						211
Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala						
	25				35	
att gat acg gaa cgc gcg tcc ggt ttt aga tac gat gac cgc gca ttt						259
Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe						
	40				50	
ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg						307
Leu Ile Gln Ile Arg Arg Gly Ser Gly Thr Leu Leu Phe Asp Pro						
	55				65	
gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat						355
Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn						
	70				80	85
ggt caa gag tgg atc att cac gca gca agc acc gat ttg ccg agc ctt						403
Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu						
	90				95	100
gcg tgg ctt gat ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct						451
Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala						
	105				110	115
ggc cgc tta gcc gga ttt gat cac gtt aat ctc gct gcc atg gtg gaa						499
Gly Arg Leu Ala Gly Phe Asp His Val Asn Leu Ala Ala Met Val Glu						
	120				125	130
cag att ttt gat ctc cac ttg ctc aaa ggc cac cgt tcg gaa gat tgg						547
Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Arg Ser Glu Asp Trp						
	135				140	145
tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat						595
Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp						
	150				155	160
gtg gag atg ctg ctg gag ctt gcc gat gtc atg gct gaa atc ctg gat						643
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp						
	170				175	180
cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg						691
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val						
	185				190	195
gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac						739
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp						
	200				205	210
ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc						787
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala						
	215				220	225
cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg						835
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu						

230	235	240	245	
gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt				883
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg				
250		255	260	
ggt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc				931
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro				
265		270	275	
ggt cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg				979
Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg				
280		285	290	
gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag				1027
Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys				
295		300	305	
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag				1075
Asp Gly Ile Pro Asp Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu				
310		315	320	325
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc				1123
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala				
330		335	340	
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga				1171
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg				
345		350	355	
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa				1219
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu				
360		365	370	
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att				1267
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile				
375		380	385	
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc				1309
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu				
390		395	400	
taaacctaaa gcccgcggt aag				1332

&lt;210&gt; 218

&lt;211&gt; 403

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 218

Met	Val	Ser	Asp	Leu	Leu	Gln	Pro	Arg	Asp	Gly	Ile	Pro	Pro	Leu	Leu
1				5					10					15	

Ser	Thr	Pro	Gly	Glu	Phe	Thr	Ala	Ala	Ala	Asp	Leu	Leu	Ala	Ser	Gly
			20					25					30		

Thr	Gly	Pro	Phe	Ala	Ile	Asp	Thr	Glu	Arg	Ala	Ser	Gly	Phe	Arg	Tyr
			35				40					45			

Asp	Asp	Arg	Ala	Phe	Leu	Ile	Gln	Ile	Arg	Arg	Arg	Gly	Ser	Gly	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Leu Leu Phe Asp Pro Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu 65 70 75 80		
Lys Pro Val Leu Asn Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr 85 90 95		
Asp Leu Pro Ser Leu Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe 100 105 110		
Asp Thr Glu Leu Ala Gly Arg Leu Ala Gly Phe Asp His Val Asn Leu 115 120 125		
Ala Ala Met Val Glu Gln Ile Phe Asp Leu His Leu Leu Lys Gly His 130 135 140		
Arg Ser Glu Asp Trp Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn 145 150 155 160		
Tyr Ala Ala Leu Asp Val Glu Met Leu Leu Glu Leu Ala Asp Val Met 165 170 175		
Ala Glu Ile Leu Asp Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu 180 185 190		
Phe Val His Ile Val Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu 195 200 205		
Thr Ser Trp Gln Asp Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp 210 215 220		
Gln Leu Val Val Ala Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala 225 230 235 240		
Ala Ser Arg Asp Leu Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile 245 250 255		
Val Glu Val Ala Arg Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln 260 265 270		
Val Lys Gly Phe Pro Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe 275 280 285		
Arg Ile Ile Thr Arg Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys 290 295 300		
Pro Gln Gln Arg Lys Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser 305 310 315 320		
Tyr Tyr Pro Glu Glu His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile 325 330 335		
Asp Asp Leu Ala Ala Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln 340 345 350		
Pro Ser Thr Leu Arg Val Ala Val Trp Met Ala Lys His Thr Gly Glu 355 360 365		
Ile His Asn Ala Glu Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala 370 375 380		

Arg Gln Trp Gln Ile Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu  
 385 390 395 400

Leu Lys Leu

<210> 219  
 <211> 833  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(810)  
 <223> FRXA01563

<400> 219  
 cag att ttt gat ctc cac ttg ctc aaa ggc cac ggt tcg gaa gat tgg 48  
 Gln Ile Phe Asp Leu His Leu Leu Lys Gly His Gly Ser Glu Asp Trp  
 1 5 10 15  
 tcc aag cgt cct ctg ccg gaa tct tgg ctc aac tac gca gca ctc gat 96  
 Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp  
 20 25 30  
 gtg gag atg ctg ctg gag ctt gcc gat gtc atg gct gaa atc ctg gat 144  
 Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp  
 35 40 45  
 cag cag gga aaa ctc ccc tgg gct gaa cag gaa ttt gtc cat att gtg 192  
 Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val  
 50 55 60  
 gat caa ttc gcc acg atg acc gaa cct tcc gaa acg tcc tgg cag gac 240  
 Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp  
 65 70 75 80  
 ctt aaa ggg ctg tcc act ctc aaa cga cca gac caa tta gtt gtg gcc 288  
 Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala  
 85 90 95  
 cgt gaa atg tgg ttg gaa cgc gac tct ttc gca gcc tcc cgc gac ctg 336  
 Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu  
 100 105 110  
 gcg ccc ggt aaa gtg ctg tcc aac aaa gtc atc gtg gaa gtc gcc cgt 384  
 Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg  
 115 120 125  
 gtt ctc ccc cgc acc ccg gca gaa tta gcg cag gtc aag gga ttc ccc 432  
 Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro  
 130 135 140  
 ggt cga tcc cag ggt gcc acc aaa cgc tgg ttc cgc atc atc acc cgg 480  
 Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg  
 145 150 155 160  
 gcg ctc aaa tcc cct cgc agg aac tgg cca aag cct cag cag cgc aag 528  
 Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys

165	170	175	
gac ggc atc ccc gat cgt cgc gcg tgg gcg tcc tac tac cca gaa gag			576
Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu			
180	185	190	
cac gaa gtg ctc caa gag att aga gcg ctt atc gac gac ctc gcc gcc			624
His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala			
195	200	205	
gat atc aac gtt ccc ggc gag aat atc ctt cag cct tca act ctg cga			672
Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg			
210	215	220	
gta gct gtg tgg atg gct aaa cac acc ggc gag atc cat aat gct gaa			720
Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu			
225	230	235	240
aca ctc aac gct gta ctt cgc gat tat ggt gcc cgc cag tgg caa att			768
Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile			
245	250	255	
gac cag act ttt ccg att ctg tcc gcc aac ttg ctg aag ctc			810
Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu			
260	265	270	
taaacctaaa gcccgcggt aag			833
<210> 220			
<211> 270			
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<213> Corynebacterium glutamicum			
<400> 220			
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Ser Lys Arg Pro Leu Pro Glu Ser Trp Leu Asn Tyr Ala Ala Leu Asp			
20	25	30	
Val Glu Met Leu Leu Glu Leu Ala Asp Val Met Ala Glu Ile Leu Asp			
35	40	45	
Gln Gln Gly Lys Leu Pro Trp Ala Glu Gln Glu Phe Val His Ile Val			
50	55	60	
Asp Gln Phe Ala Thr Met Thr Glu Pro Ser Glu Thr Ser Trp Gln Asp			
65	70	75	80
Leu Lys Gly Leu Ser Thr Leu Lys Arg Pro Asp Gln Leu Val Val Ala			
85	90	95	
Arg Glu Met Trp Leu Glu Arg Asp Ser Phe Ala Ala Ser Arg Asp Leu			
100	105	110	
Ala Pro Gly Lys Val Leu Ser Asn Lys Val Ile Val Glu Val Ala Arg			
115	120	125	
Val Leu Pro Arg Thr Pro Ala Glu Leu Ala Gln Val Lys Gly Phe Pro			
130	135	140	

Gly Arg Ser Gln Gly Ala Thr Lys Arg Trp Phe Arg Ile Ile Thr Arg  
145 150 155 160

Ala Leu Lys Ser Pro Arg Arg Asn Trp Pro Lys Pro Gln Gln Arg Lys  
165 170 175

Asp Gly Ile Pro Asp Arg Arg Ala Trp Ala Ser Tyr Tyr Pro Glu Glu  
180 185 190

His Glu Val Leu Gln Glu Ile Arg Ala Leu Ile Asp Asp Leu Ala Ala  
195 200 205

Asp Ile Asn Val Pro Gly Glu Asn Ile Leu Gln Pro Ser Thr Leu Arg  
210 215 220

Val Ala Val Trp Met Ala Lys His Thr Gly Glu Ile His Asn Ala Glu  
225 230 235 240

Thr Leu Asn Ala Val Leu Arg Asp Tyr Gly Ala Arg Gln Trp Gln Ile  
245 250 255

Asp Gln Thr Phe Pro Ile Leu Ser Ala Asn Leu Leu Lys Leu  
260 265 270

<210> 221

<211> 454

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> FRXA01713

<400> 221

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ccagagggcg tcaccgaact acgaaggttag attggacacc atg gtt tcc gat ctc 115  
Met Val Ser Asp Leu  
1 5

ctt caa ccc cgc gac ggc att ccg cct ttg cta tct acc cct ggt gag 163  
Leu Gln Pro Arg Asp Gly Ile Pro Pro Leu Leu Ser Thr Pro Gly Glu  
10 15 20

ttc act gct gcg gca gat ctc ttg gct agc gga act ggg ccc ttc gcc 211  
Phe Thr Ala Ala Ala Asp Leu Leu Ala Ser Gly Thr Gly Pro Phe Ala  
25 30 35

att gat acg gaa cgc gcg tcc ggt ttt aga tac gat gac cgc gca ttt 259  
Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr Asp Asp Arg Ala Phe  
40 45 50

ttg att cag atc cgg cgc cgt ggc agc gga act ctc cta ttc gac ccg 307  
Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr Leu Leu Phe Asp Pro  
55 60 65

gag cag ttc cgt cct gaa tta act cag gcg tta aag ccg gtg ctc aat 355  
Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu Lys Pro Val Leu Asn

70 75 80 85

ggt caa gag tgg atc att cac gca gca agc acc gat ttg ccg agc ctt 403  
 Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr Asp Leu Pro Ser Leu  
                   90                  95                  100

gcg tgg ctt gat ctt cac ccc gga tta ctc ttt gat aca gaa ctt gct 451  
 Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe Asp Thr Glu Leu Ala  
                   105                  110                  115

ggc 454  
 Gly

<210> 222  
 <211> 118  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 222  
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   1                  5                  10                  15

Ser Thr Pro Gly Glu Phe Thr Ala Ala Asp Leu Leu Ala Ser Gly  
                   20                  25                  30

Thr Gly Pro Phe Ala Ile Asp Thr Glu Arg Ala Ser Gly Phe Arg Tyr  
                   35                  40                  45

Asp Asp Arg Ala Phe Leu Ile Gln Ile Arg Arg Arg Gly Ser Gly Thr  
   50                  55                  60

Leu Leu Phe Asp Pro Glu Gln Phe Arg Pro Glu Leu Thr Gln Ala Leu  
   65                  70                  75                  80

Lys Pro Val Leu Asn Gly Gln Glu Trp Ile Ile His Ala Ala Ser Thr  
                   85                  90                  95

Asp Leu Pro Ser Leu Ala Trp Leu Asp Leu His Pro Gly Leu Leu Phe  
                   100                  105                  110

Asp Thr Glu Leu Ala Gly  
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<210> 223  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(2389)  
 <223> RXA02369

<400> 223  
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cattgctcaa tcgtggagat aagaaaatag gagtgtcgct gtg cca aat aac aag 115  
                   Val Pro Asn Asn Lys

	1	5	
gca gta gaa gca gaa atc tct ccc tcg gct gtg ctg gcc gcg gaa ttt			163
Ala Val Glu Ala Glu Ile Ser Pro Ser Ala Val Leu Ala Ala Glu Phe			
	10	20	
gat cga gat tca ttg agc gaa aaa acc cgc gta cat caa ctg gcc aaa			211
Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val His Gln Leu Ala Lys			
	25	35	
cga ctt gga atg gtt tcc aag gac gtc gtt gtt gcg ctc gat ggc atc			259
Arg Leu Gly Met Val Ser Lys Asp Val Val Val Ala Leu Asp Gly Ile			
	40	50	
ggc ctg gtc aag gtt gcg cag tca aac ctg agc aaa gaa gaa gta gaa			307
Gly Leu Val Lys Val Ala Gln Ser Asn Leu Ser Lys Glu Glu Val Glu			
	55	65	
aag ctt ctc gac gcc ctg tct cag ccc gta ctc aac gct gcc cca gct			355
Lys Leu Leu Asp Ala Leu Ser Gln Pro Val Leu Asn Ala Ala Pro Ala			
	70	85	
gcc gtc ccc gac gtt gaa ccg gtg gag aag att cgt cga cgc gtt gag			403
Ala Val Pro Asp Val Glu Pro Val Glu Lys Ile Arg Arg Arg Val Glu			
	90	100	
aag aat gtg gaa aat gaa atc cac caa atc gaa gaa aaa gta gag cgc			451
Lys Asn Val Glu Asn Glu Ile His Gln Ile Glu Glu Lys Val Glu Arg			
	105	115	
gaa ctc gcg gca gtc gcg caa cct act gac ttc gag gcg gca gcc cgc			499
Glu Leu Ala Ala Val Ala Gln Pro Thr Asp Phe Glu Ala Ala Ala Arg			
	120	130	
gaa gaa gcc act gca gaa ctg ctg gaa gat atc gtc cca gag atc acc			547
Glu Glu Ala Thr Ala Glu Leu Leu Glu Asp Ile Val Pro Glu Ile Thr			
	135	145	
ccg gcg ccg gtg gaa gca tct gtg tac acg ccg atc ttt gtg gca cct			595
Pro Ala Pro Val Glu Ala Ser Val Tyr Thr Pro Ile Phe Val Ala Pro			
	150	165	
gca gtt gta cct act gaa aac gtc caa gac acc gac gat gaa cag gtc			643
Ala Val Val Pro Thr Glu Asn Val Gln Asp Thr Asp Asp Glu Gln Val			
	170	180	
cgc gaa cgc acg gcg cgg aag cgc cgt ggg cgt cgt ggc acc ggc cgc			691
Arg Glu Arg Thr Ala Arg Lys Arg Arg Gly Arg Arg Gly Thr Gly Arg			
	185	195	
gga cgt gga gct gaa gct gaa acc gtc acc gaa gtg agt gag gag gcg			739
Gly Arg Gly Ala Glu Ala Glu Thr Val Thr Glu Val Ser Glu Glu Ala			
	200	210	
tcg aca agc gaa gta gaa gag gta aac gag cca atc gga att aag ggc			787
Ser Thr Ser Glu Val Glu Glu Val Asn Glu Pro Ile Gly Ile Lys Gly			
	215	225	
tcc act cgc ttg gag gcg caa cgc cgc cgt cgc acg gaa atg cgc gaa			835
Ser Thr Arg Leu Glu Ala Gln Arg Arg Arg Arg Thr Glu Met Arg Glu			
	230	245	



gaa aac aaa aaa cgc cgc cat gtg gtc agc acc cag gag ttc atg gaa	883
Glu Asn Lys Lys Arg Arg His Val Val Ser Thr Gln Glu Phe Met Glu	
250 255 260	
cgc cgt gaa tcg atg gaa cgt cgc atg att gtg cgc gag cgc caa cgc	931
Arg Arg Glu Ser Met Glu Arg Arg Met Ile Val Arg Glu Arg Gln Arg	
265 270 275	
cac gat cac cca ggt ctg gtc act cag gtt ggt gtg ctg gaa gac gat	979
His Asp His Pro Gly Leu Val Thr Gln Val Gly Val Leu Glu Asp Asp	
280 285 290	
cag ctg gtt gag cag ttt gtt acc tct gat gcg cag atg tct atg gtg	1027
Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala Gln Met Ser Met Val	
295 300 305	
ggc aat att tat ctg ggg cgc gtt caa aat gtg ctg cca agc atg gaa	1075
Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val Leu Pro Ser Met Glu	
310 315 320 325	
gct gcc ttc att gac att gga aaa ggt cgc aac ggt gtg ttg tat gcc	1123
Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn Gly Val Leu Tyr Ala	
330 335 340	
ggc gaa gtc gac tgg aaa gct gct gga ctt ggc gga cgt gga cgt cgc	1171
Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly Gly Arg Gly Arg Arg	
345 350 355	
att gag cag gcg ctg aaa gcc gcc gac cag gtt ctc gtc cag gtc tcc	1219
Ile Glu Gln Ala Leu Lys Ala Gly Asp Gln Val Leu Val Gln Val Ser	
360 365 370	
aag gat cca ttg ggc cat aag ggt gcg cgt ttg acc acc caa att tcc	1267
Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu Thr Thr Gln Ile Ser	
375 380 385	
ctg gcg gga cgt tac ctg gtg tac gtt cca ggt ggt cgc agc gct ggc	1315
Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly Gly Arg Ser Ala Gly	
390 395 400 405	
att tcc cgc aaa ctg cct gga cct gag cgc aag cgt ctg aag gaa atc	1363
Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys Arg Leu Lys Glu Ile	
410 415 420	
ctt ggc cgc gtt gtc cca gcg cag ggt gga acc atc atc cga act gct	1411
Leu Gly Arg Val Val Pro Ala Gln Gly Gly Thr Ile Ile Arg Thr Ala	
425 430 435	
gct gaa ggt gtg tcg gaa gaa aac atc gca gct gac gtg aac cgt ctg	1459
Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala Asp Val Asn Arg Leu	
440 445 450	
cac acc ctg tgg gag cag atc aag gaa cgc act gcg gag gaa aag aag	1507
His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr Ala Glu Glu Lys Lys	
455 460 465	
tcc cgc ggt tct aag ccg atc acc atg tat gaa gag cca gac atg ctg	1555
Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu Glu Pro Asp Met Leu	
470 475 480 485	

gtg aag gtg atc cgt gac ctc ttc aat gaa gat ttc acc tca ctg atc 1603  
Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp Phe Thr Ser Leu Ile  
490 495 500

gtt gac ggc gac cgt gcc tgg aac acc gtg cgt gcc tac atc caa tca 1651  
Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg Ala Tyr Ile Gln Ser  
505 510 515

gtc gct cct gat ttg gtg tcc cgc gtg gaa cac ttc aat cgc gca gac 1699  
Val Ala Pro Asp Leu Val Ser Arg Val Glu His Phe Asn Arg Ala Asp  
520 525 530

ttt gac ggc aag gat gct ttc gaa gca ttc gac ctg aac acc cag ctt 1747  
Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp Leu Asn Thr Gln Leu  
535 540 545

gag gaa gcg ctg tcc cga aag gtg aac ctg cca tcg ggt gga tcg ctg 1795  
Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro Ser Gly Gly Ser Leu  
550 555 560 565

atc atc gac cgc acc gaa gcc atg acg gtg atc gat gtg aac acc gga 1843  
Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile Asp Val Asn Thr Gly  
570 575 580

cgc tac acc ggc aag ggt ggt ggc aac ttg gaa gaa acc gtc acg ctc 1891  
Arg Tyr Thr Gly Lys Gly Gly Gly Asn Leu Glu Glu Thr Val Thr Leu  
585 590 595

aac aac att gaa gct gcc gaa gaa atc gtg cgc caa atg cgc ctg cgg 1939  
Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg Gln Met Arg Leu Arg  
600 605 610

gat ctc ggt ggc atg atc gtt gtc gac ttc atc gat atg gtg ctg cca 1987  
Asp Leu Gly Gly Met Ile Val Val Asp Phe Ile Asp Met Val Leu Pro  
615 620 625

gaa aac caa gaa ttg gtc ctg cgc cga ctc aat gaa gcg cta gaa aac 2035  
Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn Glu Ala Leu Glu Asn  
630 635 640 645

gat cgc acc cgc cac caa gtc tct gag gta acc tca ctg gga ctt gtt 2083  
Asp Arg Thr Arg His Gln Val Ser Glu Val Thr Ser Leu Gly Leu Val  
650 655 660

cag atg acc cgc aaa cgc atc ggc gcg ggc ctg ctg gaa acc ttc tct 2131  
Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu Leu Glu Thr Phe Ser  
665 670 675

tca ccg tgt gag cac tgt gaa ggc cga ggc atc atc gtt cat gtt gat 2179  
Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile Ile Val His Val Asp  
680 685 690

cca gta gac acc gtt gac gag cgc gtt gag gcg aaa gcg gaa gag cgt 2227  
Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala Lys Ala Glu Glu Arg  
695 700 705

agc cgt cgt cac cag cgt tcc aat agc act aac aag gca gct gcg gag 2275  
Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn Lys Ala Ala Ala Glu  
710 715 720 725

cac ccg atg gtt gtt gcc atg cgt gat ctc gtg gaa agc gat gaa cac 2323

His Pro Met Val Val Ala Met Arg Asp Leu Val Glu Ser Asp Glu His  
 730 735 740

gat ctg gat caa gaa ttt gag gaa ctc gct gca tca atg atc gtt ctc 2371  
 Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala Ser Met Ile Val Leu  
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gat gac tcc gat cta tta tgatgtggac aacgacaagc tcg 2412  
 Asp Asp Ser Asp Leu Leu  
 760

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 224  
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 Leu Ala Ala Glu Phe Asp Arg Asp Ser Leu Ser Glu Lys Thr Arg Val  
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 His Gln Leu Ala Lys Arg Leu Gly Met Val Ser Lys Asp Val Val Val  
 35 40 45  
 Ala Leu Asp Gly Ile Gly Leu Val Lys Val Ala Gln Ser Asn Leu Ser  
 50 55 60  
 Lys Glu Glu Val Glu Lys Leu Leu Asp Ala Leu Ser Gln Pro Val Leu  
 65 70 75 80  
 Asn Ala Ala Pro Ala Ala Val Pro Asp Val Glu Pro Val Glu Lys Ile  
 85 90 95  
 Arg Arg Arg Val Glu Lys Asn Val Glu Asn Glu Ile His Gln Ile Glu  
 100 105 110  
 Glu Lys Val Glu Arg Glu Leu Ala Ala Val Ala Gln Pro Thr Asp Phe  
 115 120 125  
 Glu Ala Ala Ala Arg Glu Glu Ala Thr Ala Glu Leu Leu Glu Asp Ile  
 130 135 140  
 Val Pro Glu Ile Thr Pro Ala Pro Val Glu Ala Ser Val Tyr Thr Pro  
 145 150 155 160  
 Ile Phe Val Ala Pro Ala Val Val Pro Thr Glu Asn Val Gln Asp Thr  
 165 170 175  
 Asp Asp Glu Gln Val Arg Glu Arg Thr Ala Arg Lys Arg Arg Gly Arg  
 180 185 190  
 Arg Gly Thr Gly Arg Gly Arg Gly Ala Glu Ala Glu Thr Val Thr Glu  
 195 200 205  
 Val Ser Glu Glu Ala Ser Thr Ser Glu Val Glu Glu Val Asn Glu Pro  
 210 215 220  
 Ile Gly Ile Lys Gly Ser Thr Arg Leu Glu Ala Gln Arg Arg Arg

225	230	235	240
Thr Glu Met Arg Glu Glu Asn Lys Lys Arg Arg His Val Val Ser Thr	245	250	255
Gln Glu Phe Met Glu Arg Arg Glu Ser Met Glu Arg Arg Met Ile Val	260	265	270
Arg Glu Arg Gln Arg His Asp His Pro Gly Leu Val Thr Gln Val Gly	275	280	285
Val Leu Glu Asp Asp Gln Leu Val Glu Gln Phe Val Thr Ser Asp Ala	290	295	300
Gln Met Ser Met Val Gly Asn Ile Tyr Leu Gly Arg Val Gln Asn Val	305	310	315
Leu Pro Ser Met Glu Ala Ala Phe Ile Asp Ile Gly Lys Gly Arg Asn	325	330	335
Gly Val Leu Tyr Ala Gly Glu Val Asp Trp Lys Ala Ala Gly Leu Gly	340	345	350
Gly Arg Gly Arg Arg Ile Glu Gln Ala Leu Lys Ala Gly Asp Gln Val	355	360	365
Leu Val Gln Val Ser Lys Asp Pro Leu Gly His Lys Gly Ala Arg Leu	370	375	380
Thr Thr Gln Ile Ser Leu Ala Gly Arg Tyr Leu Val Tyr Val Pro Gly	385	390	395
Gly Arg Ser Ala Gly Ile Ser Arg Lys Leu Pro Gly Pro Glu Arg Lys	405	410	415
Arg Leu Lys Glu Ile Leu Gly Arg Val Val Pro Ala Gln Gly Gly Thr	420	425	430
Ile Ile Arg Thr Ala Ala Glu Gly Val Ser Glu Glu Asn Ile Ala Ala	435	440	445
Asp Val Asn Arg Leu His Thr Leu Trp Glu Gln Ile Lys Glu Arg Thr	450	455	460
Ala Glu Glu Lys Lys Ser Arg Gly Ser Lys Pro Ile Thr Met Tyr Glu	465	470	475
Glu Pro Asp Met Leu Val Lys Val Ile Arg Asp Leu Phe Asn Glu Asp	485	490	495
Phe Thr Ser Leu Ile Val Asp Gly Asp Arg Ala Trp Asn Thr Val Arg	500	505	510
Ala Tyr Ile Gln Ser Val Ala Pro Asp Leu Val Ser Arg Val Glu His	515	520	525
Phe Asn Arg Ala Asp Phe Asp Gly Lys Asp Ala Phe Glu Ala Phe Asp	530	535	540
Leu Asn Thr Gln Leu Glu Glu Ala Leu Ser Arg Lys Val Asn Leu Pro	545	550	555
			560

Ser Gly Gly Ser Leu Ile Ile Asp Arg Thr Glu Ala Met Thr Val Ile  
565 570 575

Asp Val Asn Thr Gly Arg Tyr Thr Gly Lys Gly Gly Gly Asn Leu Glu  
580 585 590

Glu Thr Val Thr Leu Asn Asn Ile Glu Ala Ala Glu Glu Ile Val Arg  
595 600 605

Gln Met Arg Leu Arg Asp Leu Gly Gly Met Ile Val Val Asp Phe Ile  
610 615 620

Asp Met Val Leu Pro Glu Asn Gln Glu Leu Val Leu Arg Arg Leu Asn  
625 630 635 640

Glu Ala Leu Glu Asn Asp Arg Thr Arg His Gln Val Ser Glu Val Thr  
645 650 655

Ser Leu Gly Leu Val Gln Met Thr Arg Lys Arg Ile Gly Ala Gly Leu  
660 665 670

Leu Glu Thr Phe Ser Ser Pro Cys Glu His Cys Glu Gly Arg Gly Ile  
675 680 685

Ile Val His Val Asp Pro Val Asp Thr Val Asp Glu Arg Val Glu Ala  
690 695 700

Lys Ala Glu Glu Arg Ser Arg Arg His Gln Arg Ser Asn Ser Thr Asn  
705 710 715 720

Lys Ala Ala Ala Glu His Pro Met Val Val Ala Met Arg Asp Leu Val  
725 730 735

Glu Ser Asp Glu His Asp Leu Asp Gln Glu Phe Glu Glu Leu Ala Ala  
740 745 750

Ser Met Ile Val Leu Asp Asp Ser Asp Leu Leu  
755 760

<210> 225

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXN02370

<400> 225

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caagaatttg aggaactcgc tgcatacatg atcggtctcg atg act ccg atc tat 115  
Met Thr Pro Ile Tyr  
1 5

gat gat gtg gac aac gac aag ctc gag gag cct gag cgc att ctt gct 163  
Asp Asp Val Asp Asn Asp Lys Leu Asp Glu Pro Glu Arg Ile Leu Ala  
10 15 20

gaa tcc acc gtg gaa ccg gag gaa gga cca cgc atg agg gcc cgc cgt 211  
 Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg Met Arg Ala Arg Arg  
 25 30 35

caa cgt cag gaa tct gct gcg gat gat att gcc gcg att gca gct gct 259  
 Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala Ala Ile Ala Ala Ala  
 40 45 50

gcc gtg gac att gct tct gaa gaa gac cct gat gag cct tcg gga tcg 307  
 Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp Glu Pro Ser Gly Ser  
 55 60 65

tcg tat gtg tct gac ttt gag gca gag cct att gca cct gta gtt gag 355  
 Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile Ala Pro Val Val Glu  
 70 75 80 85

aag gct gct gaa cct gtg gct gag cca acc gct gat tat gaa aag gca 403  
 Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala Asp Tyr Glu Lys Ala  
 90 95 100

cgt gcc gaa ttt gag gca agc cca cgc agg cgc cgc aag act cgt ggc 451  
 Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg Arg Lys Thr Arg Gly  
 105 110 115

aat tca cgt tcg gat cat gct cca aag cca gag gat ttc gca cct gta 499  
 Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu Asp Phe Ala Pro Val  
 120 125 130

gtt gaa gag gtt gct gag act cca gtg aag aca cct gcg cgg aag gct 547  
 Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr Pro Ala Arg Lys Ala  
 135 140 145

cca cgc cgt aac cgt cca agt gag ctc agt tcc ggt gcg ccg tcc tct 595  
 Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser Gly Ala Pro Ser Ser  
 150 155 160 165

gca cca tcg acc agg aac cgt cgc cgc gca gtg cgc cgt caa ctg gtg 643  
 Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val Arg Arg Gln Leu Val  
 170 175 180

gaa gct cct gag acc gtc gtt gag ata gca cct gaa gca gca cca gaa 691  
 Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro Glu Ala Ala Pro Glu  
 185 190 195

cag gtt gca gag cct cag gtt gaa ttc gac cag cca gac aac cgc cga 739  
 Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln Pro Asp Asn Arg Arg  
 200 205 210

aag cgt cgt cgt gct gtg cgc gtg aca gcg gcg ccg gtg gag aag aag 787  
 Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala Pro Val Glu Lys Lys  
 215 220 225

gtg gcg tcg aca agc aat gcg cgg gcg ccg aag aag gaa cct cag gcg 835  
 Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys Lys Glu Pro Gln Ala  
 230 235 240 245

gcg agc acc acc aac cca ggc cgc cgt agg cgg gct acc cga cga ggc 883  
 Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg Ala Thr Arg Arg Gly  
 250 255 260

cca cga agc tagggtataa gggcgggttg tgt  
Pro Arg Ser

<210> 226  
<211> 264  
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<213> Corynebacterium glutamicum

<400> 226  
Met Thr Pro Ile Tyr Asp Asp Val Asp Asn Asp Lys Leu Asp Glu Pro  
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Glu Arg Ile Leu Ala Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg  
20 25 30  
Met Arg Ala Arg Arg Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala  
35 40 45  
Ala Ile Ala Ala Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp  
50 55 60  
Glu Pro Ser Gly Ser Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile  
65 70 75 80  
Ala Pro Val Val Glu Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala  
85 90 95  
Asp Tyr Glu Lys Ala Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg  
100 105 110  
Arg Lys Thr Arg Gly Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu  
115 120 125  
Asp Phe Ala Pro Val Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr  
130 135 140  
Pro Ala Arg Lys Ala Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser  
145 150 155 160  
Gly Ala Pro Ser Ser Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val  
165 170 175  
Arg Arg Gln Leu Val Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro  
180 185 190  
Glu Ala Ala Pro Glu Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln  
195 200 205  
Pro Asp Asn Arg Arg Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala  
210 215 220  
Pro Val Glu Lys Lys Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys  
225 230 235 240  
Lys Glu Pro Gln Ala Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Arg  
245 250 255  
Ala Thr Arg Arg Gly Pro Arg Ser  
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<221> CDS
<222> (101)..(892)
<223> FRXA02370
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Met Thr Pro Ile Tyr																	
1 5																	
tat gat gtg gac aac gac aag ctc gac gag cct gag cgc att ctt gct																	163
Tyr Asp Val Asp Asn Asp Lys Leu Asp Glu Pro Glu Arg Ile Leu Ala																	
10 15 20																	
gaa tcc acc gtg gaa ccg gag gaa gga cca cgc atg agg gcc cgc cgt																	211
Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg Met Arg Ala Arg Arg																	
25 30 35																	
caa cgt cag gaa tct gct gcg gat gat att gcc gcg att gca gct gct																	259
Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala Ala Ile Ala Ala Ala																	
40 45 50																	
gcc gtg gac att gct tct gaa gaa gac cct gat gag cct tcg gga tcg																	307
Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp Glu Pro Ser Gly Ser																	
55 60 65																	
tcg tat gtg tct gac ttt gag gca gag cct att gca cct gta gtt gag																	355
Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile Ala Pro Val Val Glu																	
70 75 80 85																	
aag gct gct gaa cct gtg gct gag cca acc gct gat tat gaa aag gca																	403
Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala Asp Tyr Glu Lys Ala																	
90 95 100																	
cgt gcc gaa ttt gag gca agc cca cgc agg cgc cgc aag act cgt ggc																	451
Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg Arg Lys Thr Arg Gly																	
105 110 115																	
aat tca cgt tcg gat cat gct cca aag cca gag gat ttc gca cct gta																	499
Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu Asp Phe Ala Pro Val																	
120 125 130																	
gtt gaa gag gtt gct gag act cca gtg aag aca cct gcg cgg aag gct																	547
Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr Pro Ala Arg Lys Ala																	
135 140 145																	
cca cgc cgt aac cgt cca agt gag ctc agt tcc ggt gcg ccg tcc tct																	595
Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser Gly Ala Pro Ser Ser																	
150 155 160 165																	
gca cca tcg acc agg aac cgt cgc cgc gca gtg cgc cgt caa ctg gtg																	643
Ala Pro Ser Thr Arg Asn Arg Arg Arg Ala Val Arg Arg Gln Leu Val																	



170	175	180	
gaa gct cct gag acc gtc gtt gag ata gca cct gaa gca gca cca gaa			691
Glu Ala Pro Glu Thr Val Val Glu Ile Ala Pro Glu Ala Ala Pro Glu			
185	190	195	
cag gtt gca gag cct cag gtt gaa ttc gac cag cca gac aac cgc cga			739
Gln Val Ala Glu Pro Gln Val Glu Phe Asp Gln Pro Asp Asn Arg Arg			
200	205	210	
aag cgt cgt cgt gct gtg cgc gtg aca gcg gcg ccg gtg gag aag aag			787
Lys Arg Arg Arg Ala Val Arg Val Thr Ala Ala Pro Val Glu Lys Lys			
215	220	225	
gtg gcg tcg aca agc aat gcg cgg gcg ccg aag aag gaa cct cag gcg			835
Val Ala Ser Thr Ser Asn Ala Arg Ala Pro Lys Lys Glu Pro Gln Ala			
230	235	240	245
gcg agc acc acc aac cca ggc cgc cgt agg cgg gct acc cga cga ggc			883
Ala Ser Thr Thr Asn Pro Gly Arg Arg Arg Ala Thr Arg Arg Gly			
250	255	260	
cca cga agc tagggtataa gggcggtttg tgt			915
Pro Arg Ser			
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Met Thr Pro Ile Tyr Tyr Asp Val Asp Asn Asp Lys Leu Asp Glu Pro			
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Glu Arg Ile Leu Ala Glu Ser Thr Val Glu Pro Glu Glu Gly Pro Arg			
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Met Arg Ala Arg Arg Gln Arg Gln Glu Ser Ala Ala Asp Asp Ile Ala			
35	40	45	
Ala Ile Ala Ala Ala Ala Val Asp Ile Ala Ser Glu Glu Asp Pro Asp			
50	55	60	
Glu Pro Ser Gly Ser Ser Tyr Val Ser Asp Phe Glu Ala Glu Pro Ile			
65	70	75	80
Ala Pro Val Val Glu Lys Ala Ala Glu Pro Val Ala Glu Pro Thr Ala			
85	90	95	
Asp Tyr Glu Lys Ala Arg Ala Glu Phe Glu Ala Ser Pro Arg Arg Arg			
100	105	110	
Arg Lys Thr Arg Gly Asn Ser Arg Ser Asp His Ala Pro Lys Pro Glu			
115	120	125	
Asp Phe Ala Pro Val Val Glu Glu Val Ala Glu Thr Pro Val Lys Thr			
130	135	140	
Pro Ala Arg Lys Ala Pro Arg Arg Asn Arg Pro Ser Glu Leu Ser Ser			

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<211> 750
<212> DNA
<213> Corynebacterium glutamicum
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Leu Gly Pro Val Ala Gly Val Asp Glu Ala Gly Arg Gly Ala Cys Cys  
10 15 20

gga ccc att tca att gcc gca tgc ata ctc ccg gac aaa ccc atc cag 211  
Gly Pro Ile Ser Ile Ala Ala Cys Ile Leu Pro Asp Lys Pro Ile Gln  
25 30 35

gag cta gcc gca ctg aca gac tcc aaa aag ctc agt gcc agc acc cgc 259  
Glu Leu Ala Ala Leu Thr Asp Ser Lys Lys Leu Ser Ala Ser Thr Arg  
40 45 50

gaa aaa ctc atg cca ctg atc aaa aaa cac gca ctc gct tgg tca gtc 307  
Glu Lys Leu Met Pro Leu Ile Lys Lys His Ala Leu Ala Trp Ser Val  
55 60 65

atc gtg atc tcc gcc caa gac atc gac cga ttt ggc atc caa cac gca 355  
Ile Val Ile Ser Ala Gln Asp Ile Asp Arg Phe Gly Ile Gln His Ala  
70 75 80 85

aac atc tcc ggc atg cga cga gcc gta gcc gcc cta ggc acc caa ccc 403  
 Asn Ile Ser Gly Met Arg Arg Ala Val Ala Ala Leu Gly Thr Gln Pro  
 90 95 100

ggc tac gta ctt acc gac gcc atg aaa gtc ccc ggc ttc aca gtc cca 451  
 Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro Gly Phe Thr Val Pro  
 105 110 115

tac cta ccc atc atc ggc gga gac gcc tcc gcc cga tgc atc gcc gcc 499  
 Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala Arg Cys Ile Ala Ala  
 120 125 130

gca agt gta tta gcc aaa caa acc cgc gac gac atc atg acc gac atg 547  
 Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp Ile Met Thr Asp Met  
 135 140 145

gcc aac gac tac ccg cac tac ggt ctc gaa att cac aaa ggc tac agt 595  
 Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile His Lys Gly Tyr Ser  
 150 155 160 165

acg aag atc cac atg gat gcg gtg cgc cac cac ggc gca agt ccc gag 643  
 Thr Lys Ile His Met Asp Ala Val Arg His His Gly Ala Ser Pro Glu  
 170 175 180

cac aga tat agt tat gca aat gtg gcc aag gca cac caa gaa tgg cta 691  
 His Arg Tyr Ser Tyr Ala Asn Val Ala Lys Ala His Gln Glu Trp Leu  
 185 190 195

cac gct gca gat aat gac acg acg gaa ggt gga gca tgagcgctga 737  
 His Ala Ala Asp Asn Asp Thr Thr Glu Gly Gly Ala  
 200 205

agaactcgac aac 750

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 <212> PRT  
 <213> Corynebacterium glutamicum

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Arg Gly Ala Cys Cys Gly Pro Ile Ser Ile Ala Ala Cys Ile Leu Pro  
 20 25 30

Asp Lys Pro Ile Gln Glu Leu Ala Ala Leu Thr Asp Ser Lys Lys Leu  
 35 40 45

Ser Ala Ser Thr Arg Glu Lys Leu Met Pro Leu Ile Lys Lys His Ala  
 50 55 60

Leu Ala Trp Ser Val Ile Val Ile Ser Ala Gln Asp Ile Asp Arg Phe  
 65 70 75 80

Gly Ile Gln His Ala Asn Ile Ser Gly Met Arg Arg Ala Val Ala Ala  
 85 90 95

Leu Gly Thr Gln Pro Gly Tyr Val Leu Thr Asp Ala Met Lys Val Pro  
 100 105 110

Gly Phe Thr Val Pro Tyr Leu Pro Ile Ile Gly Gly Asp Ala Ser Ala  
115 120 125

Arg Cys Ile Ala Ala Ala Ser Val Leu Ala Lys Gln Thr Arg Asp Asp  
130 135 140

Ile Met Thr Asp Met Ala Asn Asp Tyr Pro His Tyr Gly Leu Glu Ile  
145 150 155 160

His Lys Gly Tyr Ser Thr Lys Ile His Met Asp Ala Val Arg His His  
165 170 175

Gly Ala Ser Pro Glu His Arg Tyr Ser Tyr Ala Asn Val Ala Lys Ala  
180 185 190

His Gln Glu Trp Leu His Ala Ala Asp Asn Asp Thr Thr Glu Gly Gly  
195 200 205

Ala

<210> 231

<211> 807

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> RXN01786

<400> 231

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ttccagcttt tctcgttttg atggccgcgc acaggatcag atg cgt gcc gcc aaa 115  
Met Arg Ala Ala Lys  
1 5

atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa 163  
Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu  
10 15 20

ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg 211  
Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val  
25 30 35

cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac 259  
Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr  
40 45 50

gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg 307  
Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met  
55 60 65

gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt 355  
Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly  
70 75 80 85

cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc 403

Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln Leu Gly Glu Asn Thr  
                     90                    95                    100  
  
 att gcg att gac tgc gat gtt ctg caa gct gac ggc ggt act cgt act 451  
 Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp Gly Gly Thr Arg Thr  
                     105                    110                    115  
  
 gca tcg atc acc ggt gcg tat gtg gcg ctg gct gat gcc atc aag gtt 499  
 Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala Asp Ala Ile Lys Val  
                     120                    125                    130  
  
 ctg cag gag cgc ggg gtt gtt cca ggc agc cca ctt ctt gca cca gtt 547  
 Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro Leu Leu Ala Pro Val  
                     135                    140                    145  
  
 gct gct gtt tcc gtt ggt ctg gtc gac ggt aat gta tgc ctt gac ttg 595  
 Ala Ala Val Ser Val Gly Leu Val Asp Gly Asn Val Cys Leu Asp Leu  
                     150                    155                    160                    165  
  
 cca tat gaa gaa gat tcc cgc gcc gat gtt gac ctc aac gtt gtt atg 643  
 Pro Tyr Glu Glu Asp Ser Arg Ala Asp Val Asp Leu Asn Val Val Met  
                     170                    175                    180  
  
 acc gaa cac ggt gaa ttc gtg gaa att cag ggc acc ggc gaa gaa act 691  
 Thr Glu His Gly Glu Phe Val Glu Ile Gln Gly Thr Gly Glu Glu Thr  
                     185                    190                    195  
  
 acc ttc acc cgc gcg cag ctc aac gac atg ctt gac cac gct gaa aag 739  
 Thr Phe Thr Arg Ala Gln Leu Asn Asp Met Leu Asp His Ala Glu Lys  
                     200                    205                    210  
  
 ggc tgc cgc gaa ttg gtt gct gcc caa aaa gct gca ctg gga atc 784  
 Gly Cys Arg Glu Leu Val Ala Ala Gln Lys Ala Ala Leu Gly Ile  
                     215                    220                    225  
  
 taaaaccaca acagagttaa gga 807

&lt;210&gt; 232

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 232

Met Arg Ala Ala Lys Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly  
           1                    5                    10                    15

Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser  
                     20                    25                    30

Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp  
                     35                    40                    45

Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn  
                     50                    55                    60

Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile  
                     65                    70                    75                    80

Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln  
                     85                    90                    95

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp  
100 105 110

Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala  
115 120 125

Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro  
130 135 140

Leu Leu Ala Pro Val Ala Ala Val Ser Val Gly Leu Val Asp Gly Asn  
145 150 155 160

Val Cys Leu Asp Leu Pro Tyr Glu Glu Asp Ser Arg Ala Asp Val Asp  
165 170 175

Leu Asn Val Val Met Thr Glu His Gly Glu Phe Val Glu Ile Gln Gly  
180 185 190

Thr Gly Glu Glu Thr Thr Phe Thr Arg Ala Gln Leu Asn Asp Met Leu  
195 200 205

Asp His Ala Glu Lys Gly Cys Arg Glu Leu Val Ala Ala Gln Lys Ala  
210 215 220

Ala Leu Gly Ile  
225

<210> 233

<211> 541

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(541)

<223> FRXA01786

<400> 233

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ttccagcttt tctcgttttg atggccgcgc acaggatcag atg cgt gcc gcc aaa 115  
Met Arg Ala Ala Lys  
1 5

atc acc cgt gga ttt act tcc aac cct gca ggc agc gtg ctt gta gaa 163  
Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly Ser Val Leu Val Glu  
10 15 20

ttc ggc aat act cgt gtc atg tgc acc gct tct gtg gaa ttg ggt gtg 211  
Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser Val Glu Leu Gly Val  
25 30 35

cct cgt ttc aag cgt gat tca ggt gaa ggc tgg ttg acc gca gag tac 259  
Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp Leu Thr Ala Glu Tyr  
40 45 50

gcg atg ctt cct gct gcg act gcg gag cgt aac cgt cgt gaa tcc atg 307  
Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn Arg Arg Glu Ser Met  
55 60 65

gcc ggc aag gtc aag gga cgc act cat gaa att tct cgt ctg att ggt 355  
 Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile Ser Arg Leu Ile Gly  
 70 75 80 85

cgt tct ttg cgt gca gct gtg gat ctt tcc cag ctg ggt gag aac acc 403  
 Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln Leu Gly Glu Asn Thr  
 90 95 100

att gcg att gac tgc gat gtt ctg caa gct gac ggc ggt act cgt act 451  
 Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp Gly Gly Thr Arg Thr  
 105 110 115

gca tcg atc acc ggt gcg tat gtg gcg ctg gct gat gcc atc aag gtt 499  
 Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala Asp Ala Ile Lys Val  
 120 125 130

ctg cag gag cgc ggg gtt gtt cca ggc agc cca ctt ctt gca 541  
 Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro Leu Leu Ala  
 135 140 145

<210> 234

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

Met Arg Ala Ala Lys Ile Thr Arg Gly Phe Thr Ser Asn Pro Ala Gly  
 1 5 10 15

Ser Val Leu Val Glu Phe Gly Asn Thr Arg Val Met Cys Thr Ala Ser  
 20 25 30

Val Glu Leu Gly Val Pro Arg Phe Lys Arg Asp Ser Gly Glu Gly Trp  
 35 40 45

Leu Thr Ala Glu Tyr Ala Met Leu Pro Ala Ala Thr Ala Glu Arg Asn  
 50 55 60

Arg Arg Glu Ser Met Ala Gly Lys Val Lys Gly Arg Thr His Glu Ile  
 65 70 75 80

Ser Arg Leu Ile Gly Arg Ser Leu Arg Ala Ala Val Asp Leu Ser Gln  
 85 90 95

Leu Gly Glu Asn Thr Ile Ala Ile Asp Cys Asp Val Leu Gln Ala Asp  
 100 105 110

Gly Gly Thr Arg Thr Ala Ser Ile Thr Gly Ala Tyr Val Ala Leu Ala  
 115 120 125

Asp Ala Ile Lys Val Leu Gln Glu Arg Gly Val Val Pro Gly Ser Pro  
 130 135 140

Leu Leu Ala  
 145

<210> 235

<211> 741

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(718)

&lt;223&gt; RXN00163

&lt;400&gt; 235

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cactgggaat ctaaaaccac aacagagtta aggcacccgg atg aaa ctt ctt ctt 115  
 Met Lys Leu Leu Leu  
 1 5

gca tcc aac aac gca aag aaa ctc aaa gaa ctc cag cgg att ttg gat 163  
 Ala Ser Asn Asn Ala Lys Lys Leu Lys Glu Leu Gln Arg Ile Leu Asp  
 10 15 20

caa gca ggc ctg gat tcc gtt gaa ttg ctt gcg ctg cgt gat gtc gag 211  
 Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp Val Glu  
 25 30 35

gca tac gac gag ccg atc gaa gac ggc cgc act ttt gcc gac aac gca 259  
 Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp Asn Ala  
 40 45 50

cag atc aaa gcg cgc gcc ggg gta acc cac aca ggc atc gcc acg atc 307  
 Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala Thr Ile  
 55 60 65

gcc gat gat tcc ggc atc gct gtc gaa gaa ctc aac gga atg ccc ggc 355  
 Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met Pro Gly  
 70 75 80 85

gtt ttg tcc gca cgc tgg tcc ggc gca cac ggc aac gac acc gcc aac 403  
 Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr Ala Asn  
 90 95 100

aac gag ctg ctt ctt gcc caa atg gaa cat gtt ccc gac gag cgc cgc 451  
 Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu Arg Arg  
 105 110 115

aac gca gcc ttc gtg tcc gta tgc gtg ctt gca ctt ccg gac ggc caa 499  
 Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp Gly Gln  
 120 125 130

gaa ttt gtt cag gaa ggc cgt tgg gaa ggc caa ctc cta cgc gga cct 547  
 Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg Gly Pro  
 135 140 145

aag ggc gaa aac ggt ttc gga tac gat cca ctg ttc att cca gca gag 595  
 Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro Ala Glu  
 150 155 160 165

gaa atc gat gga caa gga cgc agc tcc gct gaa ctt tcc gca gag gaa 643  
 Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala Glu Glu  
 170 175 180

aag gac gct ttg tcc cac cga ggt caa gcg ctg cgc gga ttg gtt gag 691  
 Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu Val Glu



185 190 195  
aag atc gca cag gta gct gcg gct agc taaggcctta aggaaaacta 738  
Lys Ile Ala Gln Val Ala Ala Ala Ser  
200 205

aaa 741

<210> 236  
<211> 206  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 236  
Met Lys Leu Leu Leu Ala Ser Asn Asn Ala Lys Lys Leu Lys Glu Leu  
1 5 10 15  
Gln Arg Ile Leu Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala  
20 25 30  
Leu Arg Asp Val Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr  
35 40 45  
Phe Ala Asp Asn Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr  
50 55 60  
Gly Ile Ala Thr Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu  
65 70 75 80  
Asn Gly Met Pro Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly  
85 90 95  
Asn Asp Thr Ala Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val  
100 105 110  
Pro Asp Glu Arg Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala  
115 120 125  
Leu Pro Asp Gly Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln  
130 135 140  
Leu Leu Arg Gly Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu  
145 150 155 160  
Phe Ile Pro Ala Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu  
165 170 175  
Leu Ser Ala Glu Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu  
180 185 190  
Arg Gly Leu Val Glu Lys Ile Ala Gln Val Ala Ala Ala Ser  
195 200 205

<210> 237  
<211> 641  
<212> DNA  
<213> Corynebacterium glutamicum  
<220>

&lt;221&gt; CDS

&lt;222&gt; (58)..(618)

&lt;223&gt; FRXA00163

&lt;400&gt; 237

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Leu

1

gat caa gca ggc ctg gat tcc gtt gaa ttg ctt gcg ctg cgt gat gtc 108

Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp Val

5

10

15

gag gca tac gac gag ccg atc gaa gac ggc cgc act ttt gcc gac aac 156

Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp Asn

20

25

30

gca cag atc aaa gcg cgc gcc ggg gta acc cac aca gcc atc gcc acg 204

Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala Thr

35

40

45

atc gcc gat gat tcc ggc atc gct gtc gaa gaa ctc aac gga atg ccc 252

Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met Pro

50

55

60

65

ggc gtt ttg tcc gca cgc tgg tcc ggc gca cac ggc aac gac acc gcc 300

Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr Ala

70

75

80

aac aac gag ctg ctt ctt gcc caa atg gaa cat gtt ccc gac gag cgc 348

Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu Arg

85

90

95

cgc aac gca gcc ttc gtg tcc gta tgc gtg ctt gca ctt ccg gac ggc 396

Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp Gly

100

105

110

caa gaa ttt gtt cag gaa ggc cgt tgg gaa ggc caa ctc cta cgc gga 444

Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg Gly

115

120

125

cct aag ggc gaa aac ggt ttc gga tac gat cca ctg ttc att cca gca 492

Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro Ala

130

135

140

145

gag gaa atc gat gga caa gga cgc agc tcc gct gaa ctt tcc gca gag 540

Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala Glu

150

155

160

gaa aag gac gct ttg tcc cac cga ggt caa gcg ctg cgc gga ttg gtt 588

Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu Val

165

170

175

gag aag atc gca cag gta gct gcg gct agc taaggcctta aggaaaacta 638

Glu Lys Ile Ala Gln Val Ala Ala Ala Ser

180

185

aaa

641

&lt;210&gt; 238

&lt;211&gt; 187

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 238

Leu Asp Gln Ala Gly Leu Asp Ser Val Glu Leu Leu Ala Leu Arg Asp  
 1 5 10 15

Val Glu Ala Tyr Asp Glu Pro Ile Glu Asp Gly Arg Thr Phe Ala Asp  
 20 25 30

Asn Ala Gln Ile Lys Ala Arg Ala Gly Val Thr His Thr Gly Ile Ala  
 35 40 45

Thr Ile Ala Asp Asp Ser Gly Ile Ala Val Glu Glu Leu Asn Gly Met  
 50 55 60

Pro Gly Val Leu Ser Ala Arg Trp Ser Gly Ala His Gly Asn Asp Thr  
 65 70 75 80

Ala Asn Asn Glu Leu Leu Leu Ala Gln Met Glu His Val Pro Asp Glu  
 85 90 95

Arg Arg Asn Ala Ala Phe Val Ser Val Cys Val Leu Ala Leu Pro Asp  
 100 105 110

Gly Gln Glu Phe Val Gln Glu Gly Arg Trp Glu Gly Gln Leu Leu Arg  
 115 120 125

Gly Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Ile Pro  
 130 135 140

Ala Glu Glu Ile Asp Gly Gln Gly Arg Ser Ser Ala Glu Leu Ser Ala  
 145 150 155 160

Glu Glu Lys Asp Ala Leu Ser His Arg Gly Gln Ala Leu Arg Gly Leu  
 165 170 175

Val Glu Lys Ile Ala Gln Val Ala Ala Ser  
 180 185

&lt;210&gt; 239

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(409)

&lt;223&gt; RXA01424

&lt;400&gt; 239

gtaagcaaca gtgcttccag cgcaacataa gctgaactct tccatgcaat ttgcgacggt 60

gatgaggaaa gggcgtcgcg ctggcagtaa aactgtcgtt gtg cac ctg tgg gat 115  
 Val His Leu Trp Asp  
 1 5

agt gcc gaa tcg ttg gat ggc acc gaa aaa cag ggc gaa gtc gcc tca 163  
 Ser Ala Glu Ser Leu Asp Gly Thr Glu Lys Gln Gly Glu Val Ala Ser

	10	15	20	
ttc ggt ggt ccg cgg ttc ggc ctt gtc gtt tct aag gcc gtc gga aat				211
Phe Gly Gly Pro Arg Phe Gly Leu Val Val Ser Lys Ala Val Gly Asn				
	25	30	35	
gcg gtg gtt cgt cac cgc acc tcc cga cgg ctt cgt cat atc tgt gca				259
Ala Val Val Arg His Arg Thr Ser Arg Arg Leu Arg His Ile Cys Ala				
	40	45	50	
agc att gca gaa aaa tca cca gag cta ctc tcc ccc act cat cac gtg				307
Ser Ile Ala Glu Lys Ser Pro Glu Leu Leu Ser Pro Thr His His Val				
	55	60	65	
gtg atc cgc gcg ttg gcg ggg gct ggg aat gca acc tcg gcg gaa ctt				355
Val Ile Arg Ala Leu Ala Gly Ala Gly Asn Ala Thr Ser Ala Glu Leu				
	70	75	80	85
gaa cga gac atc cgc tac ggg ttg ggg aaa gct agc cgt gtg cgc acc				403
Glu Arg Asp Ile Arg Tyr Gly Leu Gly Lys Ala Ser Arg Val Arg Thr				
	90	95	100	
aac aag tgatgatcct ttcgacatcc cag				432
Asn Lys				

&lt;210&gt; 240

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 240

Val	His	Leu	Trp	Asp	Ser	Ala	Glu	Ser	Leu	Asp	Gly	Thr	Glu	Lys	Gln
1				5					10					15	

Gly	Glu	Val	Ala	Ser	Phe	Gly	Gly	Pro	Arg	Phe	Gly	Leu	Val	Val	Ser
		20						25					30		

Lys	Ala	Val	Gly	Asn	Ala	Val	Val	Arg	His	Arg	Thr	Ser	Arg	Arg	Leu
	35					40					45				

Arg	His	Ile	Cys	Ala	Ser	Ile	Ala	Glu	Lys	Ser	Pro	Glu	Leu	Leu	Ser
	50					55				60					

Pro	Thr	His	His	Val	Val	Ile	Arg	Ala	Leu	Ala	Gly	Ala	Gly	Asn	Ala
	65				70					75				80	

Thr	Ser	Ala	Glu	Leu	Glu	Arg	Asp	Ile	Arg	Tyr	Gly	Leu	Gly	Lys	Ala
			85					90						95	

Ser	Arg	Val	Arg	Thr	Asn	Lys
						100

&lt;210&gt; 241

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

<221> CDS  
 <222> (101)..(592)  
 <223> RXA01481

<400> 241

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tcacttttagc ccgtcccttt agtgtgccta tattggttgt atg caa aac agc aag 115
                                         Met Gln Asn Ser Lys
                                         1           5

aag acc ctc ggc gga gtg ctc gga gtc atc gtt gtc ctc gct gct gca 163
Lys Thr Leu Gly Gly Val Leu Gly Val Ile Val Val Leu Ala Ala Ala
              10              15              20

tgg ttt gga att gat ctg tcc act tca ggt gaa gcc acc agc caa gca 211
Trp Phe Gly Ile Asp Leu Ser Thr Ser Gly Glu Ala Thr Ser Gln Ala
              25              30              35

tca agc tca gca act act acc act att act agc tct aac act cca aca 259
Ser Ser Ser Ala Thr Thr Thr Thr Ile Thr Ser Ser Asn Thr Pro Thr
              40              45              50

tct gag tcc atc tcc agc aac agc gac tta gac ggt gac agc tgc tcc 307
Ser Glu Ser Ile Ser Ser Asn Ser Asp Leu Asp Gly Asp Ser Cys Ser
              55              60              65

atg agt gag ctg cca caa gaa gct gat gag gtg gtc gac gat atc ctc 355
Met Ser Glu Leu Pro Gln Glu Ala Asp Glu Val Val Asp Asp Ile Leu
              70              75              80              85

gcc ggt ggt cct ttt gat tac cca gac aat gac ggc gtg cgc ttt gga 403
Ala Gly Gly Pro Phe Asp Tyr Pro Asp Asn Asp Gly Val Arg Phe Gly
              90              95              100

aac tac gaa ggc gta cta ccg aaa gag tcc agc aac tac tac cgc gaa 451
Asn Tyr Glu Gly Val Leu Pro Lys Glu Ser Ser Asn Tyr Tyr Arg Glu
              105              110              115

tac acc gtg gaa acc cca gga ctt agc cac cgc ggt cca ctg cgc att 499
Tyr Thr Val Glu Thr Pro Gly Leu Ser His Arg Gly Pro Leu Arg Ile
              120              125              130

gtc acc ggt gga tca aac cca act gat cca gag gtg tgg tac tac acc 547
Val Thr Gly Gly Ser Asn Pro Thr Asp Pro Glu Val Trp Tyr Tyr Thr
              135              140              145

tca gat cac tat gaa act ttc tgt gcc atc acc gat gcg gag aac 592
Ser Asp His Tyr Glu Thr Phe Cys Ala Ile Thr Asp Ala Glu Asn
              150              155              160

taaatgaata tcgtcttgca ggg 615

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<210> 242  
 <211> 164  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 242  
 Met Gln Asn Ser Lys Lys Thr Leu Gly Gly Val Leu Gly Val Ile Val

1	5	10	15
Val Leu Ala Ala Ala Trp Phe Gly Ile Asp Leu Ser Thr Ser Gly Glu			
	20	25	30
Ala Thr Ser Gln Ala Ser Ser Ser Ala Thr Thr Thr Thr Ile Thr Ser			
	35	40	45
Ser Asn Thr Pro Thr Ser Glu Ser Ile Ser Ser Asn Ser Asp Leu Asp			
	50	55	60
Gly Asp Ser Cys Ser Met Ser Glu Leu Pro Gln Glu Ala Asp Glu Val			
	65	70	75
Val Asp Asp Ile Leu Ala Gly Gly Pro Phe Asp Tyr Pro Asp Asn Asp			
	85	90	95
Gly Val Arg Phe Gly Asn Tyr Glu Gly Val Leu Pro Lys Glu Ser Ser			
	100	105	110
Asn Tyr Tyr Arg Glu Tyr Thr Val Glu Thr Pro Gly Leu Ser His Arg			
	115	120	125
Gly Pro Leu Arg Ile Val Thr Gly Gly Ser Asn Pro Thr Asp Pro Glu			
	130	135	140
Val Trp Tyr Tyr Thr Ser Asp His Tyr Glu Thr Phe Cys Ala Ile Thr			
	145	150	155
			160
Asp Ala Glu Asn			

<210> 243  
 <211> 2100  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2077)  
 <223> RXN00724

<400> 243  
 cgccaaagga agccacagcg attaaaaagg cgctgggcta caccactgcg gaagagttgc 60  
 tccgccacca tgtgcgcaaa tactccacca cggtcttggc gtg gga att ggt gat 115  
 Val Gly Ile Gly Asp 5  
 gcc act gag ggc gat ctt gtt acc atc gtg ggt cag gtc gcc ttt gcc 163  
 Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly Gln Val Ala Phe Ala 20  
 10 15  
 aag cag tcc tat acc cag tcc ggc aag atg ctg tac aag gtt aca gtc 211  
 Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu Tyr Lys Val Thr Val 35  
 25 30  
 ttg act gag acg gaa cgc atc ggc att tcc ttc ttc gga gcc aag cac 259  
 Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe Phe Gly Ala Lys His 50  
 40 45

att ccg cgt ctt ctc cca gaa ggc act cgt gcg ctt ttt acc ggc aag 307  
 Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala Leu Phe Thr Gly Lys  
 55 60 65

gtg aag ttt ttt cgc aac gaa cct cag cta tct cat cca gag ttc att 355  
 Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser His Pro Glu Phe Ile  
 70 75 80 85

gtg atc cca gat cct gga tca ggc cgc cga ctc acc gcc act ggc ggt 403  
 Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu Thr Ala Thr Gly Gly  
 90 95 100

atg aaa tct ctg gct gcc tac ggc gat gtg gaa gaa gtg gca ctt cgt 451  
 Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu Glu Val Ala Leu Arg  
 105 110 115

ttg gtg gat cgc gaa tac atc ccg atc tat gcc ggc acc gcc acc atg 499  
 Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala Gly Thr Ala Thr Met  
 120 125 130

act acc tgg cgg atc atg gct gca gtg caa cgg gta ctg gaa acc atg 547  
 Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg Val Leu Glu Thr Met  
 135 140 145

ccg gtg atc aaa gaa cca ctg agc gtg gtg ccc gaa ggc atg ccc agt 595  
 Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro Glu Gly Met Pro Ser  
 150 155 160 165

ttc gac gag gcc atc cgc ggc att cac gat cca ggc cat gaa tct ccc 643  
 Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro Gly His Glu Ser Pro  
 170 175 180

agc acg ttt atc aac cgt ctg aaa tac aac gaa gca cta tcg ctg gcc 691  
 Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu Ala Leu Ser Leu Ala  
 185 190 195

acg gtg atg gcg atc cgg cgt gcc gat acc aag aac cgc aaa gca cca 739  
 Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys Asn Arg Lys Ala Pro  
 200 205 210

ccc atg ccg cgc gca ctc aaa ggg cat cag cac atg ctc atc gat gca 787  
 Pro Met Pro Arg Ala Leu Lys Gly His Gln His Met Leu Ile Asp Ala  
 215 220 225

ctc aac ttt cag ctc aca gtg gga cag aag caa gtg atc cgt gag atc 835  
 Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln Val Ile Arg Glu Ile  
 230 235 240 245

agc gcg gac att gaa caa cgc gtt ccc atg tct cgt ctg ctc caa ggt 883  
 Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser Arg Leu Leu Gln Gly  
 250 255 260

gag gtt ggt tcg ggt aaa acc atc gtg tcg ttg atc gcg atg ctg cag 931  
 Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu Ile Ala Met Leu Gln  
 265 270 275

gca att gat tcc ggt agg cag tgc gcc atg ctc gcc ccg acg gaa gtg 979  
 Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu Ala Pro Thr Glu Val  
 280 285 290

ttg gcc acc cag cat gcc cgc agc ctg agc aaa act ctc gac gac gca	1027
Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys Thr Leu Asp Asp Ala	
295 300 305	
ggc ctt gat atc aat gtt gtg ctc ttg act ggc tcg atg ccc acg gga	1075
Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly Ser Met Pro Thr Gly	
310 315 320 325	
gcc aag aag gag gct ctg ctg gaa atc atc tcc ggt gac gca gac att	1123
Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser Gly Asp Ala Asp Ile	
330 335 340	
gtg gtc ggc acg cat gcg ctg atc cag gac acc gtg gag ttc ttc gac	1171
Val Val Gly Thr His Ala Leu Ile Gln Asp Thr Val Glu Phe Phe Asp	
345 350 355	
ctt ggc ctc gtg gtg gtg gat gag cag cac cgt ttc ggc gtg gag caa	1219
Leu Gly Leu Val Val Val Asp Glu Gln His Arg Phe Gly Val Glu Gln	
360 365 370	
cgc gat caa ctg cgg acc aag ggc agg gaa ggc ctg acc ccg cac cta	1267
Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly Leu Thr Pro His Leu	
375 380 385	
ttg gtt atg act gcg acc cca att ccg cgc acc atc gcc atg acg gtg	1315
Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr Ile Ala Met Thr Val	
390 395 400 405	
ttc ggc gac ttg gcg gtg tcc acg ttg cgt gaa ctt cca ggc ggg cgc	1363
Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu Leu Pro Gly Gly Arg	
410 415 420	
cgg ccg att caa acc tcg gtg ata ccc gat cac aaa cct ggc tgg gtt	1411
Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His Lys Pro Gly Trp Val	
425 430 435	
aaa cgc ggt tgg gaa cgc atc ggt gag gaa gtc ctc gcc gga cgc caa	1459
Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val Leu Ala Gly Arg Gln	
440 445 450	
gcc tat gtg gtg tgt ccg cgc att gaa ggc gaa ggc ggc gtg ctg gaa	1507
Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu Gly Gly Val Leu Glu	
455 460 465	
atc cac gcc tat ctt tcc gaa cag gta tat cca gga ttg aat gtt gga	1555
Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro Gly Leu Asn Val Gly	
470 475 480 485	
atg ctg cac ggt cgc atg gac acg gat ctc aaa gat tcg gtc atg cag	1603
Met Leu His Gly Arg Met Asp Thr Asp Leu Lys Asp Ser Val Met Gln	
490 495 500	
gaa ttc gcc caa ggt gag atc gat att ttg gtc gcc acc acg gtc att	1651
Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val Ala Thr Thr Val Ile	
505 510 515	
gag gtc ggt att gac gtt gcc aac gcc acc gtc atg ctc atc cgc gag	1699
Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val Met Leu Ile Arg Glu	
520 525 530	
gcg gaa cgc ttc ggc gtt tcc cag atc cac cag ctg cgc ggc cgt gtt	1747



Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln Leu Arg Gly Arg Val  
 535 540 545

ggc cgt ggg cag cac gat tcc ctc tgc ctg ctg cac acc acc ttc gac 1795  
 Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu His Thr Thr Phe Asp  
 550 555 560 565

gag gac tcc cca caa ggc caa cgc ctc gcc gca att tcc acc aca acc 1843  
 Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr  
 570 575 580

gac ggt ttt caa ctc tct gaa ctt gat ttg cag gta cgc caa gaa ggc 1891  
 Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln Val Arg Gln Glu Gly  
 585 590 595

gac gtg ttg ggc acc cgc cag tcc ggc agc gac acc aaa ctc cgt cac 1939  
 Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp Thr Lys Leu Arg His  
 600 605 610

ctc tcg ttt atc agc gac caa aaa atc atc gag cgt gcg ctt atc gac 1987  
 Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp  
 615 620 625

gcc acc gag ctg gtt gcc gcc agc cgt tcc agg gcg ctt gag ctg gtc 2035  
 Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg Ala Leu Glu Leu Val  
 630 635 640 645

agc gac atc gca atg atc aac cag gaa tac ctg gaa aag agc 2077  
 Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu Glu Lys Ser  
 650 655

tgatattgat aggggtttaag tca 2100

<210> 244

<211> 659

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Val Gly Ile Gly Asp Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly  
 1 5 10 15

Gln Val Ala Phe Ala Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu  
 20 25 30

Tyr Lys Val Thr Val Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe  
 35 40 45

Phe Gly Ala Lys His Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala  
 50 55 60

Leu Phe Thr Gly Lys Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser  
 65 70 75 80

His Pro Glu Phe Ile Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu  
 85 90 95

Thr Ala Thr Gly Gly Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu  
 100 105 110

Glu Val Ala Leu Arg Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala  
 115 120 125  
 Gly Thr Ala Thr Met Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg  
 130 135 140  
 Val Leu Glu Thr Met Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro  
 145 150 155 160  
 Glu Gly Met Pro Ser Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro  
 165 170 175  
 Gly His Glu Ser Pro Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu  
 180 185 190  
 Ala Leu Ser Leu Ala Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys  
 195 200 205  
 Asn Arg Lys Ala Pro Pro Met Pro Arg Ala Leu Lys Gly His Gln His  
 210 215 220  
 Met Leu Ile Asp Ala Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln  
 225 230 235 240  
 Val Ile Arg Glu Ile Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser  
 245 250 255  
 Arg Leu Leu Gln Gly Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu  
 260 265 270  
 Ile Ala Met Leu Gln Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu  
 275 280 285  
 Ala Pro Thr Glu Val Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys  
 290 295 300  
 Thr Leu Asp Asp Ala Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly  
 305 310 315 320  
 Ser Met Pro Thr Gly Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser  
 325 330 335  
 Gly Asp Ala Asp Ile Val Val Gly Thr His Ala Leu Ile Gln Asp Thr  
 340 345 350  
 Val Glu Phe Phe Asp Leu Gly Leu Val Val Val Asp Glu Gln His Arg  
 355 360 365  
 Phe Gly Val Glu Gln Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly  
 370 375 380  
 Leu Thr Pro His Leu Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr  
 385 390 395 400  
 Ile Ala Met Thr Val Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu  
 405 410 415  
 Leu Pro Gly Gly Arg Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His  
 420 425 430  
 Lys Pro Gly Trp Val Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val

435                      440                      445  
 Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu  
     450                      455                      460  
 Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro  
     465                      470                      475                      480  
 Gly Leu Asn Val Gly Met Leu His Gly Arg Met Asp Thr Asp Leu Lys  
                     485                      490                      495  
 Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val  
                     500                      505                      510  
 Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val  
                     515                      520                      525  
 Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln  
                     530                      535                      540  
 Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu  
     545                      550                      555                      560  
 His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala  
                     565                      570                      575  
 Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln  
                     580                      585                      590  
 Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp  
                     595                      600                      605  
 Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu  
                     610                      615                      620  
 Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg  
     625                      630                      635                      640  
 Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu  
                     645                      650                      655  
 Glu Lys Ser

<210> 245  
 <211> 1604  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1581)  
 <223> RXN01979

<400> 245  
 ctg ggt cac gat ttc cgc ccc gat tat cgc cgc atc cgc gac ctg tta   48  
 Leu Gly His Asp Phe Arg Pro Asp Tyr Arg Arg Ile Arg Asp Leu Leu  
     1                      5                      10                      15  
 gcg gga ctt gcg ccc aat att ccc gtg cta gca acc aca gcc acc gcc   96

Ala Gly Leu Ala Pro Asn Ile Pro Val Leu Ala Thr Thr Ala Thr Ala	
20 25 30	
aat gac cgc gtg gtt gaa gat gtc cgt gcc caa cta gaa gat ggc aca	144
Asn Asp Arg Val Val Glu Asp Val Arg Ala Gln Leu Glu Asp Gly Thr	
35 40 45	
ggt ttg ttt cgt ggt ggg ata gac cgt gaa tcc ctt tac cta tca gtg	192
Gly Leu Phe Arg Gly Gly Ile Asp Arg Glu Ser Leu Tyr Leu Ser Val	
50 55 60	
gtg aac ctg ctc aac ccc acc gaa cgc cca gct tgg ctt gcc acc cac	240
Val Asn Leu Leu Asn Pro Thr Glu Arg Pro Ala Trp Leu Ala Thr His	
65 70 75 80	
ctc aaa gaa ctg acg ggt tgc ggc atc att tac tgc ctc act gtg tca	288
Leu Lys Glu Leu Thr Gly Ser Gly Ile Ile Tyr Cys Leu Thr Val Ser	
85 90 95	
gct gca cat gat ctt gcc gat gca ctt aat tct gtt gga tgg aat gtt	336
Ala Ala His Asp Leu Ala Asp Ala Leu Asn Ser Val Gly Trp Asn Val	
100 105 110	
gcc gcg tac acc ggt cga acc gaa gca gga gag cgc gaa cgt tta gaa	384
Ala Ala Tyr Thr Gly Arg Thr Glu Ala Gly Glu Arg Glu Arg Leu Glu	
115 120 125	
cat gcc ttg atc aac aac gag atc aaa gca cta gta gca acc tct gca	432
His Ala Leu Ile Asn Asn Glu Ile Lys Ala Leu Val Ala Thr Ser Ala	
130 135 140	
ctg gga atg ggc ttt gac aaa cct gac ctt gga ttt gtt gtg cac atg	480
Leu Gly Met Gly Phe Asp Lys Pro Asp Leu Gly Phe Val Val His Met	
145 150 155 160	
ggc agc ccc agc tca ccg gtg tct tat tac cag cag att ggt cgc gcc	528
Gly Ser Pro Ser Ser Pro Val Ser Tyr Tyr Gln Gln Ile Gly Arg Ala	
165 170 175	
ggg cgc ggc acc gct cgt gcc gat gtc atc ctg ctg cca gga act gaa	576
Gly Arg Gly Thr Ala Arg Ala Asp Val Ile Leu Leu Pro Gly Thr Glu	
180 185 190	
gac aaa gag atc tgg gag tac ttt gca tca gta tgc ttc cca cgc gaa	624
Asp Lys Glu Ile Trp Glu Tyr Phe Ala Ser Val Ser Phe Pro Arg Glu	
195 200 205	
gag gta gtc cgc caa ctg ctt gcg gtg tta acc gat gag gcg caa tcc	672
Glu Val Val Arg Gln Leu Leu Ala Val Leu Thr Asp Glu Ala Gln Ser	
210 215 220	
act gtc aaa ttg gaa tca caa gta gat ctt tcc cga tca cgc ctt gaa	720
Thr Val Lys Leu Glu Ser Gln Val Asp Leu Ser Arg Ser Arg Leu Glu	
225 230 235 240	
caa gta ctt aaa gtg cta gac gta gat ggc gca gtc aaa cgt gta cgt	768
Gln Val Leu Lys Val Leu Asp Val Asp Gly Ala Val Lys Arg Val Arg	
245 250 255	
ggc gga tgg gtc tcc acc ggg caa gag tgg atc tac gat gcg gaa cgc	816
Gly Gly Trp Val Ser Thr Gly Gln Glu Trp Ile Tyr Asp Ala Glu Arg	

260	265	270	
tac gca gga ctt gaa caa gca agg aaa att gaa cag caa agc atg gtg			864
Tyr Ala Gly Leu Glu Gln Ala Arg Lys Ile Glu Gln Gln Ser Met Val			
275	280	285	
aac tac cag aac acc act gag tgc cgc atg ctg tac ctc cgc aaa gaa			912
Asn Tyr Gln Asn Thr Thr Glu Cys Arg Met Leu Tyr Leu Arg Lys Glu			
290	295	300	
cta gac gat gtg gag gca act act ccg tgc ggg cgc tgc gac aat tgc			960
Leu Asp Asp Val Glu Ala Thr Thr Pro Cys Gly Arg Cys Asp Asn Cys			
305	310	315	320
acg ggc aaa acg tgg ggg ctc gac acc gat gcc tcg atc act ttg aaa			1008
Thr Gly Lys Thr Trp Gly Leu Asp Thr Asp Ala Ser Ile Thr Leu Lys			
325	330	335	
gtg gac caa cag ctt caa aca ccc gga gtg aaa ata gcc cca cga aaa			1056
Val Asp Gln Gln Leu Gln Thr Pro Gly Val Lys Ile Ala Pro Arg Lys			
340	345	350	
atg tgg ccg act ggc att agt gtc aga gga aaa atc gca ggg cta gaa			1104
Met Trp Pro Thr Gly Ile Ser Val Arg Gly Lys Ile Ala Gly Leu Glu			
355	360	365	
gaa gga cga gca ctg gga cga ctc aat gac att gcc cgt gga cct gca			1152
Glu Gly Arg Ala Leu Gly Arg Leu Asn Asp Ile Ala Arg Gly Pro Ala			
370	375	380	
cta aag gcc ctg ctg gac agc gga gct tat tct gat gat cca tgg atg			1200
Leu Lys Ala Leu Leu Asp Ser Gly Ala Tyr Ser Asp Asp Pro Trp Met			
385	390	395	400
gca cgc atc atc gaa gtg ctg aaa aac tgg gat tgg acc aac cgg cct			1248
Ala Arg Ile Ile Glu Val Leu Lys Asn Trp Asp Trp Thr Asn Arg Pro			
405	410	415	
gcc aac gtg gtc gct ctc ggc aat acc aac ttt gga tca act gag atg			1296
Ala Asn Val Val Ala Leu Gly Asn Thr Asn Phe Gly Ser Thr Glu Met			
420	425	430	
atc atc cag gta gct caa tca atc gca gcg gtg gga cga atg aac ttt			1344
Ile Ile Gln Val Ala Gln Ser Ile Ala Ala Val Gly Arg Met Asn Phe			
435	440	445	
gcg ggt gta ctt ccc gcc gcg ccg ggt gct gaa gaa gtc atg gct cag			1392
Ala Gly Val Leu Pro Ala Ala Pro Gly Ala Glu Glu Val Met Ala Gln			
450	455	460	
aat tcc gca tac cga gta gaa gcc cta ttg aaa caa tgg gac tgg tcg			1440
Asn Ser Ala Tyr Arg Val Glu Ala Leu Leu Lys Gln Trp Asp Trp Ser			
465	470	475	480
caa ggc ttg caa cta gtt ccc ggt ccc att ttg ctg gtg aca gac ctt			1488
Gln Gly Leu Gln Leu Val Pro Gly Pro Ile Leu Leu Val Thr Asp Leu			
485	490	495	
att gat act ggc tgg tcg gtg aca gtt gca gga aat ggc att gcg cag			1536
Ile Asp Thr Gly Trp Ser Val Thr Val Ala Gly Asn Gly Ile Ala Gln			
500	505	510	

1581

1604

<210> 246

<211> 527

<212> PRT

<213> *Corynebacterium glutamicum*

 $\langle 400 \rangle$  246

Ala Gly Leu Ala Pro Asn Ile Pro Val Leu Ala Thr Thr Ala Thr Ala  
20 25 30

Asn Asp Arg Val Val Glu Asp Val Arg Ala Gln Leu Glu Asp Gly Thr  
35 40 45

Gly Leu Phe Arg Gly Gly Ile Asp Arg Glu Ser Leu Tyr Leu Ser Val  
50 55 60

Val Asn Leu Leu Asn Pro Thr Glu Arg Pro Ala Trp Leu Ala Thr His  
65 70 75 80

Leu Lys Glu Leu Thr Gly Ser Gly Ile Ile Tyr Cys Leu Thr Val Ser  
85 90 95

Ala Ala His Asp Leu Ala Asp Ala Leu Asn Ser Val Gly Trp Asn Val  
100 105 110

Ala Ala Tyr Thr Gly Arg Thr Glu Ala Gly Glu Arg Glu Arg Leu Glu  
115 120 125

His Ala Leu Ile Asn Asn Glu Ile Lys Ala Leu Val Ala Thr Ser Ala  
130 135 140

Leu Gly Met Gly Phe Asp Lys Pro Asp Leu Gly Phe Val Val His Met  
145 150 155 160

Gly Ser Pro Ser Ser Pro Val Ser Tyr Tyr Gln Gln Ile Gly Arg Ala  
165 170 175

Gly Arg Gly Thr Ala Arg Ala Asp Val Ile Leu Leu Pro Gly Thr Glu  
180 185 190

Asp Lys Glu Ile Trp Glu Tyr Phe Ala Ser Val Ser Phe Pro Arg Glu  
195 200 205

Glu Val Val Arg Gln Leu Leu Ala Val Leu Thr Asp Glu Ala Gln Ser  
210 215 220

Thr Val Lys Leu Glu Ser Gln Val Asp Leu Ser Arg Ser Arg Leu Glu  
225 230 235 240

Gln Val Leu Lys Val Leu Asp Val Asp Gly Ala Val Lys Arg Val Arg  
245 250 255

Gly Gly Trp Val Ser Thr Gly Gln Glu Trp Ile Tyr Asp Ala Glu Arg  
 260 265 270  
 Tyr Ala Gly Leu Glu Gln Ala Arg Lys Ile Glu Gln Gln Ser Met Val  
 275 280 285  
 Asn Tyr Gln Asn Thr Thr Glu Cys Arg Met Leu Tyr Leu Arg Lys Glu  
 290 295 300  
 Leu Asp Asp Val Glu Ala Thr Thr Pro Cys Gly Arg Cys Asp Asn Cys  
 305 310 315 320  
 Thr Gly Lys Thr Trp Gly Leu Asp Thr Asp Ala Ser Ile Thr Leu Lys  
 325 330 335  
 Val Asp Gln Gln Leu Gln Thr Pro Gly Val Lys Ile Ala Pro Arg Lys  
 340 345 350  
 Met Trp Pro Thr Gly Ile Ser Val Arg Gly Lys Ile Ala Gly Leu Glu  
 355 360 365  
 Glu Gly Arg Ala Leu Gly Arg Leu Asn Asp Ile Ala Arg Gly Pro Ala  
 370 375 380  
 Leu Lys Ala Leu Leu Asp Ser Gly Ala Tyr Ser Asp Asp Pro Trp Met  
 385 390 395 400  
 Ala Arg Ile Ile Glu Val Leu Lys Asn Trp Asp Trp Thr Asn Arg Pro  
 405 410 415  
 Ala Asn Val Val Ala Leu Gly Asn Thr Asn Phe Gly Ser Thr Glu Met  
 420 425 430  
 Ile Ile Gln Val Ala Gln Ser Ile Ala Ala Val Gly Arg Met Asn Phe  
 435 440 445  
 Ala Gly Val Leu Pro Ala Ala Pro Gly Ala Glu Glu Val Met Ala Gln  
 450 455 460  
 Asn Ser Ala Tyr Arg Val Glu Ala Leu Leu Lys Gln Trp Asp Trp Ser  
 465 470 475 480  
 Gln Gly Leu Gln Leu Val Pro Gly Pro Ile Leu Leu Val Thr Asp Leu  
 485 490 495  
 Ile Asp Thr Gly Trp Ser Val Thr Val Ala Gly Asn Gly Ile Ala Gln  
 500 505 510  
 Arg Thr Ser Glu Lys Val Leu Pro Phe Ala Leu Ala Ser Arg Gly  
 515 520 525

&lt;210&gt; 247

&lt;211&gt; 3888

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3865)

<400> 247

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Met Pro Ile Ile Ile  
1 5

gat aac ctc aat tct gac gac gac tcc acc atc ggc act gcc acc gaa 163  
Asp Asn Leu Asn Ser Asp Asp Asp Ser Thr Ile Gly Thr Ala Thr Glu  
10 15 20

tac aac cct gac act gac gcc gat tta ctt gat gct att aac gct gat 211  
Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp Ala Ile Asn Ala Asp  
25 30 35

gct gac ctt gat ggc gac gcc acc atc agc act aac gcg aca gaa gaa 259  
Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu  
40 45 50

ggt gta gac gca gca gct gaa aaa cct aag aaa aag cgt aaa gcc cct 307  
Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro  
55 60 65

gct ctg aag cct aaa gga ctc acg gca aag ttc ttc cac cgt gat ctt 355  
Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe Phe His Arg Asp Leu  
70 75 80 85

act ggc gta ggt ggt agg acc ggt cgc ctc aac aag aac gta cac ccg 403  
Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn Lys Asn Val His Pro  
90 95 100

acc aac cca gat ctg tcc tac cag cca gtc tct gat gtc tac acc cca 451  
Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro  
105 110 115

caa tca gca gat cac aag ggt att aag acc cgc tac atc ctt acc cat 499  
Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His  
120 125 130

cca acc ccc gct gtt gtt ctc agt gag tcc atc agc aac gcg ttt cat 547  
Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His  
135 140 145

gtc tct acc ctg cgt cgc aac aat aat gtc aac aac tct gat tcg gaa 595  
Val Ser Thr Leu Arg Asn Asn Asn Val Asn Asn Ser Asp Ser Glu  
150 155 160 165

ttg	gct	gcc	tgg	ccg	tac	ctc	tac	caa	ctc	gat	att	ccg	cag	ctg	gac	643
Leu	Ala	Ala	Trp	Pro	Tyr	Leu	Tyr	Gln	Leu	Asp	Ile	Pro	Gln	Leu	Asp	
				170					175					180		

cag atg att aat gtc gct gac atc tgt gat tac cat ttc cac gga tat 691  
Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr  
185 190 195

aac ctg tgg gtg gat ttt acc ccg cag act atc gct cta cga tcc ggt 739  
Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile Ala Leu Arg Ser Gly  
200 205 210



aag acg gta ctc gat gac ggt acc acc gcc tct gat aac acc act cat	787
Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser Asp Asn Thr Thr His	
215 220 225	
gtc tat tac cgc gtc acc gtt cac gtt att gcc ggt caa gat cat gga	835
Val Tyr Tyr Arg Val Thr Val His Val Ile Ala Gly Gln Asp His Gly	
230 235 240 245	
tct act ctg ctt gat gac cag ggc aac cag gtg ctt gat agg gat gat	883
Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val Leu Asp Arg Asp Asp	
250 255 260	
aat cct att tct acc cca agt atc aag cgt att ggc gct gtc act gat	931
Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile Gly Ala Val Thr Asp	
265 270 275	
ctt ttc gat cac aat cct ttt ggc ttc gct agt gta aac tct ttc gca	979
Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser Val Asn Ser Phe Ala	
280 285 290	
ttt gtc gat ttc tca tgg gac cca gcc acc acc ttg gtc gat atg ctc	1027
Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr Leu Val Asp Met Leu	
295 300 305	
aac aac ctt gat tca tat ctc tct aat cac atc aat att gcc agc tcc	1075
Asn Asn Leu Asp Ser Tyr Leu Ser Asn His Ile Asn Ile Ala Ser Ser	
310 315 320 325	
cca acc ccc att gcc ctc gat atg gtt gtg ctc aat gaa tgg tct gaa	1123
Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu Asn Glu Trp Ser Glu	
330 335 340	
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Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala Gln Ala Lys Leu Ile	
345 350 355	
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Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp Val Ile Lys Gln Asn	
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Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met Asn Pro Gly Thr Thr	
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Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser Met Leu Pro Met Ser	
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Arg Gln Leu Arg Ile Leu Glu His Tyr Asp Val Pro Leu Thr Ala Tyr	
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Ser Ala Leu Phe Thr Trp Thr Val Ser Ala Ile Lys Asn Glu Ser Met Val	
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Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr Leu Ser Ser Asn Leu	
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Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro Val Pro Asp Lys Asp	
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Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro His Phe Ser Thr Gln	
470 475 480 485	
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Gln Arg Glu Ala Ile Thr Thr Asp Asn Pro Leu Ala Ile Ile Gln Ala	
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Gly Ala Gly Thr Gly Lys Ser Thr Val Ile Leu Glu Arg Ile Glu Tyr	
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Thr Asn Ala Ala Ala Asp Asn Ile Thr Ala Lys Asn Asp Lys Val Thr	
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Ser Met Thr Ile Ser Lys Met Val His Glu Ile Tyr Ala His Asn Phe	
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Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile Ile Asn Thr Leu Asp	
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Ile Glu Tyr Gly Asp Gln Met Val Thr Ser Asp Tyr Met Ile Gln Leu	
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Arg Asp Leu Leu Tyr Lys Val Met Thr Gln Gly Gly Asn Ala Asn Leu	
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Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro His Ala Ser Pro Lys	
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Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser Val Phe Glu Phe Val	
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acc acc aat tac cgt tcc aac cag gaa att ctt gac ttc gct aat atc			2323
Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu Asp Phe Ala Asn Ile			
	730	735	740
cac ctc tcg gat att gaa gct aac cag ttc gca ggt att cag ctc tac			2371
His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala Gly Ile Gln Leu Tyr			
	745	750	755
gcc aac tct ttt gat gca cct act gcg gac agc ttc aaa gaa aag gtt			2419
Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser Phe Lys Glu Lys Val			
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Glu Leu Asp Met His His Val Ser Lys Gln Ser Glu Phe Thr Asp Ser			
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Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His Ser Gly Arg Glu Ile			
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Phe Ile Lys Asp Phe Trp Phe Glu Val Thr Ala Val Asp Pro Ala His			
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Ala Ala Phe Thr Phe Thr Ser Gln Val Thr Ala His Leu Asp Lys Leu			
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Val Arg Gly Lys Arg Glu Gln Met Glu Asp Arg Val Ile Arg Ser Met			
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caa act cag tcc ggt gcg atc acc aac gaa gag ttc ttc tac cgt ctt			2899
Gln Thr Gln Ser Gly Ala Ile Thr Asn Glu Glu Phe Phe Tyr Arg Leu			
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cgt cag tgc att ctt gac tat gaa atc agg aat aac cga gca cgt cag			2947
Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn Asn Arg Ala Arg Gln			
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 Pro Ala Leu Gln Ile Glu Glu Glu Glu Glu Ala Arg Ala Leu Ala  
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gca gca gag cca gca att cag cag tac ttg tct cag ttt gct ttc gat 3523  
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 1130 1135 1140

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Lys Asn Val His Pro Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser  
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Asp Val Tyr Thr Pro Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg  
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Tyr Ile Leu Thr His Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile  
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Ser Asn Ala Phe His Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn  
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Asn Ser Asp Ser Glu Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp  
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Ile Pro Gln Leu Asp Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr

180	185	190
His Phe His Gly Tyr Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile 195 200 205		
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Asp Asn Thr Thr His Val Tyr Tyr Arg Val Thr Val His Val Ile Ala 225 230 235 240		
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Val Asn Ser Phe Ala Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr 290 295 300		
Leu Val Asp Met Leu Asn Asn Leu Asp Ser Tyr Leu Ser Asn His Ile 305 310 315 320		
Asn Ile Ala Ser Ser Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu 325 330 335		
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Gln Ala Lys Leu Ile Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp 355 360 365		
Val Ile Lys Gln Asn Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met 370 375 380		
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Pro Leu Thr Ala Tyr Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys 420 425 430		
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Val Pro Asp Lys Asp Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro 465 470 475 480		
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 Tyr Met Ile Gln Leu Arg Asp Leu Leu Tyr Lys Val Met Thr Gln Gly  
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 Val Phe Glu Phe Val Phe Ala Leu Arg Phe Ala Ala Lys His Asn Thr  
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 Gly Thr Tyr Arg Leu Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu  
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 425 430 435

aca ttg agc aat cgg cgt ggc caa att gtg tct cgt tct ttt gtg gct 1459  
 Thr Leu Ser Asn Arg Arg Gly Gln Ile Val Ser Arg Ser Phe Val Ala  
 440 445 450

tct tct ggc ccc ttt gat act gag gtg ctg tcc gat ccc atc caa tgg 1507  
 Ser Ser Gly Pro Phe Asp Thr Glu Val Leu Ser Asp Pro Ile Gln Trp  
 455 460 465

tta cat tcc ata ggc ctc gat gaa acc gcc att aac cca ggt acc gct 1555  
 Leu His Ser Ile Gly Leu Asp Glu Thr Ala Ile Asn Pro Gly Thr Ala  
 470 475 480 485

gca ctc ccc gac gat att gag cag ctt att tcc ctt gct gtt cag gcc 1603  
 Ala Leu Pro Asp Ile Glu Gln Leu Ile Ser Leu Ala Val Gln Ala  
 490 495 500

gcc cgc gcc gag atc cgt cca tta atg atc gcc gcc cgc gct cag gct 1651  
 Ala Arg Gly Glu Ile Arg Pro Leu Met Ile Ala Ala Arg Ala Gln Ala  
 505 510 515

caa act cgc gtt gag cat tgg gct aag cga gcc gaa gcc tgg aat aac 1699  
 Gln Thr Arg Val Glu His Trp Ala Lys Arg Ala Glu Ala Trp Asn Asn  
 520 525 530

aaa cga agt ggc gca gcg tcc acg tcc cgt acc gcg cga act gca aaa 1747  
 Lys Arg Ser Gly Ala Ala Ser Thr Ser Arg Thr Ala Arg Thr Ala Lys  
 535 540 545

ttg att gag gag cag cag aaa ttg agt aat gct ctc gag cca gac cgt 1795  
 Leu Ile Glu Glu Gln Lys Leu Ser Asn Ala Leu Glu Pro Asp Arg  
 550 555 560 565

gaa ctt att agg cct ttg gcc gtc att ctt ccg cag ccc gca act ttg 1843  
 Glu Leu Ile Arg Pro Leu Ala Val Ile Leu Pro Gln Pro Ala Thr Leu  
 570 575 580

aac acc gag gtt taacacaatg agtgcatttg att 1878

Asn Thr Glu Val  
585

<210> 250

<211> 585

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu Gly Glu Thr Val Ser  
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Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu Lys Arg Ala Leu Glu  
20 25 30

Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro Gln Thr Ser Gln Lys  
35 40 45

Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile Gly Val Lys Lys Asn  
50 55 60

Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg Val Ala Thr Leu His  
65 70 75 80

Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys Met Pro Pro Asn Ser  
85 90 95

Ile Ala Val Met His Gly Gly Leu Pro Asp Gln Glu Gln Met Arg Leu  
100 105 110

Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile Arg Ile Met Ile Thr  
115 120 125

Gly Asp Val Ala Ser Glu Gly Val Asn Leu His Thr Leu Cys His Asn  
130 135 140

Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile Arg Ile Gln Gln Arg  
145 150 155 160

Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His Asn Pro Ser Ile Val  
165 170 175

Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys Val Gly Glu Val His  
180 185 190

Val Leu Glu Arg Leu Met Glu Arg Glu His Glu Ala His Ser Leu Leu  
195 200 205

Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser Glu Arg Leu Glu Glu  
210 215 220

Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln Asn Phe Asn Asp Ala  
225 230 235 240

Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro Ala Gly Leu Asp Asp  
245 250 255

Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala Asp Ala Lys Ala Glu  
260 265 270

Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr Ala Pro Asp Ala Ala  
 275 280 285  
 Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu Tyr Ala Gln Glu Ser  
 290 295 300  
 Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe Asn Asn Val Pro Glu  
 305 310 315 320  
 Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys Lys His Asp Asn Asp  
 325 330 335  
 Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg Arg Arg Leu Asp Phe  
 340 345 350  
 Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val Lys Glu Asp Leu Leu  
 355 360 365  
 Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg Leu Asn Ala Ala Arg  
 370 375 380  
 Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala His Tyr Leu Gly Pro  
 385 390 395 400  
 Leu His Pro Val Thr Ser Trp Ala Ala Asp Arg Ala Leu Ala Thr Met  
 405 410 415  
 Pro Arg Ser Glu Ile Pro Ala Ala Ser Gly Lys Val Thr Glu Pro Thr  
 420 425 430  
 Val Leu Leu Met Ser Thr Leu Ser Asn Arg Arg Gly Gln Ile Val Ser  
 435 440 445  
 Arg Ser Phe Val Ala Ser Ser Gly Pro Phe Asp Thr Glu Val Leu Ser  
 450 455 460  
 Asp Pro Ile Gln Trp Leu His Ser Ile Gly Leu Asp Glu Thr Ala Ile  
 465 470 475 480  
 Asn Pro Gly Thr Ala Ala Leu Pro Asp Asp Ile Glu Gln Leu Ile Ser  
 485 490 495  
 Leu Ala Val Gln Ala Ala Arg Gly Glu Ile Arg Pro Leu Met Ile Ala  
 500 505 510  
 Ala Arg Ala Gln Ala Gln Thr Arg Val Glu His Trp Ala Lys Arg Ala  
 515 520 525  
 Glu Ala Trp Asn Asn Lys Arg Ser Gly Ala Ala Ser Thr Ser Arg Thr  
 530 535 540  
 Ala Arg Thr Ala Lys Leu Ile Glu Glu Gln Gln Lys Leu Ser Asn Ala  
 545 550 555 560  
 Leu Glu Pro Asp Arg Glu Leu Ile Arg Pro Leu Ala Val Ile Leu Pro  
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 Gln Pro Ala Thr Leu Asn Thr Glu Val  
 580 585

<210> 251  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1771)  
 <223> RXN02131

<400> 251  
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 Val Ala Phe Gly Asp  
 1 5  
 gga cct tta atc gtc caa tcc gat aag aca gtc ctg cta gaa ata gat 163  
 Gly Pro Leu Ile Val Gln Ser Asp Lys Thr Val Leu Leu Glu Ile Asp  
 10 15 20  
 cac ccc caa gca ggc gaa gca cgc ata gct cta gca cct ttt gca gag 211  
 His Pro Gln Ala Gly Glu Ala Arg Ile Ala Leu Ala Pro Phe Ala Glu  
 25 30 35  
 ctc gag cgt gca ccc gag cat att cac acc tac cgc atc acc cct ctg 259  
 Leu Glu Arg Ala Pro Glu His Ile His Thr Tyr Arg Ile Thr Pro Leu  
 40 45 50  
 gcg ttg tgg aac gcg cgc acc gca ggc cac gac gcc gaa caa gtc gtg 307  
 Ala Leu Trp Asn Ala Arg Thr Ala Gly His Asp Ala Glu Gln Val Val  
 55 60 65  
 gac atg ctg gag cgt ttt tca cgc ttc ccc gtt ccg caa gcg ctc ctg 355  
 Asp Met Leu Glu Arg Phe Ser Arg Phe Pro Val Pro Gln Ala Leu Leu  
 70 75 80 85  
 atc gac atc gca gag acg atg tcc cgc tac gga cgt gtg cgc ctg cac 403  
 Ile Asp Ile Ala Glu Thr Met Ser Arg Tyr Gly Arg Val Arg Leu His  
 90 95 100  
 cgt cac ccc gca cac ggg ctg atc ctt gaa tct ggc gaa cct gcg atc 451  
 Arg His Pro Ala His Gly Leu Ile Leu Glu Ser Gly Glu Pro Ala Ile  
 105 110 115  
 ctg gtg gaa atc tcc cgg cac aaa aag atc aaa ccc atg ctg ggc gca 499  
 Leu Val Glu Ile Ser Arg His Lys Lys Ile Lys Pro Met Leu Gly Ala  
 120 125 130  
 caa gtg gat cct gaa acc atc gtg gtc cat ccg tca gaa cgc ggg cgc 547  
 Gln Val Asp Pro Glu Thr Ile Val Val His Pro Ser Glu Arg Gly Arg  
 135 140 145  
 ctc aag cag gaa ctg ctc aag gtc ggt tgg cca gcg gaa gat ctc gcg 595  
 Leu Lys Gln Glu Leu Leu Lys Val Gly Trp Pro Ala Glu Asp Leu Ala  
 150 155 160 165  
 gga tat gtg gac ggt gaa tcc cac ccc att ggt ctc tcc act gaa ttt 643  
 Gly Tyr Val Asp Gly Glu Ser His Pro Ile Gly Leu Ser Thr Glu Phe  
 170 175 180

gaa gac tgg tcg ctg cgc gat tat cag caa atg gca gcc gat tcc ttc 691  
 Glu Asp Trp Ser Leu Arg Asp Tyr Gln Gln Met Ala Ala Asp Ser Phe  
 185 190 195

tgg gaa ggc ggt tcc ggc gta gtc gtg ctg cct tgt ggc gcg ggt aaa 739  
 Trp Glu Gly Gly Ser Gly Val Val Val Leu Pro Cys Gly Ala Gly Lys  
 200 205 210

acc atg gtc ggt gca gcc tcc atg gct cgc gca cag gca acc acc ttg 787  
 Thr Met Val Gly Ala Ala Ser Met Ala Arg Ala Gln Ala Thr Thr Leu  
 215 220 225

atc ctt gtc acc aac acc gtg gcc ggc cga cag tgg aaa gac gaa ctt 835  
 Ile Leu Val Thr Asn Thr Val Ala Gly Arg Gln Trp Lys Asp Glu Leu  
 230 235 240 245

ctt cgc cgc acc aca ctc acc gaa gac gaa atc ggt gag tac tcc ggc 883  
 Leu Arg Arg Thr Thr Leu Thr Glu Asp Glu Ile Gly Glu Tyr Ser Gly  
 250 255 260

gaa cgc aaa gaa atc cga ccc gtc acc atc gcc acc tac caa gta gtc 931  
 Glu Arg Lys Glu Ile Arg Pro Val Thr Ile Ala Thr Tyr Gln Val Val  
 265 270 275

acc agg cgt acc aaa ggc gaa tac aaa gct ctc gag ctt ttt gat tcc 979  
 Thr Arg Arg Thr Lys Gly Glu Tyr Lys Ala Leu Glu Leu Phe Asp Ser  
 280 285 290

cgc gac tgg ggc tta att att tac gac gaa gtc cat ctt ctt ccc gcc 1027  
 Arg Asp Trp Gly Leu Ile Ile Tyr Asp Glu Val His Leu Leu Pro Ala  
 295 300 305

ccc gtt ttc cgc atg acc tcc gac ctg caa tcc agg cga cgc ctc gga 1075  
 Pro Val Phe Arg Met Thr Ser Asp Leu Gln Ser Arg Arg Arg Leu Gly  
 310 315 320 325

ctg act gcc acc ctc gtg cgc gaa gac gga cga gaa ggc gat gtc ttc 1123  
 Leu Thr Ala Thr Leu Val Arg Glu Asp Gly Arg Glu Gly Asp Val Phe  
 330 335 340

agc ctg atc ggc ccc aag cgt tac gac gca cca tgg aaa gac ctc gag 1171  
 Ser Leu Ile Gly Pro Lys Arg Tyr Asp Ala Pro Trp Lys Asp Leu Glu  
 345 350 355

tcc caa ggg ttc atc gcc acc gcc gac tgc gta gaa atc cga tcc acc 1219  
 Ser Gln Gly Phe Ile Ala Thr Ala Asp Cys Val Glu Ile Arg Ser Thr  
 360 365 370

atg acc gat gct gag cgc atg gtg tac gcg act gcc gag tcg gca gat 1267  
 Met Thr Asp Ala Glu Arg Met Val Tyr Ala Thr Ala Glu Ser Ala Asp  
 375 380 385

cgt tac cgt cta gcc gcc act gcc cac act aag gtg gcc gtg gtg cgc 1315  
 Arg Tyr Arg Leu Ala Ala Thr Ala His Thr Lys Val Ala Val Val Arg  
 390 395 400 405

aaa ctc ctc gaa gag cac gct ggt aag ccc acg ctg atc atc ggc gca 1363  
 Lys Leu Leu Glu Glu His Ala Gly Lys Pro Thr Leu Ile Ile Gly Ala  
 410 415 420

tac ctc gat cag ttg gaa gaa cta ggt gca gaa ttc aac gca cca gtc 1411

Tyr Leu Asp Gln Leu Glu Glu Leu Gly Ala Glu Phe Asn Ala Pro Val  
 425 430 435

atc gac ggc aaa acg ccc aac aaa aag cgt gaa gcc ctc ttt gat caa 1459  
 Ile Asp Gly Lys Thr Pro Asn Lys Lys Arg Glu Ala Leu Phe Asp Gln  
 440 445 450

ttc cgt tcc ggc tcg ctt tcc gta ctg gtt gtc tcc aaa gtg gcg aac 1507  
 Phe Arg Ser Gly Ser Leu Ser Val Leu Val Val Ser Lys Val Ala Asn  
 455 460 465

ttc tcc atc gac ctg ccc gaa gca tcc gta gcc atc cag gtc tct gga 1555  
 Phe Ser Ile Asp Leu Pro Glu Ala Ser Val Ala Ile Gln Val Ser Gly  
 470 475 480 485

aca ttc ggc agc cga caa gaa gaa gcc caa cgc tta ggc cgc ctc ctg 1603  
 Thr Phe Gly Ser Arg Gln Glu Glu Ala Gln Arg Leu Gly Arg Leu Leu  
 490 495 500

cga ccc aag cac gat ggc agc gaa gcc cac ttc tac tcc atc gtc agc 1651  
 Arg Pro Lys His Asp Gly Ser Glu Ala His Phe Tyr Ser Ile Val Ser  
 505 510 515

cgc gac acc ctc gac acc gaa tac gca gcc cac cgc cag cga ttc ctc 1699  
 Arg Asp Thr Leu Asp Thr Glu Tyr Ala Ala His Arg Gln Arg Phe Leu  
 520 525 530

gcc gaa caa ggc tac gca tac cgc atc ctc gac gcc gac gac atc ctc 1747  
 Ala Glu Gln Gly Tyr Ala Tyr Arg Ile Leu Asp Ala Asp Asp Ile Leu  
 535 540 545

ttc cca cta ccc aag aaa gag cta taacgtgcac aacttctcct tcg 1794  
 Phe Pro Leu Pro Lys Lys Glu Leu  
 550 555

<210> 252

<211> 557

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Ala Phe Gly Asp Gly Pro Leu Ile Val Gln Ser Asp Lys Thr Val  
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Leu Leu Glu Ile Asp His Pro Gln Ala Gly Glu Ala Arg Ile Ala Leu  
 20 25 30

Ala Pro Phe Ala Glu Leu Glu Arg Ala Pro Glu His Ile His Thr Tyr  
 35 40 45

Arg Ile Thr Pro Leu Ala Leu Trp Asn Ala Arg Thr Ala Gly His Asp  
 50 55 60

Ala Glu Gln Val Val Asp Met Leu Glu Arg Phe Ser Arg Phe Pro Val  
 65 70 75 80

Pro Gln Ala Leu Leu Ile Asp Ile Ala Glu Thr Met Ser Arg Tyr Gly  
 85 90 95

Arg Val Arg Leu His Arg His Pro Ala His Gly Leu Ile Leu Glu Ser



100	105	110
Gly Glu Pro Ala Ile Leu Val	Glu Ile Ser Arg His Lys Lys Ile Lys	
115	120	125
Pro Met Leu Gly Ala Gln Val Asp Pro Glu Thr	Ile Val Val His Pro	
130	135	140
Ser Glu Arg Gly Arg Leu Lys Gln Glu Leu Leu Lys Val Gly Trp Pro		
145	150	155
Ala Glu Asp Leu Ala Gly Tyr Val Asp Gly Glu Ser His Pro Ile Gly		
165	170	175
Leu Ser Thr Glu Phe Glu Asp Trp Ser Leu Arg Asp Tyr Gln Gln Met		
180	185	190
Ala Ala Asp Ser Phe Trp Glu Gly Gly Ser Gly Val Val Val Leu Pro		
195	200	205
Cys Gly Ala Gly Lys Thr Met Val Gly Ala Ala Ser Met Ala Arg Ala		
210	215	220
Gln Ala Thr Thr Leu Ile Leu Val Thr Asn Thr Val Ala Gly Arg Gln		
225	230	235
Trp Lys Asp Glu Leu Leu Arg Arg Thr Thr Leu Thr Glu Asp Glu Ile		
245	250	255
Gly Glu Tyr Ser Gly Glu Arg Lys Glu Ile Arg Pro Val Thr Ile Ala		
260	265	270
Thr Tyr Gln Val Val Thr Arg Arg Thr Lys Gly Glu Tyr Lys Ala Leu		
275	280	285
Glu Leu Phe Asp Ser Arg Asp Trp Gly Leu Ile Ile Tyr Asp Glu Val		
290	295	300
His Leu Leu Pro Ala Pro Val Phe Arg Met Thr Ser Asp Leu Gln Ser		
305	310	315
Arg Arg Arg Leu Gly Leu Thr Ala Thr Leu Val Arg Glu Asp Gly Arg		
325	330	335
Glu Gly Asp Val Phe Ser Leu Ile Gly Pro Lys Arg Tyr Asp Ala Pro		
340	345	350
Trp Lys Asp Leu Glu Ser Gln Gly Phe Ile Ala Thr Ala Asp Cys Val		
355	360	365
Glu Ile Arg Ser Thr Met Thr Asp Ala Glu Arg Met Val Tyr Ala Thr		
370	375	380
Ala Glu Ser Ala Asp Arg Tyr Arg Leu Ala Ala Thr Ala His Thr Lys		
385	390	395
Val Ala Val Val Arg Lys Leu Leu Glu Glu His Ala Gly Lys Pro Thr		
405	410	415
Leu Ile Ile Gly Ala Tyr Leu Asp Gln Leu Glu Glu Leu Gly Ala Glu		
420	425	430

Phe Asn Ala Pro Val Ile Asp Gly Lys Thr Pro Asn Lys Lys Arg Glu  
435 440 445

Ala Leu Phe Asp Gln Phe Arg Ser Gly Ser Leu Ser Val Leu Val Val  
450 455 460

Ser Lys Val Ala Asn Phe Ser Ile Asp Leu Pro Glu Ala Ser Val Ala  
465 470 475 480

Ile Gln Val Ser Gly Thr Phe Gly Ser Arg Gln Glu Glu Ala Gln Arg  
485 490 495

Leu Gly Arg Leu Leu Arg Pro Lys His Asp Gly Ser Glu Ala His Phe  
500 505 510

Tyr Ser Ile Val Ser Arg Asp Thr Leu Asp Thr Glu Tyr Ala Ala His  
515 520 525

Arg Gln Arg Phe Leu Ala Glu Gln Gly Tyr Ala Tyr Arg Ile Leu Asp  
530 535 540

Ala Asp Asp Ile Leu Phe Pro Leu Pro Lys Lys Glu Leu  
545 550 555

<210> 253

<211> 849

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXN01066

<400> 253

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tttgaaccgc ctgggcttct agctttaagg gggtaggttc atg cgt agg gac agt 115  
Met Arg Arg Asp Ser  
1 5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163  
Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala  
10 15 20

gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga 211  
Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly  
25 30 35

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259  
Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu  
40 45 50

cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307  
Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu  
55 60 65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355  
Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile

70	75	80	85	
atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc				403
Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile				
	90	95	100	
gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa				451
Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu				
	105	110	115	
acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc				499
Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu				
	120	125	130	
aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca				547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala				
	135	140	145	
cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac				595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn				
	150	155	160	165
gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg				643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro				
	170	175	180	
ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg				691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu				
	185	190	195	
gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag				739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln				
	200	205	210	
caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att				787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile				
	215	220	225	
gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag				836
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala				
	230	235	240	
gcttaggcgt ccg				849

&lt;210&gt; 254

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 254

Met	Arg	Arg	Asp	Ser	Phe	Arg	Asp	Arg	Ala	Leu	Val	Val	Lys	Thr	Tyr
1				5					10					15	

Asp	Phe	Gly	Glu	Ala	Asp	Arg	Ile	Ile	Val	Leu	Leu	Thr	Arg	Asp	His
			20					25					30		

Gly	Ile	Val	Arg	Gly	Val	Ala	Lys	Gly	Val	Arg	Arg	Ser	Lys	Ser	Arg
		35					40					45			

Phe	Gly	Ser	Arg	Leu	Gln	Leu	Phe	Val	Glu	Leu	Asp	Val	Gln	Leu	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50                      55                      60  
 Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr  
 65                      70                      75                      80  
 Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser  
 85                      90                      95  
 Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro  
 100                      105                      110  
 His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser  
 115                      120                      125  
 Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn  
 130                      135                      140  
 His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg  
 145                      150                      155                      160  
 Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys  
 165                      170                      175  
 Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu  
 180                      185                      190  
 His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg  
 195                      200                      205  
 Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His  
 210                      215                      220  
 Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp  
 225                      230                      235                      240  
 Gln Ala

<210> 255  
 <211> 707  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(684)  
 <223> RXN01389

<400> 255  
 cag gac ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc 48  
 Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val  
 1                      5                      10                      15  
 ggt aaa att ttg cct cag aaa gat atg cca ttc ctt cca gac ggc act 96  
 Gly Lys Ile Leu Pro Gln Lys Asp Met Pro Phe Leu Pro Asp Gly Thr  
 20                      25                      30  
 cct gtt gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac 144  
 Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn  
 35                      40                      45

att ggt cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt 192  
 Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly  
 50 55 60

tgg tcc gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act 240  
 Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr  
 65 70 75 80

ctg cct gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act 288  
 Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr  
 85 90 95

cct gtg ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct 336  
 Pro Val Phe Asp Gly Ala Ser Asn Glu Leu Ala Gly Leu Leu Ala  
 100 105 110

aat tca cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt 384  
 Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly  
 115 120 125

aaa gca acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg 432  
 Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro  
 130 135 140

gtt tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac 480  
 Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp  
 145 150 155 160

gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc cag 528  
 Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr Gln  
 165 170 175

cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc ggc gaa 576  
 Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe Gly Glu  
 180 185 190

atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac aca ctt cag 624  
 Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr Thr Leu Gln  
 195 200 205

gag ctg ctg mcc ann nnn nnn nnn nnn nnn nnn nnn nnn nnt nnn 672  
 Glu Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 210 215 220

nnn nnn nnn nnn naannnnnnn tgcaccccg atc 707  
 Xaa Xaa Xaa Xaa  
 225

&lt;210&gt; 256

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 256

Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val  
 1 5 10 15

Gly Lys Ile Leu Pro Gln Lys Asp Met Pro Phe Leu Pro Asp Gly Thr  
 20 25 30

Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn  
35 40 45

Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly  
50 55 60

Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr  
65 70 75 80

Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr  
85 90 95

Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala  
100 105 110

Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly  
115 120 125

Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro  
130 135 140

Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp  
145 150 155 160

Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr Gln  
165 170 175

Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe Gly Glu  
180 185 190

Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr Thr Leu Gln  
195 200 205

Glu Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
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Xaa Xaa Xaa Xaa  
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<220>

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<223> RXN02070

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tttagggagt atcaaaactt gggactacta tcgatacgtg atg act caa gta acc 115  
Met Thr Gln Val Thr  
1 5

gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc 163  
Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile  
10 15 20

ggt aag ccc atc aca gag ctc ggc atg gtc aaa tca gtg tcc atc gac	211
Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp	
25 30 35	
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Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro	
40 45 50	
atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc	307
Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile	
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gac ggg gtt ggc caa gtt cat gtc acc acc gat gtc atg agt gat gaa	355
Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu	
70 75 80 85	
cag cgc cgt gcg ctc cgc gtc tcc ctg cgc ggt gaa act tct gag cca	403
Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro	
90 95 100	
gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt	451
Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val	
105 110 115	
gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg	499
Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu	
120 125 130	
gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc	547
Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala	
135 140 145	
gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc	595
Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg	
150 155 160 165	
cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg	643
Pro His Gln Val Asp Asp Met Ile Met Pro Pro Gln Ala His Gly Val	
170 175 180	
aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg	691
Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val	
185 190 195	
tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac	739
Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp	
200 205 210	
gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga	787
Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly	
215 220 225	
act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag	835
Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu	
230 235 240 245	
ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag	883
Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Ala Glu Val Ala Glu	
250 255 260	

cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg 931  
 Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val  
 265 270 275

att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat 979  
 Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp  
 280 285 290

gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct 1027  
 Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala  
 295 300 305

gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg 1075  
 Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro  
 310 315 320 325

aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa 1123  
 Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu  
 330 335 340

cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta 1171  
 Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu Ile Ala Glu His Leu  
 345 350 355

gct cac cgc aag gta tcg ctg gtg ggt aaa acg ctt ggg ctt ggc gtt 1219  
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 Lys

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Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr  
 35 40 45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala  
 50 55 60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp  
 65 70 75 80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly  
 85 90 95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr  
 100 105 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser



115	120	125
Met Thr Val Asn Leu Ala	Ala Ala Leu Ala Lys Arg	Gly Leu Ser Val
130	135	140
Gly Ile Leu Asp Ala Asp	Ile Tyr Gly His Ser Val	Pro Gly Met Leu
145	150	155
Gly Ser Asp Gln Arg Pro	His Gln Val Asp Asp Met	Ile Met Pro Pro
	165	170
Gln Ala His Gly Val Lys	Met Ile Ser Ile Ala His	Phe Thr Glu Gly
180	185	190
Asn Ala Pro Val Val Trp	Arg Gly Pro Met Leu His	Arg Ala Ile Gln
195	200	205
Gln Phe Leu Thr Asp Val	Phe Trp Gly Asp Leu Asp	Ile Leu Leu Leu
210	215	220
Asp Leu Pro Pro Gly Thr	Gly Asp Ile Ala Ile Thr	Val Ala Gln Leu
225	230	235
Ile Pro Asn Ala Glu Leu	Leu Ile Val Thr Thr Pro	Gln Ala Ala Ala
	245	250
Ala Glu Val Ala Glu Arg	Ala Gly Thr Ile Ser Val	Gln Thr Asn Gln
260	265	270
Lys Val Ala Gly Val Ile	Glu Asn Met Ser Ala Met	Val Leu Pro Asp
275	280	285
Gly Thr Thr Met Asp Val	Phe Gly Thr Gly Gly Gly	Gln Lys Ile Ala
290	295	300
Asp Arg Leu Thr Ala Val	Thr Gly Glu Glu Val Lys	Val Ile Gly Ser
305	310	315
Val Pro Leu Asp Pro Asn	Leu Arg Ile Gly Gly Asp	Val Gly Asn Pro
	325	330
Ile Ala Ile Ser Glu Pro	His Ser Pro Thr Ala Ala	Ala Ile Asn Glu
340	345	350
Ile Ala Glu His Leu Ala	His Arg Lys Val Ser Leu	Val Gly Lys Thr
355	360	365
Leu Gly Leu Gly Val Lys		
370		

&lt;210&gt; 259

&lt;211&gt; 3010

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3010)

&lt;223&gt; RXN02082

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Met Tyr Leu Lys Ser															
1 5															
ttg acg ctc aag ggg ttt aag tct ttc gcg tct gcg acg acc ctg aaa															163
Leu Thr Leu Lys Gly Phe Lys Ser Phe Ala Ser Ala Thr Thr Leu Lys															
10 15 20															
ttt gag cca ggc att tgt gcc gtg gtg ggt ccg aat ggt tca ggc aaa															211
Phe Glu Pro Gly Ile Cys Ala Val Val Gly Pro Asn Gly Ser Gly Lys															
25 30 35															
tcc aat gtg gtt gat gcg ctg gcc tgg gtg atg ggt gaa ggt tct gcg															259
Ser Asn Val Val Asp Ala Leu Ala Trp Val Met Gly Glu Gly Ser Ala															
40 45 50															
aag acc ttg cgt ggc ggc aaa atg gaa gat gtc att ttt gct ggc gcg															307
Lys Thr Leu Arg Gly Gly Lys Met Glu Asp Val Ile Phe Ala Gly Ala															
55 60 65															
ggc gat cgt aaa ccg ttg ggt cgc gca gaa gtc acg ctg acc att gat															355
Gly Asp Arg Lys Pro Leu Gly Arg Ala Glu Val Thr Leu Thr Ile Asp															
70 75 80 85															
aac tct gat ggc gca ctg ccc att gag tac acc gaa gtg tcg gtg acc															403
Asn Ser Asp Gly Ala Leu Pro Ile Glu Tyr Thr Glu Val Ser Val Thr															
90 95 100															
aga cgg atg ttc cgt gat ggt gca agt gaa tat gag atc aat ggg gcg															451
Arg Arg Met Phe Arg Asp Gly Ala Ser Glu Tyr Glu Ile Asn Gly Ala															
105 110 115															
aaa gct cga ttg atg gat atc cag gag ctg ttg tcg gat acc ggt att															499
Lys Ala Arg Leu Met Asp Ile Gln Glu Leu Leu Ser Asp Thr Gly Ile															
120 125 130															
ggc cgt gaa atg cac atc atg gtg ggg cag gga aag ctc gca gag att															547
Gly Arg Glu Met His Ile Met Val Gly Gln Gly Lys Leu Ala Glu Ile															
135 140 145															
ttg gag tcc cgc ccc gaa gag cgc cga gcg tat atc gaa gaa gct gcg															595
Leu Glu Ser Arg Pro Glu Glu Arg Arg Ala Tyr Ile Glu Glu Ala Ala															
150 155 160 165															
ggt gtg ctc aag cac cgg cgc agg aaa gaa aag gcg cag cgc aaa ctt															643
Gly Val Leu Lys His Arg Arg Arg Lys Glu Lys Ala Gln Arg Lys Leu															
170 175 180															
cag ggc atg cag gtc aat ctt gat cgt ttg cag gat ctg acc cat gag															691
Gln Gly Met Gln Val Asn Leu Asp Arg Leu Gln Asp Leu Thr His Glu															
185 190 195															
ttg gcc aag cag ctc aag ccg ttg gct agg cag gcg gaa gca gcg cag															739
Leu Ala Lys Gln Leu Lys Pro Leu Ala Arg Gln Ala Glu Ala Ala Gln															
200 205 210															
cgt gcg gcg acg gtg cag gct gat ttg cgt gat gcg cgt ttc cag att															787
Arg Ala Ala Thr Val Gln Ala Asp Leu Arg Asp Ala Arg Phe Gln Ile															

215	220	225	
gct ggc ttt gag atc gtg aag ctc tcg gaa aag ctg gaa acc tct act			835
Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys Leu Glu Thr Ser Thr			
230	235	240	245
gag cgc gag aaa atg att cgt gag cag gcg gaa gca gca caa gag cag			883
Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu Ala Ala Gln Glu Gln			
250	255	260	
ctg gaa gaa gcc acc aca act cag atg gaa gtg gag atg gag ttg gcg			931
Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val Glu Met Glu Leu Ala			
265	270	275	
gag atc act ccg cag gct gaa gct gcg caa cag ttg tgg ttt gat ttg			979
Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln Leu Trp Phe Asp Leu			
280	285	290	
tct tcg ctg gct gag cgg gtg tcg gca acg atg cgt att gct gca gac			1027
Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met Arg Ile Ala Ala Asp			
295	300	305	
cgt gcg agt tca ggt gcc gcg gat gtg ccg tat gcg ggc cag gat cct			1075
Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr Ala Gly Gln Asp Pro			
310	315	320	325
gat gag ttg ctt ggt cgg gcc gaa act gct gac aaa gaa tta gaa gaa			1123
Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp Lys Glu Leu Glu Glu			
330	335	340	
ctc gag atg gcc gtg gaa atg acc acc gag cgt ttg acc tcc att caa			1171
Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg Leu Thr Ser Ile Gln			
345	350	355	
gag gaa gcc gag gat aag gcc gcg cag gct cgt gag gct gag cgt gaa			1219
Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg Glu Ala Glu Arg Glu			
360	365	370	
cac ttg gcg cag gtc agg gcg att tct gat cgt cgt gaa ggt gtt gtg			1267
His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg Arg Glu Gly Val Val			
375	380	385	
cgc ctg ctt gca tct gag gaa tct ttg cgc acc cag cac acg tca gca			1315
Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr Gln His Thr Ser Ala			
390	395	400	405
gag gag gaa gct gag cga ctc agt gag cag ctt gag gag ttc atc ggc			1363
Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu Glu Glu Phe Ile Gly			
410	415	420	
cgc att ttg gat gtg gaa cgt gaa cgt cgc ctc acc gat gag cgt aaa			1411
Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu Thr Asp Glu Arg Lys			
425	430	435	
cag ggc gtt gac acg gat cgt gcg ccc ttg gaa gaa gcc ctc aaa cag			1459
Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu Glu Ala Leu Lys Gln			
440	445	450	
gca aaa cat gaa gcc gaa gca gca gag act cgt ctt gag gag ctt cgt			1507
Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg Leu Glu Glu Leu Arg			
455	460	465	

act aag cgc agc gat ctg gaa aaa gaa gta tcc agg ttg cag tcg cgc 1555  
 Thr Lys Arg Ser Asp Leu Glu Lys Glu Val Ser Arg Leu Gln Ser Arg  
 470 475 480 485

att gag acg ctt aac caa aat agg cca cgt tcc gat gct gct gat gtg 1603  
 Ile Glu Thr Leu Asn Gln Asn Arg Pro Arg Ser Asp Ala Ala Asp Val  
 490 495 500

gtg gat tac ccg cag ctg gcc acg ttg att cga ccg caa cga aac gtc 1651  
 Val Asp Tyr Pro Gln Leu Ala Thr Leu Ile Arg Pro Gln Arg Asn Val  
 505 510 515

gat aag gct ctc gct gcc gcc ctg ggt gcg cat gcc gag gcg ctg gct 1699  
 Asp Lys Ala Leu Ala Ala Ala Leu Gly Ala His Ala Glu Ala Leu Ala  
 520 525 530

ggc gag gct gcg gaa ggg ctc gtc gag aag ctt atc gac gcc ggc gtt 1747  
 Gly Glu Ala Ala Glu Gly Leu Val Glu Lys Leu Ile Asp Ala Gly Val  
 535 540 545

gca cgc acc atc atc gtt gat ggc acg cag gct ggc ggc gca tgg cgc 1795  
 Ala Arg Thr Ile Ile Val Asp Gly Thr Gln Ala Gly Gly Ala Trp Arg  
 550 555 560 565

ctg gac gcg aac att ccg gcc ggg gcg agc tgg ctg ctc gac cat gtt 1843  
 Leu Asp Ala Asn Ile Pro Ala Gly Ala Ser Trp Leu Leu Asp His Val  
 570 575 580

gat ctg gat ccg gcg att gcc ggc ccg gta aac ccg ctg ctt gcc gac 1891  
 Asp Leu Asp Pro Ala Ile Ala Gly Pro Val Asn Arg Leu Leu Ala Asp  
 585 590 595

gtt gtg ctt gtc gac gac ccc tcc ctc ggc cgc caa gca atc gag gat 1939  
 Val Val Leu Val Asp Asp Pro Ser Leu Gly Arg Gln Ala Ile Glu Asp  
 600 605 610

gat ccc cgt ctg cgt gcc gtt gac cgc aat ggt gtg ctc atc ggc gct 1987  
 Asp Pro Arg Leu Arg Ala Val Asp Arg Asn Gly Val Leu Ile Gly Ala  
 615 620 625

ggg tgg att cag gtc ggc acc gaa acc tcg act gtg gaa atc aca gct 2035  
 Gly Trp Ile Gln Val Gly Thr Glu Thr Ser Thr Val Glu Ile Thr Ala  
 630 635 640 645

cat att gag gaa gca gaa gct caa ctt gct gcg gcc tct gcc gcc ttg 2083  
 His Ile Glu Glu Ala Glu Ala Gln Leu Ala Ala Ala Ser Ala Ala Leu  
 650 655 660

gac gac att gcc ggc act ttt gat ggc gcc ctc cac gct gcc gac aac 2131  
 Asp Asp Ile Ala Gly Thr Phe Asp Gly Ala Leu His Ala Ala Asp Asn  
 665 670 675

act cgc gtc gag gtg gct gcc cgc acc gca gcc ctg cgc gaa ctc gac 2179  
 Thr Arg Val Glu Val Ala Ala Arg Thr Ala Ala Leu Arg Glu Leu Asp  
 680 685 690

atg acc agg gat tcc atc acc cgc gat ctc gcg cgc ttg gac aaa caa 2227  
 Met Thr Arg Asp Ser Ile Thr Arg Asp Leu Ala Arg Leu Asp Lys Gln  
 695 700 705

cat gag gcc gcc gaa tcc gag cgc gtc cgc cat gtt gga cgc ctg cat	2275
His Glu Ala Ala Glu Ser Glu Arg Val Arg His Val Gly Arg Leu His	
710 715 720 725	
gct gcg gaa aca cgc cgt gaa gag ctg cgc gaa cag tta gaa gac atc	2323
Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu Gln Leu Glu Asp Ile	
730 735 740	
gtc gat cga ctc tcc cgc gtg gaa gac gaa gaa gac gct gac gaa ccc	2371
Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu Asp Ala Asp Glu Pro	
745 750 755	
tca acc acc gcc cgc gac caa gca aat gcc gag ctg caa caa atc cgc	2419
Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu Leu Gln Gln Ile Arg	
760 765 770	
gcc atg gaa atg gaa gca cgc ctt gcc caa cgc acc gcc gaa gag cgc	2467
Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg Thr Ala Glu Glu Arg	
775 780 785	
gcc ggg cag cag cgg ggc aag ggc gat agt ctg cga cgc cag gcc gag	2515
Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu Arg Arg Gln Ala Glu	
790 795 800 805	
cat gag cgc caa gcc aaa atc cgg cat gaa caa gcc atg gaa gcc cgt	2563
His Glu Arg Gln Ala Lys Ile Arg His Glu Gln Ala Met Glu Ala Arg	
810 815 820	
cgc agg cgc acc caa ttg gct gca gcc gtg cat aat ggc gca cgc gat	2611
Arg Arg Arg Thr Gln Leu Ala Ala Val His Asn Gly Ala Arg Asp	
825 830 835	
gtg gcc gag cgt gtc tca agt gtc ctt gcc caa gca gcc atc gaa aga	2659
Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln Ala Ala Ile Glu Arg	
840 845 850	
gat cag cac aac cgc gac aaa gcg ctg ctg acc tca cac tta gcg cgc	2707
Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr Ser His Leu Ala Arg	
855 860 865	
gcc aaa gat gct gtg agt gct gca cgc cag cac ctc aat cga ctc agc	2755
Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His Leu Asn Arg Leu Ser	
870 875 880 885	
gac aac gcc cac tcc atg gaa ctt gcg cgc agc caa gct caa gtg cgc	2803
Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser Gln Ala Gln Val Arg	
890 895 900	
atg gag gaa gcc gtt gcc aaa atc acc gag caa ctt ggc att ccg gtc	2851
Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln Leu Gly Ile Pro Val	
905 910 915	
gca gaa ttg ctg cgc gat tac acc cca gat gaa aac ttt gat gaa aag	2899
Ala Glu Leu Leu Arg Asp Tyr Thr Pro Asp Glu Asn Phe Asp Glu Lys	
920 925 930	
ttc caa cgg gca cgc ctc aaa caa gcc gaa aaa gac ctc gcc gca cta	2947
Phe Gln Arg Ala Arg Leu Lys Gln Ala Glu Lys Asp Leu Ala Ala Leu	
935 940 945	
ggc aaa gtc aac ccc ctg gcc ttg gaa gaa ttc aaa gcc ctt gga aga	2995

Gly Lys Val Asn Pro Leu Ala Leu Glu Glu Phe Lys Ala Leu Gly Arg  
 950 955 960 965

3010

gcg cta cga gtt cct  
 Ala Leu Arg Val Pro  
 970

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 35 40 45  
 Gly Glu Gly Ser Ala Lys Thr Leu Arg Gly Gly Lys Met Glu Asp Val  
 50 55 60  
 Ile Phe Ala Gly Ala Gly Asp Arg Lys Pro Leu Gly Arg Ala Glu Val  
 65 70 75 80  
 Thr Leu Thr Ile Asp Asn Ser Asp Gly Ala Leu Pro Ile Glu Tyr Thr  
 85 90 95  
 Glu Val Ser Val Thr Arg Arg Met Phe Arg Asp Gly Ala Ser Glu Tyr  
 100 105 110  
 Glu Ile Asn Gly Ala Lys Ala Arg Leu Met Asp Ile Gln Glu Leu Leu  
 115 120 125  
 Ser Asp Thr Gly Ile Gly Arg Glu Met His Ile Met Val Gly Gln Gly  
 130 135 140  
 Lys Leu Ala Glu Ile Leu Glu Ser Arg Pro Glu Glu Arg Arg Ala Tyr  
 145 150 155 160  
 Ile Glu Glu Ala Ala Gly Val Leu Lys His Arg Arg Arg Lys Glu Lys  
 165 170 175  
 Ala Gln Arg Lys Leu Gln Gly Met Gln Val Asn Leu Asp Arg Leu Gln  
 180 185 190  
 Asp Leu Thr His Glu Leu Ala Lys Gln Leu Lys Pro Leu Ala Arg Gln  
 195 200 205  
 Ala Glu Ala Ala Gln Arg Ala Ala Thr Val Gln Ala Asp Leu Arg Asp  
 210 215 220  
 Ala Arg Phe Gln Ile Ala Gly Phe Glu Ile Val Lys Leu Ser Glu Lys  
 225 230 235 240  
 Leu Glu Thr Ser Thr Glu Arg Glu Lys Met Ile Arg Glu Gln Ala Glu  
 245 250 255

Ala Ala Gln Glu Gln Leu Glu Glu Ala Thr Thr Thr Gln Met Glu Val  
 260 265 270  
 Glu Met Glu Leu Ala Glu Ile Thr Pro Gln Ala Glu Ala Ala Gln Gln  
 275 280 285  
 Leu Trp Phe Asp Leu Ser Ser Leu Ala Glu Arg Val Ser Ala Thr Met  
 290 295 300  
 Arg Ile Ala Ala Asp Arg Ala Ser Ser Gly Ala Ala Asp Val Pro Tyr  
 305 310 315 320  
 Ala Gly Gln Asp Pro Asp Glu Leu Leu Gly Arg Ala Glu Thr Ala Asp  
 325 330 335  
 Lys Glu Leu Glu Glu Leu Glu Met Ala Val Glu Met Thr Thr Glu Arg  
 340 345 350  
 Leu Thr Ser Ile Gln Glu Glu Ala Glu Asp Lys Ala Ala Gln Ala Arg  
 355 360 365  
 Glu Ala Glu Arg Glu His Leu Ala Gln Val Arg Ala Ile Ser Asp Arg  
 370 375 380  
 Arg Glu Gly Val Val Arg Leu Leu Ala Ser Glu Glu Ser Leu Arg Thr  
 385 390 395 400  
 Gln His Thr Ser Ala Glu Glu Glu Ala Glu Arg Leu Ser Glu Gln Leu  
 405 410 415  
 Glu Glu Phe Ile Gly Arg Ile Leu Asp Val Glu Arg Glu Arg Arg Leu  
 420 425 430  
 Thr Asp Glu Arg Lys Gln Gly Val Asp Thr Asp Arg Ala Pro Leu Glu  
 435 440 445  
 Glu Ala Leu Lys Gln Ala Lys His Glu Ala Glu Ala Ala Glu Thr Arg  
 450 455 460  
 Leu Glu Glu Leu Arg Thr Lys Arg Ser Asp Leu Glu Lys Glu Val Ser  
 465 470 475 480  
 Arg Leu Gln Ser Arg Ile Glu Thr Leu Asn Gln Asn Arg Pro Arg Ser  
 485 490 495  
 Asp Ala Ala Asp Val Val Asp Tyr Pro Gln Leu Ala Thr Leu Ile Arg  
 500 505 510  
 Pro Gln Arg Asn Val Asp Lys Ala Leu Ala Ala Ala Leu Gly Ala His  
 515 520 525  
 Ala Glu Ala Leu Ala Gly Glu Ala Ala Glu Gly Leu Val Glu Lys Leu  
 530 535 540  
 Ile Asp Ala Gly Val Ala Arg Thr Ile Ile Val Asp Gly Thr Gln Ala  
 545 550 555 560  
 Gly Gly Ala Trp Arg Leu Asp Ala Asn Ile Pro Ala Gly Ala Ser Trp  
 565 570 575

Leu Leu Asp His Val Asp Leu Asp Pro Ala Ile Ala Gly Pro Val Asn  
 580 585 590  
 Arg Leu Leu Ala Asp Val Val Leu Val Asp Asp Pro Ser Leu Gly Arg  
 595 600 605  
 Gln Ala Ile Glu Asp Asp Pro Arg Leu Arg Ala Val Asp Arg Asn Gly  
 610 615 620  
 Val Leu Ile Gly Ala Gly Trp Ile Gln Val Gly Thr Glu Thr Ser Thr  
 625 630 635 640  
 Val Glu Ile Thr Ala His Ile Glu Glu Ala Glu Ala Gln Leu Ala Ala  
 645 650 655  
 Ala Ser Ala Ala Leu Asp Asp Ile Ala Gly Thr Phe Asp Gly Ala Leu  
 660 665 670  
 His Ala Ala Asp Asn Thr Arg Val Glu Val Ala Ala Arg Thr Ala Ala  
 675 680 685  
 Leu Arg Glu Leu Asp Met Thr Arg Asp Ser Ile Thr Arg Asp Leu Ala  
 690 695 700  
 Arg Leu Asp Lys Gln His Glu Ala Ala Glu Ser Glu Arg Val Arg His  
 705 710 715 720  
 Val Gly Arg Leu His Ala Ala Glu Thr Arg Arg Glu Glu Leu Arg Glu  
 725 730 735  
 Gln Leu Glu Asp Ile Val Asp Arg Leu Ser Arg Val Glu Asp Glu Glu  
 740 745 750  
 Asp Ala Asp Glu Pro Ser Thr Thr Ala Arg Asp Gln Ala Asn Ala Glu  
 755 760 765  
 Leu Gln Gln Ile Arg Ala Met Glu Met Glu Ala Arg Leu Ala Gln Arg  
 770 775 780  
 Thr Ala Glu Glu Arg Ala Gly Gln Gln Arg Gly Lys Gly Asp Ser Leu  
 785 790 795 800  
 Arg Arg Gln Ala Glu His Glu Arg Gln Ala Lys Ile Arg His Glu Gln  
 805 810 815  
 Ala Met Glu Ala Arg Arg Arg Arg Thr Gln Leu Ala Ala Val His  
 820 825 830  
 Asn Gly Ala Arg Asp Val Ala Glu Arg Val Ser Ser Val Leu Ala Gln  
 835 840 845  
 Ala Ala Ile Glu Arg Asp Gln His Asn Arg Asp Lys Ala Leu Leu Thr  
 850 855 860  
 Ser His Leu Ala Arg Ala Lys Asp Ala Val Ser Ala Ala Arg Gln His  
 865 870 875 880  
 Leu Asn Arg Leu Ser Asp Asn Ala His Ser Met Glu Leu Ala Arg Ser  
 885 890 895  
 Gln Ala Gln Val Arg Met Glu Glu Ala Val Ala Lys Ile Thr Glu Gln



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<210> 261
<211> 570
<212> DNA
<213> Corynebacterium glutamicum
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<400> 261  
taggaatagc agggtagata aacttattaa aattttttcca attcagggta gaattccaaa 60

cgc gcg gct cgt atg gca aag cgc att caa act atc gtg gcc agc gcc 163  
 Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr Ile Val Ala Ser Ala  
 10 15 20

att gaa cgc gat atc aag gac cgc cga ctt gag ttc gtc aca att act 211  
Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu Phe Val Thr Ile Thr  
25 30 35

gat gtg acc atg acc ggt gac ctg cac gat gca aag gtg ttt tac acc 259  
Asp Val Thr Met Thr Gly Asp Leu His Asp Ala Lys Val Phe Tyr Thr  
40 45 50

gtt cgt gga gct tcc att gaa gaa gaa cca gat ctt gag gca gca gca 307  
Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp Leu Glu Ala Ala Ala  
55 60 65

gag gct ctt cac cga gca cgc ggc cag ctg agg aag atc gtt ggc cag 355  
Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg Lys Ile Val Gly Gln  
70 75 80 85

cag ctg ggt gtt cgg ttt acc ccg acc ctg act tac agc atc gat acc 403  
Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr Tyr Ser Ile Asp Thr  
90 95 100

gtc cca gag gca tcc gca cac atg gaa gct ttg ttg gat cgt gct cgc 451  
Val Pro Glu Ala Ser Ala His Met Glu Ala Leu Leu Asp Arg Ala Arg  
105 110 115

aag cgc gat gag gag ctg gct aaa ttg cgc gaa ggt gca gcg cct gca 499

Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu Gly Ala Ala Pro Ala  
 120 125 130

ggt gat gca gat cct tac aag act tca tcc aag tct gaa tct gag gaa 547  
 Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys Ser Glu Ser Glu Glu  
 135 140 145

taacaccagt gacggataat agt 570

<210> 262

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Ala Asp Asn Ala Arg Ala Ala Arg Met Ala Lys Arg Ile Gln Thr  
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Ile Val Ala Ser Ala Ile Glu Arg Asp Ile Lys Asp Arg Arg Leu Glu  
 20 25 30

Phe Val Thr Ile Thr Asp Val Thr Met Thr Gly Asp Leu His Asp Ala  
 35 40 45

Lys Val Phe Tyr Thr Val Arg Gly Ala Ser Ile Glu Glu Glu Pro Asp  
 50 55 60

Leu Glu Ala Ala Ala Glu Ala Leu His Arg Ala Arg Gly Gln Leu Arg  
 65 70 75 80

Lys Ile Val Gly Gln Gln Leu Gly Val Arg Phe Thr Pro Thr Leu Thr  
 85 90 95

Tyr Ser Ile Asp Thr Val Pro Glu Ala Ser Ala His Met Glu Ala Leu  
 100 105 110

Leu Asp Arg Ala Arg Lys Arg Asp Glu Glu Leu Ala Lys Leu Arg Glu  
 115 120 125

Gly Ala Ala Pro Ala Gly Asp Ala Asp Pro Tyr Lys Thr Ser Ser Lys  
 130 135 140

Ser Glu Ser Glu Glu  
 145

<210> 263

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA01893

<400> 263

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atcagaatcc acgctgtag aaaaacacag gagtgaataa atg att gat gaa att 115

Met Ile Asp Glu Ile  
1 5

ctg ttc gaa gcg gaa gag cgc atg acc gca acg gtc gag cac acc cgc 163  
Leu Phe Glu Ala Glu Glu Arg Met Thr Ala Thr Val Glu His Thr Arg  
10 15 20

gaa gac ttg acc acc att cgt acc ggt cgc gca aac ccg gct atg ttc 211  
Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala Asn Pro Ala Met Phe  
25 30 35

aac ggt gtc atg gct gaa tac tac ggc gtg cct act cct att act cag 259  
Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro Thr Pro Ile Thr Gln  
40 45 50

atg tca ggc atc act gtt cca gag cct cgc atg ctg ctg atc aag cct 307  
Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met Leu Leu Ile Lys Pro  
55 60 65

tat gag atg tct tcc atg cag gtc att gag aat gct atc cgt aac tct 355  
Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn Ala Ile Arg Asn Ser  
70 75 80 85

gac ctt ggt gtt aac ccc acc aac gat ggc cag gtg ctg cgt gtg acc 403  
Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln Val Leu Arg Val Thr  
90 95 100

atc cca cag ctt act gaa gag cgt cgt aag gac atg gtc aag ctt gct 451  
Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp Met Val Lys Leu Ala  
105 110 115

aag ggt aag ggc gaa gac ggc aag att gcc att cgt aac atc cgc cgc 499  
Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile Arg Asn Ile Arg Arg  
120 125 130

aag ggc atg gac cag cta aag aag ctg caa aaa gat ggc gac gct ggc 547  
Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys Asp Gly Asp Ala Gly  
135 140 145

gaa gat gaa gta cag gca gca gaa aaa gaa cta gat aaa gtc acc gct 595  
Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu Asp Lys Val Thr Ala  
150 155 160 165

ggt ttt gtt gcg cag gtc gat gaa gtc gtt gct cgc aag gaa aag gaa 643  
Gly Phe Val Ala Gln Val Asp Glu Val Val Ala Arg Lys Glu Lys Glu  
170 175 180

ctg atg gag gtc tagaagacct ttatcgcaat ggc 678  
Leu Met Glu Val  
185

&lt;210&gt; 264

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 264

Met Ile Asp Glu Ile Leu Phe Glu Ala Glu Glu Arg Met Thr Ala Thr  
1 5 10 15

Val Glu His Thr Arg Glu Asp Leu Thr Thr Ile Arg Thr Gly Arg Ala  
 20 25 30

Asn Pro Ala Met Phe Asn Gly Val Met Ala Glu Tyr Tyr Gly Val Pro  
 35 40 45

Thr Pro Ile Thr Gln Met Ser Gly Ile Thr Val Pro Glu Pro Arg Met  
 50 55 60

Leu Leu Ile Lys Pro Tyr Glu Met Ser Ser Met Gln Val Ile Glu Asn  
 65 70 75 80

Ala Ile Arg Asn Ser Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Gln  
 85 90 95

Val Leu Arg Val Thr Ile Pro Gln Leu Thr Glu Glu Arg Arg Lys Asp  
 100 105 110

Met Val Lys Leu Ala Lys Gly Lys Gly Glu Asp Gly Lys Ile Ala Ile  
 115 120 125

Arg Asn Ile Arg Arg Lys Gly Met Asp Gln Leu Lys Lys Leu Gln Lys  
 130 135 140

Asp Gly Asp Ala Gly Glu Asp Glu Val Gln Ala Ala Glu Lys Glu Leu  
 145 150 155 160

Asp Lys Val Thr Ala Gly Phe Val Ala Gln Val Asp Glu Val Val Ala  
 165 170 175

Arg Lys Glu Lys Glu Leu Met Glu Val  
 180 185

&lt;210&gt; 265

&lt;211&gt; 458

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(435)

&lt;223&gt; RXA01568

&lt;400&gt; 265

tgg gat aac atc acc tat ttg atg cgc gct gcg cga aaa ggc acc gtg 48  
 Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val  
 1 5 10 15

gtt ccc atg gtc atc gag ttg gat ggc cgg ttc gtg ggg cag ttg act 96  
 Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr  
 20 25 30

atc ggc aac atc cag cac ggc ggc atc tcc gat gcc tgg att ggc tat 144  
 Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr  
 35 40 45

tgg gtt tcc agc gcg gtg acg ggg cgc ggt atc gct acg gcc gcc tgc 192  
 Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys  
 50 55 60

gcg ctc ggc gtg gat cat gct ttt cga cgc ata ggt ctg cat cgc ctc 240  
 Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu  
 65 70 75 80

acc gcc acc tat cta ccc agc aac cca gca tcc ggg aag gtg ctc gga 288  
 Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly  
 85 90 95

cac agc ggt ttc cgc cca gaa ggc tat ctc att aga aat ctg cat att 336  
 His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile  
 100 105 110

gat gga caa tgg atg gat cac cat ttt gtg gca ttg ctg gcg gat gag 384  
 Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu  
 115 120 125

tat tca ata acc gcg gtg gaa cgt ctc act aga gag gga cga ttg cgc 432  
 Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg  
 130 135 140

cga tgattactaa tgcaagaaa ttt 458  
 Arg  
 145

<210> 266  
 <211> 145  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 266  
 Trp Asp Asn Ile Thr Tyr Leu Met Arg Ala Ala Arg Lys Gly Thr Val  
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Val Pro Met Val Ile Glu Leu Asp Gly Arg Phe Val Gly Gln Leu Thr  
 20 25 30

Ile Gly Asn Ile Gln His Gly Gly Ile Ser Asp Ala Trp Ile Gly Tyr  
 35 40 45

Trp Val Ser Ser Ala Val Thr Gly Arg Gly Ile Ala Thr Ala Ala Cys  
 50 55 60

Ala Leu Gly Val Asp His Ala Phe Arg Arg Ile Gly Leu His Arg Leu  
 65 70 75 80

Thr Ala Thr Tyr Leu Pro Ser Asn Pro Ala Ser Gly Lys Val Leu Gly  
 85 90 95

His Ser Gly Phe Arg Pro Glu Gly Tyr Leu Ile Arg Asn Leu His Ile  
 100 105 110

Asp Gly Gln Trp Met Asp His His Phe Val Ala Leu Leu Ala Asp Glu  
 115 120 125

Tyr Ser Ile Thr Ala Val Glu Arg Leu Thr Arg Glu Gly Arg Leu Arg  
 130 135 140

Arg  
 145

<210> 267  
 <211> 789  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(766)  
 <223> RXA01661

<400> 267  
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 gaaggccttc cttaccgcag cttgctggga ctttctgac ttg gac tca act aac 115  
 Leu Asp Ser Thr Asn  
 1 5  
 acc ccc ggc ccc acg gag tgg ggc gag tcc cgc gtg ggc aaa ggt cca 163  
 Thr Pro Gly Pro Thr Glu Trp Gly Glu Ser Arg Val Gly Lys Gly Pro  
 10 15 20  
 tgg gaa gag gaa aac ccc ggc gta cct cgg cct aca agc ccg ctt ttc 211  
 Trp Glu Glu Glu Asn Pro Gly Val Pro Arg Pro Thr Ser Pro Leu Phe  
 25 30 35  
 gac gtc acc ctc ctc aac gag ggc gat cgc cgc aac gtt gtt gac gcc 259  
 Asp Val Thr Leu Leu Asn Glu Gly Asp Arg Arg Asn Val Val Asp Ala  
 40 45 50  
 tat cgt tat tgg acc cgt gag gcg att gtt gaa gat atc gac acc cgc 307  
 Tyr Arg Tyr Trp Thr Arg Glu Ala Ile Val Glu Asp Ile Asp Thr Arg  
 55 60 65  
 cgc cac agc ctc cac gta gcg atc gaa aac ttt gaa aac gac gcc aac 355  
 Arg His Ser Leu His Val Ala Ile Glu Asn Phe Glu Asn Asp Ala Asn  
 70 75 80 85  
 atc ggc acc gtc gtg cgc acc gcc aac gcc ttt gcc gtg aac aca gtc 403  
 Ile Gly Thr Val Val Arg Thr Ala Asn Ala Phe Ala Val Asn Thr Val  
 90 95 100  
 cac att gtg ggc agg cgt cgg tgg aac cgc agg gga gcc atg gtg act 451  
 His Ile Val Gly Arg Arg Arg Trp Asn Arg Arg Gly Ala Met Val Thr  
 105 110 115  
 gac cgt tac cag cac ctc atg cac cac gaa gac gtt gat tcg ctg ctt 499  
 Asp Arg Tyr Gln His Leu Met His His Glu Asp Val Asp Ser Leu Leu  
 120 125 130  
 gcg tgg gca atc gcg gag cgg ctt acc atc gtc gcg atc gat aac acc 547  
 Ala Trp Ala Ile Ala Glu Arg Leu Thr Ile Val Ala Ile Asp Asn Thr  
 135 140 145  
 cca ggt tcc gtg cct ttg gaa acc gct gag ttg ccg aag aac tgc ctg 595  
 Pro Gly Ser Val Pro Leu Glu Thr Ala Glu Leu Pro Lys Asn Cys Leu  
 150 155 160 165  
 ttg ctg ttt ggt cag gaa ggc cca ggt gtc acc gaa gct gcg cgt gca 643  
 Leu Leu Phe Gly Gln Glu Gly Pro Gly Val Thr Glu Ala Ala Arg Ala  
 170 175 180

ggt gcg tta atg acc tgt tcg att gcc caa ttt ggt tcc act cga tcc 691  
 Gly Ala Leu Met Thr Cys Ser Ile Ala Gln Phe Gly Ser Thr Arg Ser  
 185 190 195  
  
 atc aac gcg ggt gta gct gct ggt att gca atg cat gca tgg att cgt 739  
 Ile Asn Ala Gly Val Ala Ala Gly Ile Ala Met His Ala Trp Ile Arg  
 200 205 210  
  
 caa cat gcc gac tta tcg caa gcc tgg taattttata ccctagatcg 786  
 Gln His Ala Asp Leu Ser Gln Ala Trp  
 215 220  
  
 tta 789

&lt;210&gt; 268

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 268

Leu Asp Ser Thr Asn Thr Pro Gly Pro Thr Glu Trp Gly Glu Ser Arg  
 1 5 10 15  
  
 Val Gly Lys Gly Pro Trp Glu Glu Glu Asn Pro Gly Val Pro Arg Pro  
 20 25 30  
  
 Thr Ser Pro Leu Phe Asp Val Thr Leu Leu Asn Glu Gly Asp Arg Arg  
 35 40 45  
  
 Asn Val Val Asp Ala Tyr Arg Tyr Trp Thr Arg Glu Ala Ile Val Glu  
 50 55 60  
  
 Asp Ile Asp Thr Arg Arg His Ser Leu His Val Ala Ile Glu Asn Phe  
 65 70 75 80  
  
 Glu Asn Asp Ala Asn Ile Gly Thr Val Val Arg Thr Ala Asn Ala Phe  
 85 90 95  
  
 Ala Val Asn Thr Val His Ile Val Gly Arg Arg Arg Trp Asn Arg Arg  
 100 105 110  
  
 Gly Ala Met Val Thr Asp Arg Tyr Gln His Leu Met His His Glu Asp  
 115 120 125  
  
 Val Asp Ser Leu Leu Ala Trp Ala Ile Ala Glu Arg Leu Thr Ile Val  
 130 135 140  
  
 Ala Ile Asp Asn Thr Pro Gly Ser Val Pro Leu Glu Thr Ala Glu Leu  
 145 150 155 160  
  
 Pro Lys Asn Cys Leu Leu Leu Phe Gly Gln Glu Gly Pro Gly Val Thr  
 165 170 175  
  
 Glu Ala Ala Arg Ala Gly Ala Leu Met Thr Cys Ser Ile Ala Gln Phe  
 180 185 190  
  
 Gly Ser Thr Arg Ser Ile Asn Ala Gly Val Ala Ala Gly Ile Ala Met  
 195 200 205

His Ala Trp Ile Arg Gln His Ala Asp Leu Ser Gln Ala Trp  
 210 215 220

<210> 269  
 <211> 936  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(913)  
 <223> RXA01581

<400> 269  
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 agcaaagttg accgcacggt taactgttag tgttatgagc atg gca ttg gac ttt 115  
 Met Ala Leu Asp Phe  
 1 5  
 aat gag gcg ttt acc gaa cgc acc ccg cgc atc gtc aac gca gct aaa 163  
 Asn Glu Ala Phe Thr Glu Arg Thr Pro Arg Ile Val Asn Ala Ala Lys  
 10 15 20  
 ctg cat cgc gcc gcg cag cgc aaa aaa gat aag cgt ttt cta gtt gaa 211  
 Leu His Arg Ala Ala Gln Arg Lys Lys Asp Lys Arg Phe Leu Val Glu  
 25 30 35  
 ggc gaa aat tcc gtt gaa gca gct gtc gct acc ggc gca gca act gac 259  
 Gly Glu Asn Ser Val Glu Ala Ala Val Ala Thr Gly Ala Ala Thr Asp  
 40 45 50  
 ctc ttt gtc act gaa tcc gct gcg gag cgc ttc gag gaa atc gtc cgc 307  
 Leu Phe Val Thr Glu Ser Ala Ala Glu Arg Phe Glu Glu Ile Val Arg  
 55 60 65  
 acc gcc ggt tac atg aat gtc tac acc cac gcg atc acg gac aag gcc 355  
 Thr Ala Gly Tyr Met Asn Val Tyr Thr His Ala Ile Thr Asp Lys Ala  
 70 75 80 85  
 gcg aag cat ctt agc gac acc gtc acc acc acg ggc att ttt gcg ctt 403  
 Ala Lys His Leu Ser Asp Thr Val Thr Thr Thr Gly Ile Phe Ala Leu  
 90 95 100  
 tgc gac gac gtc ctg tgg tca gtc ggc aag gcg atc acc ggc cag cca 451  
 Cys Asp Asp Val Leu Trp Ser Val Gly Lys Ala Ile Thr Gly Gln Pro  
 105 110 115  
 cgt cta gtg agc gtg ccg gtt gag acc cgc gag ccc ggt aat gcc gga 499  
 Arg Leu Val Ser Val Pro Val Glu Thr Arg Glu Pro Gly Asn Ala Gly  
 120 125 130  
 acc ttg att cgc gta tcc gac gcg gtc ggc gcc gac gcc gtc gtc ttc 547  
 Thr Leu Ile Arg Val Ser Asp Ala Val Gly Ala Asp Ala Val Val Phe  
 135 140 145  
 gct ggt gaa tca gta gat cca ctt ggc gca aaa gct gtg cgc tcc tca 595  
 Ala Gly Glu Ser Val Asp Pro Leu Gly Ala Lys Ala Val Arg Ser Ser  
 150 155 160 165



gcg gga tgc ctg ttt cac att cca gtg gca cgc aac aac aac atc gca 643  
 Ala Gly Ser Leu Phe His Ile Pro Val Ala Arg Asn Asn Asn Ile Ala  
                     170                    175                    180

gat gtc ttg ggg cag ctt cgt tcc aag ggt ctg cag atc ctt gcg acc 691  
 Asp Val Leu Gly Gln Leu Arg Ser Lys Gly Leu Gln Ile Leu Ala Thr  
                     185                    190                    195

tca gcc gat ggg gaa gta gac ctc gat gac gcc gat gag ctg cta gcc 739  
 Ser Ala Asp Gly Glu Val Asp Leu Asp Asp Ala Asp Glu Leu Leu Ala  
                     200                    205                    210

aag cca acc gca tgg ctt ttt ggt aat gaa gct cac gga ctt gat gag 787  
 Lys Pro Thr Ala Trp Leu Phe Gly Asn Glu Ala His Gly Leu Asp Glu  
                     215                    220                    225

agc ctg ctt gct cag gct gat cac cgc gtg cgt att ccg atc cgc ggc 835  
 Ser Leu Leu Ala Gln Ala Asp His Arg Val Arg Ile Pro Ile Arg Gly  
                     230                    235                    240                    245

cgc gca gaa tca ctc aat ttg gcc aca gca gcg tca att tgt ctg tac 883  
 Arg Ala Glu Ser Leu Asn Leu Ala Thr Ala Ala Ser Ile Cys Leu Tyr  
                     250                    255                    260

gaa tcc tcc aag gca cta ttc gcc ggt gag taaaccccaa ttcattgcccc 933  
 Glu Ser Ser Lys Ala Leu Phe Ala Gly Glu  
                     265                    270

gcg 936

<210> 270  
 <211> 271  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 270  
 Met Ala Leu Asp Phe Asn Glu Ala Phe Thr Glu Arg Thr Pro Arg Ile  
     1                    5                    10                    15

Val Asn Ala Ala Lys Leu His Arg Ala Ala Gln Arg Lys Lys Asp Lys  
                     20                    25                    30

Arg Phe Leu Val Glu Gly Glu Asn Ser Val Glu Ala Ala Val Ala Thr  
                     35                    40                    45

Gly Ala Ala Thr Asp Leu Phe Val Thr Glu Ser Ala Ala Glu Arg Phe  
                     50                    55                    60

Glu Glu Ile Val Arg Thr Ala Gly Tyr Met Asn Val Tyr Thr His Ala  
                     65                    70                    75                    80

Ile Thr Asp Lys Ala Ala Lys His Leu Ser Asp Thr Val Thr Thr Thr  
                     85                    90                    95

Gly Ile Phe Ala Leu Cys Asp Asp Val Leu Trp Ser Val Gly Lys Ala  
                     100                    105                    110

Ile Thr Gly Gln Pro Arg Leu Val Ser Val Pro Val Glu Thr Arg Glu  
                     115                    120                    125

Pro Gly Asn Ala Gly Thr Leu Ile Arg Val Ser Asp Ala Val Gly Ala  
130 135 140

Asp Ala Val Val Phe Ala Gly Glu Ser Val Asp Pro Leu Gly Ala Lys  
145 150 155 160

Ala Val Arg Ser Ser Ala Gly Ser Leu Phe His Ile Pro Val Ala Arg  
165 170 175

Asn Asn Asn Ile Ala Asp Val Leu Gly Gln Leu Arg Ser Lys Gly Leu  
180 185 190

Gln Ile Leu Ala Thr Ser Ala Asp Gly Glu Val Asp Leu Asp Asp Ala  
195 200 205

Asp Glu Leu Leu Ala Lys Pro Thr Ala Trp Leu Phe Gly Asn Glu Ala  
210 215 220

His Gly Leu Asp Glu Ser Leu Leu Ala Gln Ala Asp His Arg Val Arg  
225 230 235 240

Ile Pro Ile Arg Gly Arg Ala Glu Ser Leu Asn Leu Ala Thr Ala Ala  
245 250 255

Ser Ile Cys Leu Tyr Glu Ser Ser Lys Ala Leu Phe Ala Gly Glu  
260 265 270

<210> 271

<211> 1062

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1039)

<223> RXA00313

<400> 271

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ttgcagtaat tacagacact ttttaaggaga taatttaaac atg gca gga aat gac 115  
Met Ala Gly Asn Asp  
1 5

agt cgt cga ggc ggc tta cgc aag acc aat aaa aaa ggt gca acc aag 163  
Ser Arg Arg Gly Gly Leu Arg Lys Thr Asn Lys Lys Gly Ala Thr Lys  
10 15 20

ggc agt ggc gga cag gtt cgt cgc ggt ctg aaa ggt aag ggg cct acc 211  
Gly Ser Gly Gly Gln Val Arg Arg Gly Leu Lys Gly Lys Gly Pro Thr  
25 30 35

cct aaa gct gag gat cgc acc tat cac gca gct cac aag cgc aag gtg 259  
Pro Lys Ala Glu Asp Arg Thr Tyr His Ala Ala His Lys Arg Lys Val  
40 45 50

gag cgt gat cgt cgt gat cgt gga cgc cac cag cgt gaa atg cca gag 307  
Glu Arg Asp Arg Arg Asp Arg Gly Arg His Gln Arg Glu Met Pro Glu  
55 60 65

ttg gtt gtg ggc cgt aac cca gtg ctg gaa tgt ctg cat gca cgc gtt Leu Val Val Gly Arg Asn Pro Val Leu Glu Cys Leu His Ala Arg Val 70 75 80 85	355
cca gcg act gct ttg tat gtt gca gag ggt gcg gcg aac gat gag cgt Pro Ala Thr Ala Leu Tyr Val Ala Glu Gly Ala Ala Asn Asp Glu Arg 90 95 100	403
ctg agc gag gca gtg cac act gcg gct ggc cga aat ctt cca gtg ctg Leu Ser Glu Ala Val His Thr Ala Ala Gly Arg Asn Leu Pro Val Leu 105 110 115	451
gag gtt aac aag ctg gag ctg gat cgt atg acc ggc aac ggc atg cac Glu Val Asn Lys Leu Glu Leu Asp Arg Met Thr Gly Asn Gly Met His 120 125 130	499
cag ggc atc ggc ctg gcg atc cct cct tac gag tac gca gat gtt cat Gln Gly Ile Gly Leu Ala Ile Pro Pro Tyr Glu Tyr Ala Asp Val His 135 140 145	547
gat ctg atc gcc aat gct gcg gct tct aag aag cca ggc atg ttc gtg Asp Leu Ile Ala Asn Ala Ala Ser Lys Lys Pro Gly Met Phe Val 150 155 160 165	595
att ctg gat aac atc acc gac cca cgt aac ttg ggt gct gtg att cgt Ile Leu Asp Asn Ile Thr Asp Pro Arg Asn Leu Gly Ala Val Ile Arg 170 175 180	643
tcc gtc ggt gct ttc ggc ggc aac ggt gtc atc att ccg gag cgt cgt Ser Val Gly Ala Phe Gly Gly Asn Gly Val Ile Ile Pro Glu Arg Arg 185 190 195	691
tca gca tct gtg acc gct gtt gca tgg cgt act tct gct ggt acc gca Ser Ala Ser Val Thr Ala Val Ala Trp Arg Thr Ser Ala Gly Thr Ala 200 205 210	739
gcg cgt gtg cca gtg gcg aag gaa acc aac atg act cgt gtc gtg aag Ala Arg Val Pro Val Ala Lys Glu Thr Asn Met Thr Arg Val Val Lys 215 220 225	787
gaa ttc cag caa aac ggt tac cag gtc gtc ggc ctt gac gct ggc ggc Glu Phe Gln Gln Asn Gly Tyr Gln Val Val Gly Leu Asp Ala Gly Gly 230 235 240 245	835
gac cac act ttg gac acc tac gac ggc acc gac aac gtt gtc atc gtc Asp His Thr Leu Asp Thr Tyr Asp Gly Thr Asp Asn Val Val Ile Val 250 255 260	883
gtc ggt tct gag ggc aag gga att tcc cgt ctc gtt cgc gaa aac tgc Val Gly Ser Glu Gly Lys Gly Ile Ser Arg Leu Val Arg Glu Asn Cys 265 270 275	931
gac acc atc atg tcc ata ccc acc gag ggc tgg gtt gaa tcg ctg aac Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp Val Glu Ser Leu Asn 280 285 290	979
gct tcg gtt gct gcc ggc gtc gtg ctg tcg gag ttc tcg cgc cag cgt Ala Ser Val Ala Ala Gly Val Val Leu Ser Glu Phe Ser Arg Gln Arg 295 300 305	1027
cgc att aag ggt taagccggag gttggcgtcg aaa	1062

Arg Ile Lys Gly  
310

<210> 272

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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Lys Gly Ala Thr Lys Gly Ser Gly Gly Gln Val Arg Arg Gly Leu Lys  
20 25 30

Gly Lys Gly Pro Thr Pro Lys Ala Glu Asp Arg Thr Tyr His Ala Ala  
35 40 45

His Lys Arg Lys Val Glu Arg Asp Arg Arg Asp Arg Gly Arg His Gln  
50 55 60

Arg Glu Met Pro Glu Leu Val Val Gly Arg Asn Pro Val Leu Glu Cys  
65 70 75 80

Leu His Ala Arg Val Pro Ala Thr Ala Leu Tyr Val Ala Glu Gly Ala  
85 90 95

Ala Asn Asp Glu Arg Leu Ser Glu Ala Val His Thr Ala Ala Gly Arg  
100 105 110

Asn Leu Pro Val Leu Glu Val Asn Lys Leu Glu Leu Asp Arg Met Thr  
115 120 125

Gly Asn Gly Met His Gln Gly Ile Gly Leu Ala Ile Pro Pro Tyr Glu  
130 135 140

Tyr Ala Asp Val His Asp Leu Ile Ala Asn Ala Ala Ala Ser Lys Lys  
145 150 155 160

Pro Gly Met Phe Val Ile Leu Asp Asn Ile Thr Asp Pro Arg Asn Leu  
165 170 175

Gly Ala Val Ile Arg Ser Val Gly Ala Phe Gly Gly Asn Gly Val Ile  
180 185 190

Ile Pro Glu Arg Arg Ser Ala Ser Val Thr Ala Val Ala Trp Arg Thr  
195 200 205

Ser Ala Gly Thr Ala Ala Arg Val Pro Val Ala Lys Glu Thr Asn Met  
210 215 220

Thr Arg Val Val Lys Glu Phe Gln Gln Asn Gly Tyr Gln Val Val Gly  
225 230 235 240

Leu Asp Ala Gly Gly Asp His Thr Leu Asp Thr Tyr Asp Gly Thr Asp  
245 250 255

Asn Val Val Ile Val Val Gly Ser Glu Gly Lys Gly Ile Ser Arg Leu  
260 265 270

Val Arg Glu Asn Cys Asp Thr Ile Met Ser Ile Pro Thr Glu Gly Trp  
 275 280 285

Val Glu Ser Leu Asn Ala Ser Val Ala Ala Gly Val Val Leu Ser Glu  
 290 295 300

Phe Ser Arg Gln Arg Arg Ile Lys Gly  
 305 310

<210> 273

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXN00460

<400> 273

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ctattattcc acccttttcc aaggccttac aatcaaacac atg ccg gaa cac cca 115  
 Met Pro Glu His Pro  
 1 5

ctt cac gtt atc ttc gac aat cct gtc atc cct ccc aac acc gga aac 163  
 Leu His Val Ile Phe Asp Asn Pro Val Ile Pro Pro Asn Thr Gly Asn  
 10 15 20

gcc atc cga atg tgt gca gga aca ggc gct cac ctg cac ctt gtt gaa 211  
 Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His Leu His Leu Val Glu  
 25 30 35

cct tta ggc ttt gag ctg aca gaa aag cac ctt cgc cga gca ggc ctt 259  
 Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu Arg Arg Ala Gly Leu  
 40 45 50

gac tac cac gac tta gcc gat gtc aca gtg cat gca acc ttc gat gaa 307  
 Asp Tyr His Asp Leu Ala Asp Val Thr Val His Ala Thr Phe Asp Glu  
 55 60 65

gcc atg gct gca gtc cct ggt cgc gta ttt gcc ttc acc aca acg gcc 355  
 Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala Phe Thr Thr Thr Ala  
 70 75 80 85

aat acc cgc ttc acc gat atc gct ttt gaa cct ggc gat gca ctc ctt 403  
 Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro Gly Asp Ala Leu Leu  
 90 95 100

ttt gga act gaa cca aca gga ctc cct caa gaa cat gtt gag cat tcc 451  
 Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu His Val Glu His Ser  
 105 110 115

cga atc acc agt gag ctt cgg atc ccc atg ctt ccc ggt agg cgt tcc 499  
 Arg Ile Thr Ser Glu Leu Arg Ile Pro Met Leu Pro Gly Arg Arg Ser  
 120 125 130

atg aac ctt tca aat tcc gcg gcg gta gcg acc tat gaa gca tgg cgt 547  
 Met Asn Leu Ser Asn Ser Ala Ala Val Ala Thr Tyr Glu Ala Trp Arg

135

140

145

caa ctc gga ttt gtg ggt ggg gtt tagttttttg ctgggcttct ggg  
 Gln Leu Gly Phe Val Gly Gly Val  
 150 155

594

&lt;210&gt; 274

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 274

Met Pro Glu His Pro Leu His Val Ile Phe Asp Asn Pro Val Ile Pro  
 1 5 10 15

Pro Asn Thr Gly Asn Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His  
 20 25 30

Leu His Leu Val Glu Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu  
 35 40 45

Arg Arg Ala Gly Leu Asp Tyr His Asp Leu Ala Asp Val Thr Val His  
 50 55 60

Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala  
 65 70 75 80

Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro  
 85 90 95

Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu  
 100 105 110

His Val Glu His Ser Arg Ile Thr Ser Glu Leu Arg Ile Pro Met Leu  
 115 120 125

Pro Gly Arg Arg Ser Met Asn Leu Ser Asn Ser Ala Ala Val Ala Thr  
 130 135 140

Tyr Glu Ala Trp Arg Gln Leu Gly Phe Val Gly Gly Val  
 145 150 155

&lt;210&gt; 275

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(478)

&lt;223&gt; FRXA00460

&lt;400&gt; 275

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ctattattcc acccttttcc aaggccttac aatcaaacac atg ccg gaa cac cca 115  
 Met Pro Glu His Pro  
 1 5

ctt cac gtt atc ttc gac aat cct gtc atc cct ccc aac acc gga aac 163  
 Leu His Val Ile Phe Asp Asn Pro Val Ile Pro Pro Asn Thr Gly Asn  
                   10                                  15                                  20

gcc atc cga atg tgt gca gga aca ggc gct cac ctg cac ctt gtt gaa 211  
 Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His Leu His Leu Val Glu  
                   25                                  30                                  35

cct tta ggc ttt gag ctg aca gaa aag cac ctt cgc cga gca ggc ctt 259  
 Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu Arg Arg Ala Gly Leu  
                   40                                  45                                  50

gac tac cac gac tta gcc gat gtc aca gtg cat gca acc ttc gat gaa 307  
 Asp Tyr His Asp Leu Ala Asp Val Thr Val His Ala Thr Phe Asp Glu  
                   55                                  60                                  65

gcc atg gct gca gtc cct ggt cgc gta ttt gcc ttc acc aca acg gcc 355  
 Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala Phe Thr Thr Thr Ala  
                   70                                  75                                  80                                  85

aat acc cgc ttc acc gat atc gct ttt gaa cct ggc gat gca ctc ctt 403  
 Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro Gly Asp Ala Leu Leu  
                                   90                                  95                                  100

ttt gga act gaa cca aca gga ctc cct caa gaa cat gtt gag cat tcc 451  
 Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu His Val Glu His Ser  
                   105                                  110                                  115

cga atc acc agt gag ctt cgg atc cta 478  
 Arg Ile Thr Ser Glu Leu Arg Ile Leu  
                   120                                  125

&lt;210&gt; 276

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 276

Met Pro Glu His Pro Leu His Val Ile Phe Asp Asn Pro Val Ile Pro  
           1                                  5                                  10                                  15

Pro Asn Thr Gly Asn Ala Ile Arg Met Cys Ala Gly Thr Gly Ala His  
                   20                                  25                                  30

Leu His Leu Val Glu Pro Leu Gly Phe Glu Leu Thr Glu Lys His Leu  
                   35                                  40                                  45

Arg Arg Ala Gly Leu Asp Tyr His Asp Leu Ala Asp Val Thr Val His  
                   50                                  55                                  60

Ala Thr Phe Asp Glu Ala Met Ala Ala Val Pro Gly Arg Val Phe Ala  
                   65                                  70                                  75                                  80

Phe Thr Thr Thr Ala Asn Thr Arg Phe Thr Asp Ile Ala Phe Glu Pro  
                   85                                  90                                  95

Gly Asp Ala Leu Leu Phe Gly Thr Glu Pro Thr Gly Leu Pro Gln Glu  
                   100                                  105                                  110

His Val Glu His Ser Arg Ile Thr Ser Glu Leu Arg Ile Leu

115	120	125
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<213> <i>Corynebacterium glutamicum</i>		
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<223> RXA02179		
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	Met Thr Thr Arg Thr	
	1 5	
gta att tct gat ccc gca gat cct cgt ctg gat gat gtc cgc gat ctc	163	
Val Ile Ser Asp Pro Ala Asp Pro Arg Leu Asp Asp Val Arg Asp Leu		
	10 15 20	
aac cat tcc gat tcc cgg cca gac cta ccc ggt ggc aaa ggc ctt gtt	211	
Asn His Ser Asp Ser Arg Pro Asp Leu Pro Gly Gly Lys Gly Leu Val		
	25 30 35	
gtt gcc gaa ggt ccg ttg gtg gtt ggt cgg ctt ctg gaa tcg cgt tac	259	
Val Ala Glu Gly Pro Leu Val Val Gly Arg Leu Leu Glu Ser Arg Tyr		
	40 45 50	
cca gtg cgt gcg atc gtc ggg ttt aaa aac aag ctg gat tct ttc ctc	307	
Pro Val Arg Ala Ile Val Gly Phe Lys Asn Lys Leu Asp Ser Phe Leu		
	55 60 65	
gac agc atc gat gca tcc ctt gtt gaa ggc atc cca gtg tat gag gta	355	
Asp Ser Ile Asp Ala Ser Leu Val Glu Gly Ile Pro Val Tyr Glu Val		
	70 75 80 85	
tcc cgc gag ctc ctc gca gag gtc gca ggt ttt gat atg cac cgc gga	403	
Ser Arg Glu Leu Leu Ala Glu Val Ala Gly Phe Asp Met His Arg Gly		
	90 95 100	
ctt ctg gcg aca gcc gat cgc acc gag gaa gca agt gtt gcg cag gtt	451	
Leu Leu Ala Thr Ala Asp Arg Thr Glu Glu Ala Ser Val Ala Gln Val		
	105 110 115	
cta gaa aac gcc cgc acc gtg gtg gtg ctg gaa ggc gta ggc gat cac	499	
Leu Glu Asn Ala Arg Thr Val Val Val Leu Glu Gly Val Gly Asp His		
	120 125 130	
gaa aac atc gga tcc atg ttc cgc aac gca gca ggc atg ggc gtt gac	547	
Glu Asn Ile Gly Ser Met Phe Arg Asn Ala Ala Gly Met Gly Val Asp		
	135 140 145	
gcc atc ttg ttc ggc aac ggt tgt gcc gat cct ttg tat cga cgt gtc	595	
Ala Ile Leu Phe Gly Asn Gly Cys Ala Asp Pro Leu Tyr Arg Arg Val		
	150 155 160 165	
gtt cga gtc tca atg ggc cac gtg ctc cgc ctg ccg ttc gca cac ttg	643	



Val Arg Val Ser Met Gly His Val Leu Arg Leu Pro Phe Ala His Leu  
 170 175 180

gaa ggc acc tac acc acg tgg cag cgc agc tta gag cag ctc aaa gaa 691  
 Glu Gly Thr Tyr Thr Thr Trp Gln Arg Ser Leu Glu Gln Leu Lys Glu  
 185 190 195

gcc gga ttc cac ctc gtt tca ctc acc cca gat cca gag gcg gaa cac 739  
 Ala Gly Phe His Leu Val Ser Leu Thr Pro Asp Pro Glu Ala Glu His  
 200 205 210

ctc gaa gat gcg ctc gca ggc aaa gac aaa gtg gct cta ctc gtg ggc 787  
 Leu Glu Asp Ala Leu Ala Gly Lys Asp Lys Val Ala Leu Leu Val Gly  
 215 220 225

gct gaa ggc cca ggc ctg acc gag cat gcg atg cgc gcc acc gat gtc 835  
 Ala Glu Gly Pro Gly Leu Thr Glu His Ala Met Arg Ala Thr Asp Val  
 230 235 240 245

cgc gcc cgc atc ccg atg gcg ccg ggt acc gat agc ttg aac ctg gct 883  
 Arg Ala Arg Ile Pro Met Ala Pro Gly Thr Asp Ser Leu Asn Leu Ala  
 250 255 260

acc tcg gcg gcg att gcg ttt tat gaa cgg gat cgc tca cag cgt 928  
 Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp Arg Ser Gln Arg  
 265 270 275

taagtaacag cgctaagtag tag 951

<210> 278  
 <211> 276  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 278  
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 20 25 30

Gly Lys Gly Leu Val Val Ala Glu Gly Pro Leu Val Val Gly Arg Leu  
 35 40 45

Leu Glu Ser Arg Tyr Pro Val Arg Ala Ile Val Gly Phe Lys Asn Lys  
 50 55 60

Leu Asp Ser Phe Leu Asp Ser Ile Asp Ala Ser Leu Val Glu Gly Ile  
 65 70 75 80

Pro Val Tyr Glu Val Ser Arg Glu Leu Leu Ala Glu Val Ala Gly Phe  
 85 90 95

Asp Met His Arg Gly Leu Leu Ala Thr Ala Asp Arg Thr Glu Glu Ala  
 100 105 110

Ser Val Ala Gln Val Leu Glu Asn Ala Arg Thr Val Val Val Leu Glu  
 115 120 125

Gly Val Gly Asp His Glu Asn Ile Gly Ser Met Phe Arg Asn Ala Ala

130 135 140

Gly Met Gly Val Asp Ala Ile Leu Phe Gly Asn Gly Cys Ala Asp Pro  
 145 150 155 160

Leu Tyr Arg Arg Val Val Arg Val Ser Met Gly His Val Leu Arg Leu  
 165 170 175

Pro Phe Ala His Leu Glu Gly Thr Tyr Thr Thr Trp Gln Arg Ser Leu  
 180 185 190

Glu Gln Leu Lys Glu Ala Gly Phe His Leu Val Ser Leu Thr Pro Asp  
 195 200 205

Pro Glu Ala Glu His Leu Glu Asp Ala Leu Ala Gly Lys Asp Lys Val  
 210 215 220

Ala Leu Leu Val Gly Ala Glu Gly Pro Gly Leu Thr Glu His Ala Met  
 225 230 235 240

Arg Ala Thr Asp Val Arg Ala Arg Ile Pro Met Ala Pro Gly Thr Asp  
 245 250 255

Ser Leu Asn Leu Ala Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp  
 260 265 270

Arg Ser Gln Arg  
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<210> 279  
 <211> 666  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA02522

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 Met Trp Ala Arg Asp  
 1 5

ata aac ttt cta tac atg agt aca gag cag gaa ctg caa atc gga aaa 163  
 Ile Asn Phe Leu Tyr Met Ser Thr Glu Gln Glu Leu Gln Ile Gly Lys  
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gtt gta aaa tcc cac ggc att cgg ggt gaa gtc gtg gtg gaa ttg agc 211  
 Val Val Lys Ser His Gly Ile Arg Gly Glu Val Val Val Glu Leu Ser  
 25 30 35

acc gat gat cca gac att cgc ttc gcc att ggg gaa gtt ctc aac ggc 259  
 Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly Glu Val Leu Asn Gly  
 40 45 50

aag cag gca ggc aag gag cat tca ctg acc atc gat gca gcg cgc atg 307  
 Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile Asp Ala Ala Arg Met

55 60 65

cac caa ggt cga ctc ttg gtg aag ttc gca gag gtc cca gat cgt acc 355  
 His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu Val Pro Asp Arg Thr  
 70 75 80 85

gct gct gat tct ttg cgt gga act cga ttc ttt gcg gca cct ctt gag 403  
 Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe Ala Ala Pro Leu Glu  
 90 95 100

gat gaa gac gat gag gat ggc ttc tac gac cat gag ttg gaa ggt ctg 451  
 Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His Glu Leu Glu Gly Leu  
 105 110 115

cgc gtc att cac gag ggc gag gat atc ggt gaa gtc acc ggc gtg atg 499  
 Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu Val Thr Gly Val Met  
 120 125 130

cat ggc cca gcc ggt gag atc ctg gaa gtc cgc ctg acc tca ggc aag 547  
 His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg Leu Thr Ser Gly Lys  
 135 140 145

gaa aca ctg att cct ttt gtg cac gcc att gtt cct gag gtg gat ctg 595  
 Glu Thr Leu Ile Pro Phe Val His Ala Ile Val Pro Glu Val Asp Leu  
 150 155 160 165

gaa gaa gga acc gca acg atc acc cct cca gag ggc ttg tta gat ctt 643  
 Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu Gly Leu Leu Asp Leu  
 170 175 180

taggctccga cagatttaat agt 666

<210> 280  
 <211> 181  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 280  
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Leu Gln Ile Gly Lys Val Val Lys Ser His Gly Ile Arg Gly Glu Val  
 20 25 30

Val Val Glu Leu Ser Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly  
 35 40 45

Glu Val Leu Asn Gly Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile  
 50 55 60

Asp Ala Ala Arg Met His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu  
 65 70 75 80

Val Pro Asp Arg Thr Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe  
 85 90 95

Ala Ala Pro Leu Glu Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His  
 100 105 110

Glu Leu Glu Gly Leu Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu

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<210> 281
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<212> DNA
<213> Corynebacterium glutamicum
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cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga 163  
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly  
10 15 20

tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac 211  
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn  
25 30 35

aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct 259  
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala  
40 45 50

aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg 307  
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met  
55 60 65

ggt ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg 355  
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val  
70 75 80 85

ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att 403  
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile  
90 95 100

gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc 451  
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly  
105 110 115

gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc 499

Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg  
 120 125 130  
 atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt 547  
 Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg  
 135 140 145  
 ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt 595  
 Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly  
 150 155 160 165  
 gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc 643  
 Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val  
 170 175 180  
 ggt cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat 691  
 Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp  
 185 190 195  
 ggt gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag 739  
 Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys  
 200 205 210  
 act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc 787  
 Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser  
 215 220 225  
 gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac 835  
 Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp  
 230 235 240 245  
 ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc 883  
 Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile  
 250 255 260  
 gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931  
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu  
 265 270 275  
 ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979  
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val  
 280 285 290  
 cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct 1027  
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser  
 295 300 305  
 gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg 1080  
 Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 310 315 320  
 cct 1083

&lt;210&gt; 282

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser

1	5	10	15
Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly	20	25	30
Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile	35	40	45
Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp	50	55	60
Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val	65	70	75
Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His	85	90	95
Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile	100	105	110
Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg	115	120	125
Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val	130	135	140
Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly	145	150	155
Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln	165	170	175
Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu	180	185	190
Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys	195	200	205
Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr	210	215	220
Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly	225	230	235
Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys	245	250	255
Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg	260	265	270
Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr	275	280	285
Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg	290	295	300
Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu	305	310	315
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<223> RXA02615
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Trp Pro Ala Val Lys Leu Thr Leu Met Glu Arg Leu Tyr Arg His Met				
	185	190	195	
cag gtt ccc atc att ccc aac gag gca tcg ctt ttc gac gcc agc				736
Gln Val Pro Ile Ile Pro Asn Glu Ala Ser Leu Phe Asp Ala Ser				
	200	205	210	
tagcccccttt gttcacccaa acc				759

&lt;210&gt; 284

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 284

Met	Gln	Phe	Ala	Gln	Asn	Pro	Arg	Leu	Thr	Asn	Asp	Ala	Val	Ile	Leu
1				5					10					15	

Glu	Pro	Leu	Ser	His	Gln	Trp	Thr	Gln	Asp	Leu	Gln	Glu	Ala	Val	Ala
		20						25					30		

Ser	Gln	Glu	Leu	Trp	Arg	His	Trp	Phe	Val	Ala	Leu	Pro	Thr	Pro	Glu
		35					40					45			

Gly	Met	Ala	Glu	Glu	Ile	Asp	Arg	Arg	Leu	Ala	Glu	His	Ala	Asp	Gly
	50					55					60				

Leu	Cys	Ala	Pro	Trp	Ala	Ile	Ile	Ser	Ala	Ala	Thr	Gly	Arg	Ala	Val
	65				70					75					80

Gly	Met	Thr	Ser	Phe	His	Thr	Leu	Asp	His	Ala	Asn	Lys	Arg	Leu	Glu
				85					90					95	

Ile	Gly	Arg	Thr	Trp	Met	Ala	Ala	His	Val	Gln	Gly	Thr	Gly	Ile	Asn
		100						105					110		

Pro	Ser	Val	Lys	Phe	Leu	Gln	Leu	Gln	Arg	Ala	Phe	Glu	Asp	Leu	Gly
		115					120					125			

Val	Asn	Ala	Val	Glu	Phe	Arg	Thr	Asn	Trp	His	Asn	His	Arg	Ser	Arg
	130					135						140			

Ala	Ala	Ile	Glu	Arg	Leu	Gly	Ala	Lys	Gln	Asp	Gly	Val	Leu	Arg	Lys
	145				150					155					160

His	Arg	Ile	His	Pro	Asp	Gly	Thr	Val	Arg	Asp	Thr	Val	Ile	Tyr	Ser
				165					170					175	

Ile	Thr	Asn	Asp	Glu	Trp	Pro	Ala	Val	Lys	Leu	Thr	Leu	Met	Glu	Arg
		180						185					190		

Leu	Tyr	Arg	His	Met	Gln	Val	Pro	Ile	Ile	Pro	Asn	Glu	Ala	Ser	Leu
		195					200					205			

Phe	Asp	Ala	Ser
	210		



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<221> CDS  
<222> (101)..(808)  
<223> RXN01343
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ggccccgttaa accacagaat tccatgaaag ggaattttcta																	
Met Ser Lys Asn Ser																	115
1 5																	
aag gcg tac cgc gag gcc gct gag aag atc gac gct ggt cgc atc tac																	163
Lys	Ala	Tyr	Arg	Glu	Ala	Ala	Glu	Lys	Ile	Asp	Ala	Gly	Arg	Ile	Tyr		
10 15 20																	
tcc cca ctc gag gct gca aac ctg gtc aag gag acc tcc tcc aag aac																	211
Ser	Pro	Leu	Glu	Ala	Ala	Asn	Leu	Val	Lys	Glu	Thr	Ser	Ser	Lys	Asn		
25 30 35																	
tac gac gct tcc atc gac gta gct atc cgc ctg ggc gtt gac cca cgt																	259
Tyr	Asp	Ala	Ser	Ile	Asp	Val	Ala	Ile	Arg	Leu	Gly	Val	Asp	Pro	Arg		
40 45 50																	
aag gct gat cag ctt gtt cgt ggc acc gtc tcc ctg cct aac ggc acc																	307
Lys	Ala	Asp	Gln	Leu	Val	Arg	Gly	Thr	Val	Ser	Leu	Pro	Asn	Gly	Thr		
55 60 65																	
ggg aag acc gtt cgc gtt gct gtg ttc gca cag ggc gag aag gct act																	355
Gly	Lys	Thr	Val	Arg	Val	Ala	Val	Phe	Ala	Gln	Gly	Glu	Lys	Ala	Thr		
70 75 80 85																	
gag gct gag gct gct ggc gct gac ttc gtt ggc acc gac gag ctc gtt																	403
Glu	Ala	Glu	Ala	Ala	Gly	Ala	Asp	Phe	Val	Gly	Thr	Asp	Glu	Leu	Val		
90 95 100																	
gag aag atc cag ggt ggc tgg acc gac ttc gac gtt gct att gca acc																	451
Glu	Lys	Ile	Gln	Gly	Gly	Trp	Thr	Asp	Phe	Asp	Val	Ala	Ile	Ala	Thr		
105 110 115																	
cct gat cag atg gct aag atc ggc cgt atc gct cgt gtc ttg ggc cca																	499
Pro	Asp	Gln	Met	Ala	Lys	Ile	Gly	Arg	Ile	Ala	Arg	Val	Leu	Gly	Pro		
120 125 130																	
cgt ggt ctg atg cct aac cct aag acc ggc acc gtc acc aac gat gtc																	547
Arg	Gly	Leu	Met	Pro	Asn	Pro	Lys	Thr	Gly	Thr	Val	Thr	Asn	Asp	Val		
135 140 145																	
gct aag gct atc gaa gag gtc aag ggc ggc aag att tcc ttc cgc gtt																	595
Ala	Lys	Ala	Ile	Glu	Glu	Val	Lys	Gly	Gly	Lys	Ile	Ser	Phe	Arg	Val		
150 155 160 165																	
gac aag gct tcc aac ctg cac gct gca att ggt aag gct tcc ttc gat																	643
Asp	Lys	Ala	Ser	Asn	Leu	His	Ala	Ala	Ile	Gly	Lys	Ala	Ser	Phe	Asp		
170 175 180																	

gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag atc atc 691  
 Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu Ile Ile  
                   185                  190                  195

cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc gtg acc 739  
 Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg Val Thr  
                   200                  205                  210

ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac gtc acc 787  
 Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His Val Thr  
                   215                  220                  225

aag aac tac gca gaa gag gca taagccttcc cacgcgtaac tct 831  
 Lys Asn Tyr Ala Glu Glu Ala  
 230                  235

&lt;210&gt; 286

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 286

Met Ser Lys Asn Ser Lys Ala Tyr Arg Glu Ala Ala Glu Lys Ile Asp  
           1                  5                  10                  15

Ala Gly Arg Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu  
                   20                  25                  30

Thr Ser Ser Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu  
                   35                  40                  45

Gly Val Asp Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser  
           50                  55                  60

Leu Pro Asn Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln  
           65                  70                  75                  80

Gly Glu Lys Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly  
                   85                  90                  95

Thr Asp Glu Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp  
                   100                  105                  110

Val Ala Ile Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala  
                   115                  120                  125

Arg Val Leu Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr  
                   130                  135                  140

Val Thr Asn Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys  
                   145                  150                  155                  160

Ile Ser Phe Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly  
                   165                  170                  175

Lys Ala Ser Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu  
                   180                  185                  190

Leu Asp Glu Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr

195

200

205

Val Lys Arg Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val  
 210 215 220

Asp Thr His Val Thr Lys Asn Tyr Ala Glu Glu Ala  
 225 230 235

&lt;210&gt; 287

&lt;211&gt; 674

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(651)

&lt;223&gt; FRXA01343

&lt;400&gt; 287

atc tac tcc cca ctc gag gct gca aac ctg gtc aag gag acc tcc tcc 48  
 Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser  
 1 5 10 15

aag aac tac gac gct tcc atc gac gta gct atc cgc ctg ggc gtt gac 96  
 Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp  
 20 25 30

cca cgt aag gct gat cag ctt gtt cgt ggc acc gtc tcc ctg cct aac 144  
 Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn  
 35 40 45

ggc acc ggt aag acc gtt cgc gtt gct gtg ttc gca cag ggc gag aag 192  
 Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys  
 50 55 60

gct act gag gct gag gct gct ggc gct gac ttc gtt ggc acc gac gag 240  
 Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu  
 65 70 75 80

ctc gtt gag aag atc cag ggt ggc tgg acc gac ttc gac gtt gct att 288  
 Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile  
 85 90 95

gca acc cct gat cag atg gct aag atc ggc cgt atc gct cgt gtc ttg 336  
 Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu  
 100 105 110

ggc cca cgt ggt ctg atg cct aac cct aag acc ggc acc gtc acc aac 384  
 Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn  
 115 120 125

gat gtc gct aag gct atc gaa gag gtc aag ggc ggc aag att tcc ttc 432  
 Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe  
 130 135 140

cgc gtt gac aag gct tcc aac ctg cac gct gca att ggt aag gct tcc 480  
 Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser  
 145 150 155 160

ttc gat gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag 528

Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu  
 165 170 175

atc atc cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc 576  
 Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg  
 180 185 190

gtg acc ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac 624  
 Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His  
 195 200 205

gtc acc aag aac tac gca gaa gag gca taagccttcc cacgcgtaac 671  
 Val Thr Lys Asn Tyr Ala Glu Glu Ala  
 210 215

tct 674

&lt;210&gt; 288

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 288

Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser  
 1 5 10 15

Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp  
 20 25 30

Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn  
 35 40 45

Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys  
 50 55 60

Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu  
 65 70 75 80

Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile  
 85 90 95

Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu  
 100 105 110

Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn  
 115 120 125

Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe  
 130 135 140

Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser  
 145 150 155 160

Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu  
 165 170 175

Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg  
 180 185 190

Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His

195

200

205

Val Thr Lys Asn Tyr Ala Glu Glu Ala  
210 215

&lt;210&gt; 289

&lt;211&gt; 684

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(661)

&lt;223&gt; RXA01951

&lt;400&gt; 289

cgctaccgcg tcacgcgactt ccgtcgtaac gacaaggatg gcgtattggc aaaggtcgct 60

cacatcgagt acgacccaaa ccgtaccgct aacattgcac ttg ctt cac tac ttc 115  
Leu Leu His Tyr Phe  
1 5

gat ggc gag aag cgt tac atc ctc gca ccg aag ggc ctg acc cag ggc 163  
Asp Gly Glu Lys Arg Tyr Ile Leu Ala Pro Lys Gly Leu Thr Gln Gly  
10 15 20

acc gtt atc gag tcc ggc gct gca gcc gac atc aag gtt ggt aac aac 211  
Thr Val Ile Glu Ser Gly Ala Ala Asp Ile Lys Val Gly Asn Asn  
25 30 35

ctg cca ctg cgt aac atc ccg act ggt acc acc atc cac aac gtg gag 259  
Leu Pro Leu Arg Asn Ile Pro Thr Gly Thr Thr Ile His Asn Val Glu  
40 45 50

ttg aag cca ggc gca ggt gca aag ctg gca cgt tcc gct gga gct tcc 307  
Leu Lys Pro Gly Ala Gly Ala Lys Leu Ala Arg Ser Ala Gly Ala Ser  
55 60 65

atc cag ctt ctt ggt aag gaa ggc tcc tac gca gtt ctg cgt atg cca 355  
Ile Gln Leu Leu Gly Lys Glu Gly Ser Tyr Ala Val Leu Arg Met Pro  
70 75 80 85

tcc tcc gag atc cga cgc gta aac atc cgc tgc cgc gcg act gtt ggt 403  
Ser Ser Glu Ile Arg Arg Val Asn Ile Arg Cys Arg Ala Thr Val Gly  
90 95 100

gag gtc ggc aac gcc gag cag atc aac att cgt tgg ggt aaa gct ggt 451  
Glu Val Gly Asn Ala Glu Gln Ile Asn Ile Arg Trp Gly Lys Ala Gly  
105 110 115

cgt atg cgt tgg aag ggc tgg cgc cca acc gtc cgt ggt gtc gtt atg 499  
Arg Met Arg Trp Lys Gly Trp Arg Pro Thr Val Arg Gly Val Val Met  
120 125 130

aac ccg gtc gac cac cca cac ggt ggt ggt gaa ggt aag act tct ggt 547  
Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Lys Thr Ser Gly  
135 140 145

ggt cgc cac cca gtc tcc cca tgg gga cag aag gaa ggc cgc acc cgc 595  
Gly Arg His Pro Val Ser Pro Trp Gly Gln Lys Glu Gly Arg Thr Arg

150                      155                      160                      165  
aag cct aag cgt tac agc gat gac atg atc gtt cgt cgc cgt cgt gct 643  
Lys Pro Lys Arg Tyr Ser Asp Asp Met Ile Val Arg Arg Arg Arg Ala  
                         170                      175                      180  
aac aag aac aag aag cgt taagaggagg taacggtgaa tgt 684  
Asn Lys Asn Lys Lys Arg  
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<212> PRT  
<213> Corynebacterium glutamicum

<400> 290  
Leu Leu His Tyr Phe Asp Gly Glu Lys Arg Tyr Ile Leu Ala Pro Lys  
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Gly Leu Thr Gln Gly Thr Val Ile Glu Ser Gly Ala Ala Ala Asp Ile  
                         20                      25                      30  
Lys Val Gly Asn Asn Leu Pro Leu Arg Asn Ile Pro Thr Gly Thr Thr  
                         35                      40                      45  
Ile His Asn Val Glu Leu Lys Pro Gly Ala Gly Ala Lys Leu Ala Arg  
                         50                      55                      60  
Ser Ala Gly Ala Ser Ile Gln Leu Leu Gly Lys Glu Gly Ser Tyr Ala  
65                      70                      75                      80  
Val Leu Arg Met Pro Ser Ser Glu Ile Arg Arg Val Asn Ile Arg Cys  
                         85                      90                      95  
Arg Ala Thr Val Gly Glu Val Gly Asn Ala Glu Gln Ile Asn Ile Arg  
                         100                      105                      110  
Trp Gly Lys Ala Gly Arg Met Arg Trp Lys Gly Trp Arg Pro Thr Val  
                         115                      120                      125  
Arg Gly Val Val Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu  
                         130                      135                      140  
Gly Lys Thr Ser Gly Gly Arg His Pro Val Ser Pro Trp Gly Gln Lys  
145                      150                      155                      160  
Glu Gly Arg Thr Arg Lys Pro Lys Arg Tyr Ser Asp Asp Met Ile Val  
                         165                      170                      175  
Arg Arg Arg Arg Ala Asn Lys Asn Lys Lys Arg  
                         180                      185

<210> 291  
<211> 507  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS

&lt;222&gt; (101)..(484)

&lt;223&gt; FRXA01950

&lt;400&gt; 291

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cggctccgtc gcttaagacg tcgatagaaa aggacacatt atg gct att cgt aag 115  
 Met Ala Ile Arg Lys  
 1 5

tac aag ccg aca acc ccg ggt cgc cgc gca agc tcc gtt tcc atg ttc 163  
 Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser Ser Val Ser Met Phe  
 10 15 20

acg gag atc acc cgt tcg acc cct gag aag tca ctt ctc cgc cca ctg 211  
 Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser Leu Leu Arg Pro Leu  
 25 30 35

agc aag acc ggc gga cgt aac tct cac ggc cac atc acc acc cgt cac 259  
 Ser Lys Thr Gly Gly Arg Asn Ser His Gly His Ile Thr Thr Arg His  
 40 45 50

cgc ggt ggt gga cac aag cgc cgc tac cgc gtc atc gac ttc cgt cgt 307  
 Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val Ile Asp Phe Arg Arg  
 55 60 65

aac gac aag gat ggc gta ttg gca aag gtc gct cac atc gag tac gac 355  
 Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala His Ile Glu Tyr Asp  
 70 75 80 85

cca aac cgt acc gct aac att gca ctt gct tca cta ctt cga tgg cga 403  
 Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser Leu Leu Arg Trp Arg  
 90 95 100

gaa gcg tta cat cct cgc acc gaa ggg cct gac cca ggg cac cgt tat 451  
 Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp Pro Gly His Arg Tyr  
 105 110 115

cga gtc cgg cgc tgc agc cga cat caa ggt tgg taacaacctg ccaactgcgta 504  
 Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp  
 120 125

aca 507

&lt;210&gt; 292

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 292

Met Ala Ile Arg Lys Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser  
 1 5 10 15

Ser Val Ser Met Phe Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser  
 20 25 30

Leu Leu Arg Pro Leu Ser Lys Thr Gly Gly Arg Asn Ser His Gly His  
 35 40 45

Ile Thr Thr Arg His Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val

50	55	60
Ile Asp Phe Arg Arg Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala		
65	70	75 80
His Ile Glu Tyr Asp Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser		
	85	90 95
Leu Leu Arg Trp Arg Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp		
	100	105 110
Pro Gly His Arg Tyr Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp		
	115	120 125

<210> 293  
 <211> 777  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(754)  
 <223> RXA01286

<400> 293  
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 Met Ser Glu Asn Glu  
 1 5  
 atc aag ggc att ctg ggc acc aag ctc ggc atg act cag atc ttc gac 163  
 Ile Lys Gly Ile Leu Gly Thr Lys Leu Gly Met Thr Gln Ile Phe Asp  
 10 15 20  
 gag gag aac cgc gtt att ccg gtt acc gtc gtt gaa gcg ggt cca tgc 211  
 Glu Glu Asn Arg Val Ile Pro Val Thr Val Val Glu Ala Gly Pro Cys  
 25 30 35  
 gta gtt tcc cag att cgc acc gtt gag acc gat ggc tac aac gcc atc 259  
 Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp Gly Tyr Asn Ala Ile  
 40 45 50  
 cag atc gcc tac ggc gaa atc gac cca cgc aag gtg aac cag cca ttg 307  
 Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys Val Asn Gln Pro Leu  
 55 60 65  
 act ggt cac ttc aag aaa gca ggc gtt acc ccc cgc cgc cac gtc acc 355  
 Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro Arg Arg His Val Thr  
 70 75 80 85  
 gag att cgt atg gac gat gtc tcc ggt tac gag gtt gga cag gac gtt 403  
 Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu Val Gly Gln Asp Val  
 90 95 100  
 acc gtt gaa atc ttc aac gac atc aag ttc gtt gac gtc acc ggt acc 451  
 Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val Asp Val Thr Gly Thr



105	110	115	
acc aag ggt aag ggc tac gcc ggc gct atg aag cgc cat ggc ttc gct			499
Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys Arg His Gly Phe Ala			
120	125	130	
ggc cag ggt gcc ggc cac ggt aac cag gct gca cac cgc cgc gta ggt			547
Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala His Arg Arg Val Gly			
135	140	145	
ggc att ggt gca gct gct acc cca ggt cgc atc ttc aag ggc aag cgt			595
Gly Ile Gly Ala Ala Thr Pro Gly Arg Ile Phe Lys Gly Lys Arg			
150	155	160	165
atg gct ggc cgc atg ggt aat gac cgc gtc acc acc cag aac ctc aag			643
Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr Thr Gln Asn Leu Lys			
170	175	180	
gtt cag aag att gac gcc gat gcc aac atc atc ctt atc aag ggc gca			691
Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile Leu Ile Lys Gly Ala			
185	190	195	
atc cct ggt aac cgt ggt ggc atc gtt acc gtt aag acc gca gtg aag			739
Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val Lys Thr Ala Val Lys			
200	205	210	
ggc ggt gca cac gca tgacgaatct gaagctgtat gtt			777
Gly Gly Ala His Ala			
215			
<210> 294			
<211> 218			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 294			
Met Ser Glu Asn Glu Ile Lys Gly Ile Leu Gly Thr Lys Leu Gly Met			
1	5	10	15
Thr Gln Ile Phe Asp Glu Glu Asn Arg Val Ile Pro Val Thr Val Val			
20	25	30	
Glu Ala Gly Pro Cys Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp			
35	40	45	
Gly Tyr Asn Ala Ile Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys			
50	55	60	
Val Asn Gln Pro Leu Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro			
65	70	75	80
Arg Arg His Val Thr Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu			
85	90	95	
Val Gly Gln Asp Val Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val			
100	105	110	
Asp Val Thr Gly Thr Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys			
115	120	125	

Arg His Gly Phe Ala Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala  
 130 135 140

His Arg Arg Val Gly Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile  
 145 150 155 160

Phe Lys Gly Lys Arg Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr  
 165 170 175

Thr Gln Asn Leu Lys Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile  
 180 185 190

Leu Ile Lys Gly Ala Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val  
 195 200 205

Lys Thr Ala Val Lys Gly Gly Ala His Ala  
 210 215

<210> 295  
 <211> 626  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(603)  
 <223> RXA01948

<400> 295  
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 Ser Val Glu Leu Pro Ala Glu Ile Phe Asp Arg Glu Val Ser Val Ala  
 1 5 10 15

ctg ctg cac cag gtt gtc aac gca cag ctt gca gca gct cga cag ggc 96  
 Leu Leu His Gln Val Val Asn Ala Gln Leu Ala Ala Ala Arg Gln Gly  
 20 25 30

acc cac tcc acc aag acc cgt ggc gaa gta cgt ggc ggt ggc cgt aag 144  
 Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Gly Arg Lys  
 35 40 45

cca ttc cgt cag aag gga acc ggt cgc gct cgt cag ggc tcg atc cgc 192  
 Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg  
 50 55 60

gca cct cac ttc acc ggt ggt ggc atc tcc cac ggc cct aag cca cgc 240  
 Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg  
 65 70 75 80

gac tac tct cag cgc acc cct aag aag atg atc aag gct gca ctt tac 288  
 Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr  
 85 90 95

ggt gca ctg tct gat cgt gca cgc aat gca cgt atc cac gtc gtc tcc 336  
 Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser  
 100 105 110

gaa ttg gtg cct ggc cag acc cct tcg acc aag tct gca aag gct ttc 384  
 Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe  
 115 120 125

atc gag cgt ctg acc gag cgt aag tcc gtg ctg ctc gta gtg agc cgt 432  
 ile glu arg leu thr glu arg lys ser val leu leu val val ser arg  
 130 135 140

gag gat atc aac gcc cag aag agt gct aac aac ctg cct ggc gtc cac 480  
 glu asp ile asn ala gln lys ser ala asn asn leu pro gly val his  
 145 150 155 160

atc ctg gcc gct gat cag ctg aac acc tac gac gtt ctc aag tct gac 528  
 ile leu ala ala asp gln leu asn thr tyr asp val leu lys ser asp  
 165 170 175

gac gtt gtg ttc tcc gtt gag gct ctc cac acc ttc atc aac cgc gct 576  
 asp val val phe ser val glu ala leu his thr phe ile asn arg ala  
 180 185 190

tcc ggt gcg gca cag gag gag cag aac taatggctac tatcgccaac 623  
 ser gly ala ala gln glu glu gln asn  
 195 200

cca 626

<210> 296  
 <211> 201  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 296  
 ser val glu leu pro ala glu ile phe asp arg glu val ser val ala  
 1 5 10 15  
 leu leu his gln val val asn ala gln leu ala ala ala arg gln gly  
 20 25 30  
 thr his ser thr lys thr arg gly glu val arg gly gly gly arg lys  
 35 40 45  
 pro phe arg gln lys gly thr gly arg ala arg gln gly ser ile arg  
 50 55 60  
 ala pro his phe thr gly gly gly ile ser his gly pro lys pro arg  
 65 70 75 80  
 asp tyr ser gln arg thr pro lys lys met ile lys ala ala leu tyr  
 85 90 95  
 gly ala leu ser asp arg ala arg asn ala arg ile his val val ser  
 100 105 110  
 glu leu val pro gly gln thr pro ser thr lys ser ala lys ala phe  
 115 120 125  
 ile glu arg leu thr glu arg lys ser val leu leu val val ser arg  
 130 135 140  
 glu asp ile asn ala gln lys ser ala asn asn leu pro gly val his  
 145 150 155 160  
 ile leu ala ala asp gln leu asn thr tyr asp val leu lys ser asp

acc ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac 547  
Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp  
135 140 145

aag atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct 595  
 Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala  
 150 155 160 165

gta acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca 643  
 Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro  
 170 175 180

ttc aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaagc 693  
 Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln  
 185 190

act 696

<210> 298  
 <211> 191  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 298  
 Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu  
 1 5 10 15

Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln  
 20 25 30

Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala  
 35 40 45

Ala Arg Asp Ser Lys Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala  
 50 55 60

Ile Thr Gly Gln Lys Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala  
 65 70 75 80

Asn Phe Lys Leu Arg Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu  
 85 90 95

Arg Gly Asp Arg Met Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala  
 100 105 110

Leu Pro Arg Ile Arg Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp  
 115 120 125

Gly His Gly Asn Tyr Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr  
 130 135 140

Glu Ile Asp Val Asp Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr  
 145 150 155 160

Val Val Thr Thr Ala Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg  
 165 170 175

Glu Leu Gly Phe Pro Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln  
 180 185 190

<210> 299  
 <211> 256

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(256)

&lt;223&gt; FRXA00711

&lt;400&gt; 299

tggtcatcga ctccgacgga aacccaactc gcgttggcta ccgtttcgat gaaaacggca 60

agaagggtccg cgtttctcgt cgcaatggga aggatatcta atg act gag aat tac 115  
Met Thr Glu Asn Tyr  
1 5

atc cct cgt ctg aag acc cgt tac cag gac gaa atc cgc acc aag ctt 163  
Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu Ile Arg Thr Lys Leu  
10 15 20

cag ggc gag ttc gag ttc gaa aac gtc atg cag atc cca ggc gtc acc 211  
Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln Ile Pro Gly Val Thr  
25 30 35

aag att gtc gtc aac atg ggt gtc ggc gac gca gct cgt gac tcc 256  
Lys Ile Val Val Asn Met Gly Val Gly Asp Ala Ala Arg Asp Ser  
40 45 50

&lt;210&gt; 300

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 300

Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu  
1 5 10 15

Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln  
20 25 30

Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala  
35 40 45

Ala Arg Asp Ser  
50

&lt;210&gt; 301

&lt;211&gt; 290

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(267)

&lt;223&gt; FRXA00706

&lt;400&gt; 301

gag ttc ctg gac cgt ctg ctg acc gtg gca ctg cca cgt atc cgc gac 48  
Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp  
1 5 10 15

ttc cgt gga ctt tcc gac cag cag ttc gac ggc cac ggt aac tac acc 96  
 Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr  
                   20                  25                  30

ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac aag 144  
 Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys  
                   35                  40                  45

atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct gta 192  
 Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val  
                   50                  55                  60

acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca ttc 240  
 Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe  
                   65                  70                  75                  80

aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaagc 287  
 Lys Gly Glu Asp Gly Asn Arg Gln Gln  
                                   85

act 290

&lt;210&gt; 302

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 302

Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp  
                   1                  5                  10                  15

Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr  
                   20                  25                  30

Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys  
                   35                  40                  45

Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val  
                   50                  55                  60

Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe  
                   65                  70                  75                  80

Lys Gly Glu Asp Gly Asn Arg Gln Gln  
                                   85

&lt;210&gt; 303

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(634)

&lt;223&gt; RXA00695

&lt;400&gt; 303

tccacgtcac agggcctcct gaccgaccgt caggctaccg agaagggcgt aggcggagaa 60

gtcctcgcct acgtctggta atagggagga ttgactaaat atg tca cgt atc gga 115  
Met Ser Arg Ile Gly  
1 5

aaa gaa ccg atc acc atc cca tcc ggt gtc gaa acc aag att gac gga 163  
Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu Thr Lys Ile Asp Gly  
10 15 20

cag ctc gtt gag gtt aag ggt cct aag ggc acc ctg aac gtt aac gtt 211  
Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr Leu Asn Val Asn Val  
25 30 35

cca gag cca atc tcc gtt gca gtg gaa gac ggc aag att gtc gtc acc 259  
Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly Lys Ile Val Val Thr  
40 45 50

cgc ccg gat gat cac cgc act aac cgt tcc ctc cac ggt ctc tcc cgc 307  
Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu His Gly Leu Ser Arg  
55 60 65

tcc ctg gtt aac aac ctg gtt gtc ggc gtc acc gag ggc tac acc atc 355  
Ser Leu Val Asn Asn Leu Val Val Gly Val Thr Glu Gly Tyr Thr Ile  
70 75 80 85

aag atg gaa atc ttc ggt gtc ggt tac cgt gtc gcg ctg aag ggc aag 403  
Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val Ala Leu Lys Gly Lys  
90 95 100

gac ctt gag ttc tcc ctc ggc tac tca cac cca gtt ctg att gaa gct 451  
Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro Val Leu Ile Glu Ala  
105 110 115

tct gaa ggc atc act ttc gca gtt gat ggc aac acc aag ctt tca gtt 499  
Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn Thr Lys Leu Ser Val  
120 125 130

tct ggc atc gac aag cag aag gtt gga cag gtc gca gca gtg atc cgc 547  
Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val Ala Ala Val Ile Arg  
135 140 145

cgc ctg cgt aag gac gat cct tac aag ggt aag ggc atc cgc tac gag 595  
Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys Gly Ile Arg Tyr Glu  
150 155 160 165

ggt gag cag atc cgc cgc aag gtc gga aag acg ggt aag taagcaatga 644  
Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr Gly Lys  
170 175

gcaacactga aaa 657

&lt;210&gt; 304

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 304

Met Ser Arg Ile Gly Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu  
1 5 10 15



Gly Lys

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<220>
<221> CDS
<222> (101)..(526)
<223> RXA00543
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<400> 305
gctccggcgg gttcggcggc gcagacgatg agccaccggt ctaaagcttt tcttttctaa 60
aacattcaca aacactcaaa aaccacgaaa ggcagggatc atg aag ctg atc ctc 115
                                         Met Lys Leu Ile Leu
                                         1                               5
acc gcc gcc gtt gaa aac ctt ggt gtc gct ggc gac atc gta gag gtt 163
Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly Asp Ile Val Glu Val
                        10                        15                        20
aag aac ggc tac gga cgt aac ctg ctg ctc ccc cgt ggc ctg gca atc 211
Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro Arg Gly Leu Ala Ile
                        25                        30                        35
gta gcc acc ccg ggt gct gag aag cag atc gag ggc atc aag cgt gcc 259
Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu Gly Ile Lys Arg Ala

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40	45	50	
cag gag gct cgc gag att cgc gac ctc gac cac gct cgc gaa gtt aag			307
Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His Ala Arg Glu Val Lys			
55	60	65	
gta gca ctg gaa gca ctt gaa ggt gtt acc att gca gtc cgc acc tcc			355
Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile Ala Val Arg Thr Ser			
70	75	80	85
gag agc gga aaa ctg ttc ggc tcc gtt aag act gac gac atc gtc gac			403
Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr Asp Asp Ile Val Asp			
90	95	100	
gca gtc aag gca gcc ggc ggc ccg aac ctg gac aag cgt gcc att gtt			451
Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp Lys Arg Ala Ile Val			
105	110	115	
ctc ccg aag aac ctg gtt aag acc acc ggt aag tac cag gta gaa gca			499
Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys Tyr Gln Val Glu Ala			
120	125	130	
aag ctc acc gac gga att gtt tcc gcg tgaagtttga ggtcgtcgca			546
Lys Leu Thr Asp Gly Ile Val Ser Ala			
135	140		
gcg			549
<210> 306			
<211> 142			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 306			
Met Lys Leu Ile Leu Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly			
1	5	10	15
Asp Ile Val Glu Val Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro			
20	25	30	
Arg Gly Leu Ala Ile Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu			
35	40	45	
Gly Ile Lys Arg Ala Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His			
50	55	60	
Ala Arg Glu Val Lys Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile			
65	70	75	80
Ala Val Arg Thr Ser Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr			
85	90	95	
Asp Asp Ile Val Asp Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp			
100	105	110	
Lys Arg Ala Ile Val Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys			
115	120	125	
Tyr Gln Val Glu Ala Lys Leu Thr Asp Gly Ile Val Ser Ala			
130	135	140	

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<220>  
<221> CDS  
<222> (101)..(613)  
<223> RXA01335
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cggatcagta gattacacat aagaggaagg aggcgaagta atg gca aac cca aga 115  
Met Ala Asn Pro Arg  
1 5

acc gtc gtt ctc acc gag tac cgt ggc ctg acc gtg gct cag acc acc 211  
Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr Val Ala Gln Thr Thr  
25 30 35

aac acc ctt gtt aag atc gcc gct aac gaa gct ggc gtc gag ggc ctt 307  
Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala Gly Val Glu Gly Leu  
55 60 65

gca gtt gac acc gct aag gtg ctg aag aaa ttc ggc gaa gaa aac aag 403  
Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe Gly Glu Glu Asn Lys  
90 95 100

gaa cag gtc aac gca atc gcc gag ctg gac aac cgt gag acc act ctc 499  
Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn Arg Glu Thr Thr Leu  
120 125 130

ctg ttc aac gct cct gct tcc cag gtc gca cgc ctc gcc gtt gcg ctc 595  
Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg Leu Ala Val Ala Leu  
150 155 160 165

cag gac aag aag gac gca taagtgcgcca ccaggcgccac cag 636  
Gln Asp Lys Lys Asp Ala

170

&lt;210&gt; 308

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 308

Met Ala Asn Pro Arg Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg  
 1 5 10 15

Phe Ala Glu Thr Asp Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr  
 20 25 30

Val Ala Gln Thr Thr Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln  
 35 40 45

Tyr Ser Val Ala Lys Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala  
 50 55 60

Gly Val Glu Gly Leu Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala  
 65 70 75 80

Phe Ile Lys Gly Glu Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe  
 85 90 95

Gly Glu Glu Asn Lys Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly  
 100 105 110

Asn Ala Leu Thr Ala Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn  
 115 120 125

Arg Glu Thr Thr Leu Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu  
 130 135 140

Ala Lys Ala Ala Gly Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg  
 145 150 155 160

Leu Ala Val Ala Leu Gln Asp Lys Lys Asp Ala  
 165 170

&lt;210&gt; 309

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(535)

&lt;223&gt; RXN02826

&lt;400&gt; 309

agcgatcatc tgaagttgta gcgggaccga gcatccggac gggttactagt ggggtttcat 60

cgtcccagtt gtggccggta acaaggaagc aggtttaacg atg gct cct aag aag 115  
 Met Ala Pro Lys Lys  
 1 5

aag aag aag gtc act ggc ctc atc aag ctc cag atc cag gca gga cag 163

Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln Ile Gln Ala Gly Gln  
                   10                  15                  20  
 gca aac cct gct cct cca gtt ggc cca gca ctt ggt gct cac ggc gtc 211  
 Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu Gly Ala His Gly Val  
                   25                  30                  35  
 aac atc atg gaa ttc tgc aag gct tac aac gct gcg act gaa aac cag 259  
 Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala Ala Thr Glu Asn Gln  
                   40                  45                  50  
 cgc ggc aac gtt gtt cct gtt gag atc acc gtt tac gaa gac cgt tca 307  
 Arg Gly Asn Val Val Pro Val Glu Ile Thr Val Tyr Glu Asp Arg Ser  
                   55                  60                  65  
 ttc gac ttc aag ctg aag act cct cca gct gca aag ctt ctt ctg aag 355  
 Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala Lys Leu Leu Leu Lys  
                   70                  75                  80                  85  
 gct gct ggc ctg cag aag ggc tcc ggc gtt cct cac acc cag aag gtc 403  
 Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro His Thr Gln Lys Val  
                   90                  95                  100  
 ggc aag gtt tcc atg gct cag gtt cgt gag atc gct gag acc aag aag 451  
 Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile Ala Glu Thr Lys Lys  
                   105                  110                  115  
 gaa gac ctg aac gct cgc gat atc gac gct gct gcg aag atc atc gct 499  
 Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala Lys Ile Ile Ala  
                   120                  125                  130  
 ggt acc gct cgt tcc atg ggc atc acc gtc gaa ggc taaaagcttt 545  
 Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu Gly  
                   135                  140                  145  
 cacaccggtt agt 558

&lt;210&gt; 310

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 310

Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln  
                   1                  5                  10                  15

Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu  
                   20                  25                  30

Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala  
                   35                  40                  45

Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val  
                   50                  55                  60

Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala  
                   65                  70                  75                  80

Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro  
                   85                  90                  95

His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile  
 100 105 110

Ala Glu Thr Lys Lys Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala  
 115 120 125

Ala Lys Ile Ile Ala Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu  
 130 135 140

Gly  
 145

<210> 311

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (67)..(465)

<223> FRXA02826

<400> 311

ccggacggtt tctagtgggg ttctcatcgctc ccagttgtgg ccggttaacaa ggaagcaggt 60

ttaacgatg gct cct aag aag aag aag aag gtc act ggc ctc atc aag ctc 111  
 Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu  
 1 5 10 15

cag atc cag gca gga cag gca aac cct gct cct cca gtt ggc cca gaa 159  
 Gln Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu  
 20 25 30

ctt ggt gct cac ggc gtc aac atc atg gaa ttc tgc aag gct tac aac 207  
 Leu Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn  
 35 40 45

gct gcg act gaa aac cag cgc ggg aac gtt gtt cct gtt gag atc acc 255  
 Ala Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr  
 50 55 60

gtt tac gaa gac cgt tca ttc gac ttc aag ctg aag act cct cca gct 303  
 Val Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala  
 65 70 75

gca aag ctt ctt ctg aaa gct gct ggc ctg cag aag ggc tcc ggc gtt 351  
 Ala Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val  
 80 85 90 95

cct cac acc cag aag gtc ggc aag gtt tcc atg gct cag gtt cgt gag 399  
 Pro His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu  
 100 105 110

atc cct gcg acc aag aac gaa gac ctg acg ctc gcg ata tcg acg ctg 447  
 Ile Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu  
 115 120 125

ctg cga aga tca tcg ctg 465  
 Leu Arg Arg Ser Ser Leu

130

&lt;210&gt; 312

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 312

Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln  
 1 5 10 15

Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu Leu  
 20 25 30

Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala  
 35 40 45

Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val  
 50 55 60

Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala  
 65 70 75 80

Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro  
 85 90 95

His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile  
 100 105 110

Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu Leu  
 115 120 125

Arg Arg Ser Ser Leu  
 130

&lt;210&gt; 313

&lt;211&gt; 507

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(484)

&lt;223&gt; RXA01334

&lt;400&gt; 313

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togagcgtgt taaacgctca acaacaggaa ggatgccacc atg gct aag ctc acc 115  
 Met Ala Lys Leu Thr  
 1 5

aaa gac gag ctc atc gag gct ttc aag gaa atg acc ctc atc gag ctc 163  
 Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met Thr Leu Ile Glu Leu  
 10 15 20

tcc gag ttc gtt aag gaa ttc gaa gag gtc ttc gac gta acc gca gct 211  
 Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe Asp Val Thr Ala Ala  
 25 30 35





<210> 315  
 <211> 353  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(330)  
 <223> RXA02037

<400> 315  
 ggc aag ggc aag cct ttg tac gca cct aac gtt gac tgc ggc gac cac 48  
 Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His  
 1 5 10 15  
 gta atc gtg atc aac gct gac aag gtt gca gtt acc tcc aac aag cgc 96  
 Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg  
 20 25 30  
 gag cgc gaa atg cgt tac cgc cac tcc ggt tac cct ggt ggc ctg aag 144  
 Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys  
 35 40 45  
 tcc atg acc ctg ggt cgt tcc ctg gat ctg cac cca gag cgc acc atc 192  
 Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile  
 50 55 60  
 gag gat tcc atc gtc ggc atg atg cca cac aac aag ctc act gct gct 240  
 Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala  
 65 70 75 80  
 tcc gca aag aag ctg cac gtt ttc tcc ggc tcc gag cac cca tac gct 288  
 Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala  
 85 90 95  
 gct cag aag cct gag gcc tac gag atc aag aag gtg gcc cag 330  
 Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln  
 100 105 110  
 taatgtcaga gcctatccag aac 353

<210> 316  
 <211> 110  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 316  
 Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His  
 1 5 10 15  
 Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg  
 20 25 30  
 Glu Arg Glu Met Arg Tyr Arg His Ser Gly Tyr Pro Gly Gly Leu Lys  
 35 40 45  
 Ser Met Thr Leu Gly Arg Ser Leu Asp Leu His Pro Glu Arg Thr Ile  
 50 55 60

Glu Asp Ser Ile Val Gly Met Met Pro His Asn Lys Leu Thr Ala Ala  
 65 70 75 80  
 Ser Ala Lys Lys Leu His Val Phe Ser Gly Ser Glu His Pro Tyr Ala  
 85 90 95  
 Ala Gln Lys Pro Glu Ala Tyr Glu Ile Lys Lys Val Ala Gln  
 100 105 110

<210> 317  
 <211> 567  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(544)  
 <223> RXA00699

<400> 317  
 ccacaccgtg atccgccccg ataccccaga ggtacgtggc atgacacctgg cagttcgcca 60  
 cctgatcgtc gtcgaagaag tggcggggga gtaggtaaca atg agc gaa cca att 115  
 Met Ser Glu Pro Ile  
 1 5  
 aag ctc cac gat ttg cgc cca gca gcg ggc tca aac aaa gct aag acc 163  
 Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser Asn Lys Ala Lys Thr  
 10 15 20  
 cgc gtt ggt cga ggc gaa gca tcc aag ggt aag act gca ggt cgc ggt 211  
 Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys Thr Ala Gly Arg Gly  
 25 30 35  
 acc aag ggt acc aag gca cgc aag cag gtt tct gca gca ttc gaa ggt 259  
 Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser Ala Ala Phe Glu Gly  
 40 45 50  
 ggc cag atg cca ctg cag atg cgt ctt cct aag ctg aag ggc ttc aag 307  
 Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys Leu Lys Gly Phe Lys  
 55 60 65  
 aac cct aac aag gtt gac tac cag gta gtt aac att gca gat ctc gca 355  
 Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn Ile Ala Asp Leu Ala  
 70 75 80 85  
 gag aag ttc cca cag ggc ggc gac gtc agc att gct gac atc gtt gca 403  
 Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile Ala Asp Ile Val Ala  
 90 95 100  
 gca gga ctt gtc cgc aag aac gaa ctg gtt aag gtt ctt ggc aac ggc 451  
 Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys Val Leu Gly Asn Gly  
 105 110 115  
 gac atc agc gtc aag ctg aac gtc acc gct aac aag ttc tcc ggc tct 499  
 Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn Lys Phe Ser Gly Ser  
 120 125 130  
 gcc aag gaa aag atc gaa gcc gct ggc ggc tcc gca acc gtg gca 544  
 Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser Ala Thr Val Ala

135 140 145 567  
 taagttcacc agaactttaa aaa

<210> 318  
 <211> 148  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 318  
 Met Ser Glu Pro Ile Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser  
 1 5 10 15  
 Asn Lys Ala Lys Thr Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys  
 20 25 30  
 Thr Ala Gly Arg Gly Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser  
 35 40 45  
 Ala Ala Phe Glu Gly Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys  
 50 55 60  
 Leu Lys Gly Phe Lys Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn  
 65 70 75 80  
 Ile Ala Asp Leu Ala Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile  
 85 90 95  
 Ala Asp Ile Val Ala Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys  
 100 105 110  
 Val Leu Gly Asn Gly Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn  
 115 120 125  
 Lys Phe Ser Gly Ser Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser  
 130 135 140  
 Ala Thr Val Ala  
 145

<210> 319  
 <211> 537  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(514)  
 <223> RXA02042

<400> 319  
 atgcacccgc agagcgtcgc ggccgcggcg accgcaacgc acgtccgcgt cgtggtggcc 60  
 agcgtcgtca gcgctgctgag cagaagcagg agggctaaac atg ctt att cct aag 115  
 Met Leu Ile Pro Lys  
 1 5  
 cgc gtt aag tac cgt cgc cag cac cgt cct acc cgt agt ggt atc tcc 163  
 Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr Arg Ser Gly Ile Ser

	10	15	20	
aag ggc ggc aac cgc gtc act ttc ggt gag tac ggc atc cag gct ctc				211
Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr Gly Ile Gln Ala Leu				
	25	30	35	
gag cct gcc tac atc acc aac cgt cag att gaa tct gca cgt att gca				259
Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu Ser Ala Arg Ile Ala				
	40	45	50	
atc aac cgc cac gtc agg cgt ggt ggc aag gtt tgg atc aac atc ttc				307
Ile Asn Arg His Val Arg Arg Gly Gly Lys Val Trp Ile Asn Ile Phe				
	55	60	65	
cca gac cgc cca ctg acc cag aag cca ctc ggc gtt cgt atg ggt tcc				355
Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly Val Arg Met Gly Ser				
	70	75	80	85
ggt aag ggc cct gtg gag aag tgg gtt gca aac atc aag ccg ggc cgt				403
Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn Ile Lys Pro Gly Arg				
	90	95	100	
atc ctc ttc gag atg agc tac ccg gac gaa gct act gct ctc gag gct				451
Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala Thr Ala Leu Glu Ala				
	105	110	115	
ctg cgc cgc gct ggc cag aag ctt cca tgc aag gtc cgt atc gtc aag				499
Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys Val Arg Ile Val Lys				
	120	125	130	
agg gag gat cag ctc taatggctat cggtacccca gca				537
Arg Glu Asp Gln Leu				
	135			

&lt;210&gt; 320

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 320

Met	Leu	Ile	Pro	Lys	Arg	Val	Lys	Tyr	Arg	Arg	Gln	His	Arg	Pro	Thr
1				5					10					15	

Arg	Ser	Gly	Ile	Ser	Lys	Gly	Gly	Asn	Arg	Val	Thr	Phe	Gly	Glu	Tyr
		20						25					30		

Gly	Ile	Gln	Ala	Leu	Glu	Pro	Ala	Tyr	Ile	Thr	Asn	Arg	Gln	Ile	Glu
		35					40					45			

Ser	Ala	Arg	Ile	Ala	Ile	Asn	Arg	His	Val	Arg	Arg	Gly	Gly	Lys	Val
	50					55				60					

Trp	Ile	Asn	Ile	Phe	Pro	Asp	Arg	Pro	Leu	Thr	Gln	Lys	Pro	Leu	Gly
65					70				75					80	

Val	Arg	Met	Gly	Ser	Gly	Lys	Gly	Pro	Val	Glu	Lys	Trp	Val	Ala	Asn
			85					90						95	

Ile	Lys	Pro	Gly	Arg	Ile	Leu	Phe	Glu	Met	Ser	Tyr	Pro	Asp	Glu	Ala
		100						105					110		

Thr Ala Leu Glu Ala Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys  
 115 120 125

Val Arg Ile Val Lys Arg Glu Asp Gln Leu  
 130 135

<210> 321

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA00670

<400> 321

gaaactggtg gctacatcga tgtcgaggcg gaagattccg agtaagtcgc atggtccaat 60

tcatggggccg cgctaaatca acgtacaagg agtacatcta atg cct acc cct aag 115  
 Met Pro Thr Pro Lys  
 1 5

aag ggc gcc cgc ctc ggc gga tcc gca agc cac cag aag aag atc ctc 163  
 Lys Gly Ala Arg Leu Gly Gly Ser Ala Ser His Gln Lys Lys Ile Leu  
 10 15 20

tct aac ctg gct gca tct ctg ttc gag cat ggc gca atc aag acc acc 211  
 Ser Asn Leu Ala Ala Ser Leu Phe Glu His Gly Ala Ile Lys Thr Thr  
 25 30 35

gat gct aag gca aag gct ctg cgt cca tac gct gag aag ctg atc acc 259  
 Asp Ala Lys Ala Lys Ala Leu Arg Pro Tyr Ala Glu Lys Leu Ile Thr  
 40 45 50

aag gct aag tcc ggt tcc gtt gca gat cgt cgt aac gtt ctc gca ctg 307  
 Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg Asn Val Leu Ala Leu  
 55 60 65

gtt cct aac aag gaa atc gtg gct tac ctg ttc aac gaa ctt gct cct 355  
 Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe Asn Glu Leu Ala Pro  
 70 75 80 85

aag ttc gag aac cgt cca ggt ggt tac acc cgc atc atc aag ctg gag 403  
 Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg Ile Ile Lys Leu Glu  
 90 95 100

aac cgt aag ggc gac aac gct cct atg tcc cag atc tcc ctc gtt ctc 451  
 Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln Ile Ser Leu Val Leu  
 105 110 115

gag gag acc gtc tcc gca gaa gca tcc cgc gca acc cgc gca tct gct 499  
 Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala Thr Arg Ala Ser Ala  
 120 125 130

tcc aag aag gct gct gaa gag gct gag acc gaa gag gta gtc gag gct 547  
 Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu Glu Val Val Glu Ala  
 135 140 145

cca gct gag gag acc gca acc gaa gag gct gca gaa gag aag 589  
 Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala Glu Glu Lys  
 150 155 160

taaattttctc taactccgca tag 612

<210> 322

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Met Pro Thr Pro Lys Lys Gly Ala Arg Leu Gly Gly Ser Ala Ser His  
 1 5 10 15

Gln Lys Lys Ile Leu Ser Asn Leu Ala Ala Ser Leu Phe Glu His Gly  
 20 25 30

Ala Ile Lys Thr Thr Asp Ala Lys Ala Lys Ala Leu Arg Pro Tyr Ala  
 35 40 45

Glu Lys Leu Ile Thr Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg  
 50 55 60

Asn Val Leu Ala Leu Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe  
 65 70 75 80

Asn Glu Leu Ala Pro Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg  
 85 90 95

Ile Ile Lys Leu Glu Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln  
 100 105 110

Ile Ser Leu Val Leu Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala  
 115 120 125

Thr Arg Ala Ser Ala Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu  
 130 135 140

Glu Val Val Glu Ala Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala  
 145 150 155 160

Glu Glu Lys

<210> 323

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA00696

<400> 323

gatccgccgc ctgcgtaagg acgataccta caagggtgaag ggcataccgct acgagggtga 60

gcagatccgc cgcaagggtcg gaaagacggg taagtaagca atg agc aac act gaa 115

[illegible]

<211> 134

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 324

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<400> 324
Met Ser Asn Thr Glu Asn Lys Gln Lys Arg Val Ser Val Gly Lys Asp
  1                               10                      15

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Ile Ala Thr Arg Arg Arg Val Ala Arg Ala Arg Arg His Phe Arg Ile  
20 25 30

Arg Lys Asn Leu Arg Gly Thr Pro Glu Ala Pro Arg Leu Val Val His  
35 40 45

Arg Ser Ser Arg His Met His Val Gln Ile Ile Asp Asp Val Ala Gly  
50 55 60

His Thr Leu Ala Ala Ala Ser Ser Ile Glu Ala Glu Val Arg Ala Thr  
65 70 75 80

Glu Gly Asp Lys Lys Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala  
                   85                  90                  95

Glu Arg Ala Lys Ala Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala  
                   100                  105                  110

Gly Tyr Lys Tyr His Gly Arg Val Ala Ala Leu Ala Asp Ala Ala Arg  
                   115                  120                  125

Glu Gly Gly Leu Lys Phe  
                   130

&lt;210&gt; 325

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(439)

&lt;223&gt; RXA01353

&lt;400&gt; 325

cagcctcgaa aattgaaacg gaaacgaacc ggccgagcac cccaaacctg gggaagtgcc 60

gccagggtcc tctttcccta ctagtaaaag gattgtttat atg aac att ctg gat 115  
   Met Asn Ile Leu Asp  
   1                  5

aag atc gac gca gca tcc ctg cgc gac gac gtt cct gca ttc cgc gcc 163  
  Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val Pro Ala Phe Arg Ala  
                                   10                                  15                                  20

ggc gac acc ctc gac gta cac gtc aag gtc atc gaa ggc acc acc acc 211  
  Gly Asp Thr Leu Asp Val His Val Lys Val Ile Glu Gly Thr Thr Thr  
                                   25                                  30                                  35

cgt acc cag ctg ttc aag ggt gtt gtc att cgc cgt cag ggc ggc gga 259  
  Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg Arg Gln Gly Gly Gly  
                                   40                                  45                                  50

atc cgc gag acc ttc acc gta cgt aag gtt tcc ttc ggc atc ggt gtt 307  
  Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser Phe Gly Ile Gly Val  
                                   55                                  60                                  65

gag cgt acc ttc cca gta cac tcc cca aac atc gag aag atc gag gtc 355  
  Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile Glu Lys Ile Glu Val  
                                   70                                  75                                  80                                  85

att cgt cgt ggt gac gtt cgt cgt gcg aag ctg tac tac ctg cgc gaa 403  
  Ile Arg Arg Gly Asp Val Arg Arg Ala Lys Leu Tyr Tyr Leu Arg Glu  
                                   90                                  95                                  100

ctg cgc ggc aag gct gca cgt att aag gag aag cgc taattattta 449  
  Leu Arg Gly Lys Ala Ala Arg Ile Lys Glu Lys Arg  
                                   105                                  110

gcgtttgtta ggt 462



<210> 326  
 <211> 113  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 326  
 Met Asn Ile Leu Asp Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val  
           1                  5                  10                  15  
 Pro Ala Phe Arg Ala Gly Asp Thr Leu Asp Val His Val Lys Val Ile  
                   20                  25                  30  
 Glu Gly Thr Thr Thr Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg  
                   35                  40                  45  
 Arg Gln Gly Gly Gly Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser  
           50                  55                  60  
 Phe Gly Ile Gly Val Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile  
           65                  70                  75                  80  
 Glu Lys Ile Glu Val Ile Arg Arg Gly Asp Val Arg Arg Ala Lys Leu  
                   85                  90                  95  
 Tyr Tyr Leu Arg Glu Leu Arg Gly Lys Ala Ala Arg Ile Lys Glu Lys  
           100                  105                  110

Arg

<210> 327  
 <211> 504  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(481)  
 <223> RXA02420

<400> 327  
 cgacaccaag cgcatagaag gcctgctcgg caaggcttaa gtttaaaacc ttgcgctaaa 60  
 cccctccacc tttcaagaca agatttaagg aagtaccacc gtg gca cgt gtc aag 115  
   Val Ala Arg Val Lys  
   1                  5  
 cgg tcc gtt aac gca aag aag aag cgt cgc gaa att ctg aag tcc gca 163  
 Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu Ile Leu Lys Ser Ala  
                   10                  15                  20  
 aag ggc tac cgc ggc cag cgc tca cgc ctt tac cgt aag gct aag gag 211  
 Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr Arg Lys Ala Lys Glu  
                   25                  30                  35  
 cag tgg ctg cac tcc atg act tac tct tac cgc gat cgt cgc gcc cgt 259  
 Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg Asp Arg Arg Ala Arg  
           40                  45                  50  
 aag agc gag ttc cgt aag ctg tgg atc cag cgt atc aac gct gct gca 307

Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg Ile Asn Ala Ala Ala  
 55 60 65  
 cgt atg aac ggc atc acc tac aac cgt ctc atc cag ggc ctt cgc ctt 355  
 Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile Gln Gly Leu Arg Leu  
 70 75 80 85  
 gct gag atc gag gtc gac cgc aag atc ctc gct gat ctc gca gtc aac 403  
 Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala Asp Leu Ala Val Asn  
 90 95 100  
 gac ttt gca acc ttc tcc gca atc tgc gag gct gca aag gct gca ctt 451  
 Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala Ala Lys Ala Ala Leu  
 105 110 115  
 cct gag gac gtt aac gct cca aag gct gct taagcttaca aacgaattga 501  
 Pro Glu Asp Val Asn Ala Pro Lys Ala Ala  
 120 125  
 cct 504

<210> 328  
 <211> 127  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 328  
 Val Ala Arg Val Lys Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu  
 1 5 10 15  
 Ile Leu Lys Ser Ala Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr  
 20 25 30  
 Arg Lys Ala Lys Glu Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg  
 35 40 45  
 Asp Arg Arg Ala Arg Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg  
 50 55 60  
 Ile Asn Ala Ala Ala Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile  
 65 70 75 80  
 Gln Gly Leu Arg Leu Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala  
 85 90 95  
 Asp Leu Ala Val Asn Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala  
 100 105 110  
 Ala Lys Ala Ala Leu Pro Glu Asp Val Asn Ala Pro Lys Ala Ala  
 115 120 125

<210> 329  
 <211> 415  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(415)

&lt;223&gt; RXN02371

&lt;400&gt; 329

ttggctccgc atgtctaaaa cgcaattgta aaacgtaagt ccaatcaggg actcatcatc 60

cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115  
 Met Tyr Ala Ile Val  
 1 5

aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163  
 Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys  
 10 15 20

gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211  
 Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro  
 25 30 35

gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259  
 Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu  
 40 45 50

gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307  
 Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro  
 55 60 65

aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355  
 Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg  
 70 75 80 85

cag gga cac cgt cag ccc ctg acc gtt ctg aag gta acc gga aat caa 403  
 Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys Val Thr Gly Asn Gln  
 90 95 100

gta agc cct cgg 415  
 Val Ser Pro Arg  
 105

&lt;210&gt; 330

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 330

Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu  
 1 5 10 15

Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser  
 20 25 30

Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr  
 35 40 45

Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu  
 50 55 60

His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr  
 65 70 75 80

Gly Tyr Lys Lys Arg Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys  
 85 90 95

Val Thr Gly Asn Gln Val Ser Pro Arg  
100 105

<210> 331  
<211> 370  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(370)  
<223> FRXA02371

<400> 331  
ttggctccgc atgtctaaaa cgcaattgta aaacgtaagt ccaatcaggg actcatcatc 60  
cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115  
Met Tyr Ala Ile Val  
1 5  
aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163  
Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys  
10 15 20  
gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211  
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro  
25 30 35  
gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259  
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu  
40 45 50  
gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307  
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro  
55 60 65  
aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355  
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg  
70 75 80 85  
cag gga cac cgt cag 370  
Gln Gly His Arg Gln  
90

<210> 332  
<211> 90  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 332  
Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu  
1 5 10 15  
Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser  
20 25 30  
Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr  
35 40 45

Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu  
50 55 60

His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr  
65 70 75 80

Gly Tyr Lys Lys Arg Gln Gly His Arg Gln  
85 90

<210> 333

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(403)

<223> RXA01949

<400> 333

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tcaaccgcgc ttccggtgcg gcacaggagg agcagaacta atg gct act atc gcc 115  
Met Ala Thr Ile Ala  
1 5

aac cca cgc gac atc atc atc gca ccg gtc gtt tct gag aag tcc tac 163  
Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val Ser Glu Lys Ser Tyr  
10 15 20

ggc ctc atg gag cag aac gtt tac acg ttc ttc gtc tcc act gac gct 211  
Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe Val Ser Thr Asp Ala  
25 30 35

aac aag act cag atc aag att gcc atc gaa gag atc ttc ggc gtc aag 259  
Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu Ile Phe Gly Val Lys  
40 45 50

gtt gca tct gtg aac acc gtt aac cgt gca ggt aag cgc aag cgc tcc 307  
Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly Lys Arg Lys Arg Ser  
55 60 65

cgc acc ggc ttc ggt act cgc aag gct acc aag cgc gct tat gtg act 355  
Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys Arg Ala Tyr Val Thr  
70 75 80 85

ctt cgc gaa ggc agc gac tcc atc gac atc ttc agc ggc tcc gtc gct 403  
Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe Ser Gly Ser Val Ala  
90 95 100

taagacgtcg atagaaaagg aca 426

<210> 334

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Met Ala Thr Ile Ala Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val  
 1 5 10 15  
 Ser Glu Lys Ser Tyr Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe  
 20 25 30  
 Val Ser Thr Asp Ala Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu  
 35 40 45  
 Ile Phe Gly Val Lys Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly  
 50 55 60  
 Lys Arg Lys Arg Ser Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys  
 65 70 75 80  
 Arg Ala Tyr Val Thr Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe  
 85 90 95  
 Ser Gly Ser Val Ala  
 100

<210> 335  
 <211> 489  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(466)  
 <223> RXN00709

<400> 335  
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 Val Ile Gln Gln Glu  
 1 5  
 tcg cgt ctg aag gtc gcc gac aac act ggt gca cgt gaa att ctg tgc 163  
 Ser Arg Leu Lys Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys  
 10 15 20  
 atc cgc gtt ctc ggt gga tcc acc cga cgt ttt gct ggc att ggt gac 211  
 Ile Arg Val Leu Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp  
 25 30 35  
 gtc atc gtc gcc act gtc aag gaa gca acc cca ggc ggc aac gta aag 259  
 Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys  
 40 45 50  
 tct ggc gaa atc gtc aag gct gtt atc gtt cgc acc aag aag gag acc 307  
 Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr  
 55 60 65  
 cgt cgt gca gac ggt tct tac atc tcc ttc gat gag aac gct gcc gtc 355  
 Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val  
 70 75 80 85  
 atc atc aag aac gac aac gag cca cgt ggc acc cgt atc ttc gga cca 403  
 Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro

	90	95	100	
ggt gct cgt gaa ctt cgt gag aag aag ttc atg aag atc gtt tct ctc				451
Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu				
	105	110	115	

gca ccg gag gtg att taagaatgaa ggtccacaag ggc	489
Ala Pro Glu Val Ile	
120	

<210> 336  
 <211> 122  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 336	
Val Ile Gln Gln Glu Ser Arg Leu Lys Val Ala Asp Asn Thr Gly Ala	
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Arg Glu Ile Leu Cys Ile Arg Val Leu Gly Gly Ser Thr Arg Arg Phe	
20 25 30	
Ala Gly Ile Gly Asp Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro	
35 40 45	
Gly Gly Asn Val Lys Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg	
50 55 60	
Thr Lys Lys Glu Thr Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp	
65 70 75 80	
Glu Asn Ala Ala Val Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr	
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Arg Ile Phe Gly Pro Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met	
100 105 110	
Lys Ile Val Ser Leu Ala Pro Glu Val Ile	
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<210> 337  
 <211> 362  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(339)  
 <223> FRXA00709

<400> 337	
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Val Ala Asp Asn Thr Gly Ala Arg Glu Ile Leu Cys Ile Arg Val Leu	
1 5 10 15	
ggt gga tcc acc cga cgt ttt gct ggc att ggt gac gtc atc gtc gcc	96
Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala	
20 25 30	

act gtc aag gaa gca acc cca ggc ggc aac gta aag tct ggc gaa atc 144  
 Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile  
           35                  40                  45

gtc aag gct gtt atc gtt cgc acc aag aag gag acc cgt cgt gca gac 192  
 Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp  
           50                  55                  60

ggc tct tac atc tcc ttc gat gag aac gct gcc gtc atc atc aag aac 240  
 Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Val Ile Ile Lys Asn  
           65                  70                  75                  80

gac aac gag cca cgt ggc acc cgt atc ttc gga cca gtt gct cgt gaa 288  
 Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu  
                   85                  90                  95

ctt cgt gag aag aag ttc atg aag atc gtt tct ctc gca ccg gag gtg 336  
 Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val  
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 Ile

<210> 338  
 <211> 113  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 338  
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Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala  
                   20                  25                  30

Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile  
                   35                  40                  45

Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp  
                   50                  55                  60

Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val Ile Ile Lys Asn  
           65                  70                  75                  80

Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu  
                   85                  90                  95

Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val  
                   100                  105                  110

Ile

<210> 339  
 <211> 435  
 <212> DNA  
 <213> Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(412)

&lt;223&gt; RXA00710

&lt;400&gt; 339

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tcatgaagat	cgtttctctc	gcaccggagg	tgatttaaga	atg aag gtc cac aag	115
				Met Lys Val His Lys	
				1 5	

ggc gat atg gtt ctg gtc atc tca ggt cca gac aag ggt gct aag gga	163
Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp Lys Gly Ala Lys Gly	
10 15 20	

cag gtc atc gcg gct ttc cct aag acc gaa aag gtt ctc gtc gaa ggc	211
Gln Val Ile Ala Ala Phe Pro Lys Thr Glu Lys Val Leu Val Glu Gly	
25 30 35	

gtt aac cgc atc aag aag cac gta gct aac tcc gca cca gag cgt ggc	259
Val Asn Arg Ile Lys Lys His Val Ala Asn Ser Ala Pro Glu Arg Gly	
40 45 50	

gca gag tcc ggc gga atc gtg acc cag gaa gct ccg atc cat gtc tct	307
Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala Pro Ile His Val Ser	
55 60 65	

aac gtc atg gtc atc gac tcc gac gga aac cca act cgc gtt ggc tac	355
Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro Thr Arg Val Gly Tyr	
70 75 80 85	

cgt ttc gat gaa aac ggc aag aag gtc cgc gtt tct cgt cgc aat ggg	403
Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val Ser Arg Arg Asn Gly	
90 95 100	

aag gat atc taatgactga gaattacatc cct	435
Lys Asp Ile	

&lt;210&gt; 340

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 340

Met Lys Val His Lys Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp
1 5 10 15

Lys Gly Ala Lys Gly Gln Val Ile Ala Ala Phe Pro Lys Thr Glu Lys
20 25 30

Val Leu Val Glu Gly Val Asn Arg Ile Lys Lys His Val Ala Asn Ser
35 40 45

Ala Pro Glu Arg Gly Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala
50 55 60

Pro Ile His Val Ser Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro
65 70 75 80

Thr Arg Val Gly Tyr Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val  
                   85                  90                  95

Ser Arg Arg Asn Gly Lys Asp Ile  
                   100

<210> 341  
 <211> 357  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(334)  
 <223> RXA02635

<400> 341  
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 gtcttctaac tgaatgtggg cggctaggag aaagtaagtt atg tcg gca cat tgc 115  
   Met Ser Ala His Cys  
   1                  5  
 cag gta acg gga cgc aag ccg agt ttc ggc aag tct gtc tca cac tcg 163  
 Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys Ser Val Ser His Ser  
                   10                  15                  20  
 cac cga cgc act tcc cgc cgt tgg aac ccc aac gtg cag cgt cgc aag 211  
 His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn Val Gln Arg Arg Lys  
                   25                  30                  35  
 ttc tat gtc cct tcc gag gga cgc acc atc act ctg acc gtt tcc acc 259  
 Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr Leu Thr Val Ser Thr  
                   40                  45                  50  
 aag ggt ctg aag gtc att gac cgc gac ggc atc gaa gcc gtt gtt gct 307  
 Lys Gly Leu Lys Val Ile Asp Arg Asp Gly Ile Glu Ala Val Val Ala  
                   55                  60                  65  
 cag att cgc gca cgt ggg gag aag atc taaagatggc acgtaatgat 354  
 Gln Ile Arg Ala Arg Gly Glu Lys Ile  
                   70                  75  
 atc 357

<210> 342  
 <211> 78  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 342  
 Met Ser Ala His Cys Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys  
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 Ser Val Ser His Ser His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn  
                   20                  25                  30  
 Val Gln Arg Arg Lys Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr

<220>

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aaccgacctg aagtttcaat cctgagggaa tgcagagtaa atg aaa aag gat atc 115
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Met Lys Lys Asp Ile  
1 5

cac cct gac tac cat gcg gta gtc ttc cag gac gca ggt act ggc ttc 163  
His Pro Asp Tyr His Ala Val Val Phe Gln Asp Ala Gly Thr Gly Phe  
10 15 20

cag ttc ctg acc aag tcc acc gct tcc agc gac cgc acc gtg tcc tgg 211  
Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp Arg Thr Val Ser Trp  
25 30 35

gaa gat ggt aac gag tac cca ctg atc gtc gtt gac gtc acc agc gag 259  
Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val Asp Val Thr Ser Glu  
40 45 50

tct cac cca ttc tgg acc ggc gct cag cgt gtc atg gac acc gct ggt 307  
Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val Met Asp Thr Ala Gly  
55 60 65

cgt gtt gag aag ttc gag cgt cgc ttc ggt ggc atg gct cgc cgc aag 355  
Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly Met Ala Arg Arg Lys  
70 75 80 85

aag aag gca taggagggaa aacaatggca gtt 387  
Lys Lys Ala

<210> 348

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Lys Lys Asp Ile His Pro Asp Tyr His Ala Val Val Phe Gln Asp  
1 5 10 15

Ala Gly Thr Gly Phe Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp  
20 25 30

Arg Thr Val Ser Trp Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val  
35 40 45

Asp Val Thr Ser Glu Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val  
50 55 60

Met Asp Thr Ala Gly Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly  
65 70 75 80

Met Ala Arg Arg Lys Lys Lys Ala  
85

<210> 349

<211> 285

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(262)

&lt;223&gt; RXA02636

&lt;400&gt; 349

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ttgtttgctca gattcgcgca cgtggggaga agatctaaag atg gca cgt aat gat 115  
Met Ala Arg Asn Asp  
1 5

atc cgc cct atc atc aag ctg aag tct act gct ggc act ggt tac acc 163  
Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala Gly Thr Gly Tyr Thr  
10 15 20

tat gtc acc cgt aag aac aag cgc aac aac ccg gac cgt att tcc ctc 211  
Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro Asp Arg Ile Ser Leu  
25 30 35

atg aag tac gat cca gta gtc cgt aag cac gtc gaa ttc cgc gag gag 259  
Met Lys Tyr Arg Asp Pro Val Val Arg Lys His Val Glu Phe Arg Glu Glu  
40 45 50

cga taatcaatgg ctaagaagtc aaa 285  
Arg

&lt;210&gt; 350

&lt;211&gt; 54

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

Met Ala Arg Asn Asp Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala  
1 5 10 15

Gly Thr Gly Tyr Thr Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro  
20 25 30

Asp Arg Ile Ser Leu Met Lys Tyr Asp Pro Val Val Arg Lys His Val  
35 40 45

Glu Phe Arg Glu Glu Arg  
50

&lt;210&gt; 351

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(241)

&lt;223&gt; RXA01423

&lt;400&gt; 351

ttcccccggt atagggttag cgcggaatc ttgcgcgact ttgtccacta gaaccggtgt 60

gtccggtgat ccgtcaacaa aatatttagg agtggtttcac atg gca aag ggc aag 115  
Met Ala Lys Gly Lys  
1 5

cgg acg ttc cag ccg aac aac cgt cgt cgt gca cgt gtt cac ggt ttc 163  
 Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala Arg Val His Gly Phe  
                   10                                  15                                  20  
  
 cgt ctt cgt atg cgt acc cgt gca ggt cgt gca att gtt gcg gct cgt 211  
 Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala Ile Val Ala Ala Arg  
                   25                                  30                                  35  
  
 cgt cgc aag ggt cgc gca aag ctg acc gcg taatttttta gcgtcaccac 261  
 Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala  
                   40                                  45  
  
 aat 264

<210> 352  
 <211> 47  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 352  
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           1                                  5                                  10                                  15  
  
 Arg Val His Gly Phe Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala  
                   20                                  25                                  30  
  
 Ile Val Ala Ala Arg Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala  
                   35                                  40                                  45

<210> 353  
 <211> 315  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(292)  
 <223> RXA02419

<400> 353  
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 ggcaagaaat aatcacgaat agggtttaag gacaactttc atg aag aac aag acc 115  
   Met Lys Asn Lys Thr  
   1                                  5  
  
 cac aag ggc acc gca aag cgc gtt aag gtg act ggc tcc ggc aag ctc 163  
 His Lys Gly Thr Ala Lys Arg Val Lys Val Thr Gly Ser Gly Lys Leu  
                   10                                  15                                  20  
  
 gtt cgc gag cag gca aac cgc cgc cac ctt ctc gag ggc aag tca tct 211  
 Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu Glu Gly Lys Ser Ser  
                   25                                  30                                  35  
  
 acc cgc act cgt cgc ctg aag ggc atc gtt gag gtt gac aag gcc gac 259  
 Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu Val Asp Lys Ala Asp  
                   40                                  45                                  50

aaa

315

<210> 354  
<211> 64  
<212> PRT  
<213> Corynebacterium glutamicum

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<400> 354
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  1          5          10          15
Gly Ser Gly Lys Leu Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu
  20          25          30
Glu Gly Lys Ser Ser Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu
  35          40          45
Val Asp Lys Ala Asp Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala
  50          55          60

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<210> 355
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1558)
<223> RXA02190
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<400> 355
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ccattatcta atttcctatc catttcggag caatttacat atg ccc acc aac aat      115
                                     Met Pro Thr Asn Asn
                                           1             5

gca cct cag gta gcc atc aac gac att ggc tct gct gag gac ttc ctt      163
Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser Ala Glu Asp Phe Leu
                     10                        15                    20

gca gca atc gac gca acc atc aag tac ttc aac gat ggc gat atc gtt      211
Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn Asp Gly Asp Ile Val
                      25                          30                35

gaa ggc acc gtg gta aag gtc gat cgt gac gag gta ctt ctg gac atc      259
Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu Val Leu Leu Asp Ile
                   40                        45                    50

gga tac aag acc gag ggt gtc atc cca tcc cgc gag ctg tcc atc aag      307
Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg Glu Leu Ser Ile Lys
    55                        60                        65

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cac gat gtc gat cca gac gag gtc gtc gaa gtc ggc gac caa att gac 355  
 His Asp Val Asp Pro Asp Glu Val Val Glu Val Gly Asp Gln Ile Asp  
 70 75 80 85

gca ctt gtc ctc acc aag gaa gac aaa gaa ggt cgt ctg atc ctt tcc 403  
 Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly Arg Leu Ile Leu Ser  
 90 95 100

aag aag cgt gct cag tac gag cgt gct tgg ggc gcc atc gag gag ctc 451  
 Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly Ala Ile Glu Glu Leu  
 105 110 115

aag gaa aag gac gag cca gtt acc ggt acc gtc atc gag gtc gtc aag 499  
 Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val Ile Glu Val Val Lys  
 120 125 130

ggt ggc ctc atc atc gac atc ggt ctc cgt ggc ttc ctg cct gca tcc 547  
 Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly Phe Leu Pro Ala Ser  
 135 140 145

ctc gtt gag atg cgt cgc gtc cgc gac ctg gat ccg tac atc ggc cag 595  
 Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp Pro Tyr Ile Gly Gln  
 150 155 160 165

gag ctc gaa gct aag atc atc gag ctg gac aag aac cgc aac aac gtc 643  
 Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys Asn Arg Asn Asn Val  
 170 175 180

gtt ctg tcc cgt cgc gca ttc ctc gag cag acc cag tct gag gtc cgc 691  
 Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr Gln Ser Glu Val Arg  
 185 190 195

tcc gag ttc ctg cac cag ctc cag aag ggc cag gtc cgc aag ggc gtc 739  
 Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln Val Arg Lys Gly Val  
 200 205 210

gtc tct tcc atc gtc aac ttc ggc gca ttc gtc gat ctc ggc ggt gtc 787  
 Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val Asp Leu Gly Gly Val  
 215 220 225

gac gga ctg gtt cac gtt tcc gag ctg tcc tgg aag cac atc gac cac 835  
 Asp Gly Leu Val His Val Ser Glu Leu Ser Trp Lys His Ile Asp His  
 230 235 240 245

cca tct gag gtt gtc acc gtc ggc gac gaa gtc acc gtt gag gtt ctc 883  
 Pro Ser Glu Val Val Thr Val Gly Asp Glu Val Thr Val Glu Val Leu  
 250 255 260

gag gtc gat ctc gac cgc gag cgc gtc tcc ctg tcc ctg aag gct acc 931  
 Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu Ser Leu Lys Ala Thr  
 265 270 275

cag gaa gac cca tgg cgc gtc ttc gct cgc act cac gct gtg ggc cag 979  
 Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr His Ala Val Gly Gln  
 280 285 290

atc gtt cca ggc aag gtc acc aag ctg gtt cca ttc ggt gcg ttc gtt 1027  
 Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro Phe Gly Ala Phe Val  
 295 300 305

cgc gtc gaa gag ggc atc gaa ggc ctc gtc cac atc tcc gag ctg gct 1075  
 Arg Val Glu Glu Gly Ile Glu Gly Leu Val His Ile Ser Glu Leu Ala  
 310 315 320 325  
 cag cgc cac gtc gag gtt ccg gac cag gtt gtc gca gtt ggc gaa gag 1123  
 Gln Arg His Val Glu Val Pro Asp Gln Val Val Ala Val Gly Glu Glu  
 330 335 340  
 gtc atg gtc aag gtc atc gac atc gat ctc gag cgt cgt cgt atc tcc 1171  
 Val Met Val Lys Val Ile Asp Ile Asp Leu Glu Arg Arg Arg Ile Ser  
 345 350 355  
 ctg tcc ctc aag cag gct gac gag gac tac acc gaa gag ttc gac cca 1219  
 Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr Glu Glu Phe Asp Pro  
 360 365 370  
 tcc aag tac gga atg gct gac tcc tac gac gag cag ggt aac tac atc 1267  
 Ser Lys Tyr Gly Met Ala Asp Ser Tyr Asp Glu Gln Gly Asn Tyr Ile  
 375 380 385  
 ttc cct gag ggc ttc gac gcc gag acc aac gaa tgg ctc gaa ggc ttc 1315  
 Phe Pro Glu Gly Phe Asp Ala Glu Thr Asn Glu Trp Leu Glu Gly Phe  
 390 395 400 405  
 gat gag cag cgt cag gct tgg gaa gct cgc tac gcc gag tcc gag cgt 1363  
 Asp Glu Gln Arg Gln Ala Trp Glu Ala Arg Tyr Ala Glu Ser Glu Arg  
 410 415 420  
 cgc ttc acc gct cac acc gct cag atc gag cgt cgt cgt cag cag gct 1411  
 Arg Phe Thr Ala His Thr Ala Gln Ile Glu Arg Arg Arg Gln Gln Ala  
 425 430 435  
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 Glu Glu Ala Ala Ala Glu Ala Pro Ala Gly Asn Tyr Ser Thr Asp Ser  
 440 445 450  
 gca gaa gat gca cct gca gca gaa gca gtt gaa gag tcc gct ggc tcc 1507  
 Ala Glu Asp Ala Pro Ala Ala Glu Ala Val Glu Glu Ser Ala Gly Ser  
 455 460 465  
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 Leu Ala Ser Asp Glu Gln Leu Ala Ala Leu Arg Glu Lys Leu Ala Gly  
 470 475 480 485  
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 Asn

&lt;210&gt; 356

&lt;211&gt; 486

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Met Pro Thr Asn Asn Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser  
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Ala Glu Asp Phe Leu Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn  
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Asp Gly Asp Ile Val Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu  
 35 40 45  
 Val Leu Leu Asp Ile Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg  
 50 55 60  
 Glu Leu Ser Ile Lys His Asp Val Asp Pro Asp Glu Val Val Glu Val  
 65 70 75 80  
 Gly Asp Gln Ile Asp Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly  
 85 90 95  
 Arg Leu Ile Leu Ser Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly  
 100 105 110  
 Ala Ile Glu Glu Leu Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val  
 115 120 125  
 Ile Glu Val Val Lys Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly  
 130 135 140  
 Phe Leu Pro Ala Ser Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp  
 145 150 155 160  
 Pro Tyr Ile Gly Gln Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys  
 165 170 175  
 Asn Arg Asn Asn Val Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr  
 180 185 190  
 Gln Ser Glu Val Arg Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln  
 195 200 205  
 Val Arg Lys Gly Val Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val  
 210 215 220  
 Asp Leu Gly Gly Val Asp Gly Leu Val His Val Ser Glu Leu Ser Trp  
 225 230 235 240  
 Lys His Ile Asp His Pro Ser Glu Val Val Thr Val Gly Asp Glu Val  
 245 250 255  
 Thr Val Glu Val Leu Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu  
 260 265 270  
 Ser Leu Lys Ala Thr Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr  
 275 280 285  
 His Ala Val Gly Gln Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro  
 290 295 300  
 Phe Gly Ala Phe Val Arg Val Glu Glu Gly Ile Glu Gly Leu Val His  
 305 310 315 320  
 Ile Ser Glu Leu Ala Gln Arg His Val Glu Val Pro Asp Gln Val Val  
 325 330 335  
 Ala Val Gly Glu Glu Val Met Val Lys Val Ile Asp Ile Asp Leu Glu  
 340 345 350  
 Arg Arg Arg Ile Ser Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr

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Met Arg Arg Phe Ile  
1 5

ttc acc gag cgt aac ggc atc tac atc att gac ctt cag cag acc ctg 163  
Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp Leu Gln Gln Thr Leu  
10 15 20

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acc tac atc gat cag gct ttc gag ttc gtc aag gaa acc gtt gct cac    211
Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys Glu Thr Val Ala His
      25                      30                      35
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ggt ggc acc gtt ctt ttc gtt ggt acc aaa aag cag gct cag gaa gct 259  
 Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ala  
           40                          45                          50

gtt cag gtt gag gca gac cgc gtt ggt atg cct tac gtg aac cac cgt 307  
Val Gln Val Glu Ala Asp Arg Val Gly Met Pro Tyr Val Asn His Arg  
55 60 65

tgg ctc ggc ggc atg ctg acc aac ttc cag acc gtt tcc aag cgt ctg 355

Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr Val Ser Lys Arg Leu  
 70 75 80 85  
 aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac 403  
 Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala Ala Glu Asn Gly Tyr  
 90 95 100  
 gag ggt cgc acc aag cgc gaa gtt ctc atg ctg acc cgt gag cgc acc 451  
 Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu Thr Arg Glu Arg Thr  
 105 110 115  
 aag ctg gag cgc gtc ctc ggt ggt atc gca gag atg acc cgc gtg cct 499  
 Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu Met Thr Arg Val Pro  
 120 125 130  
 tcc gca ctg tgg atc att gac acc aac aag gag cac atc gct gtc gct 547  
 Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu His Ile Ala Val Ala  
 135 140 145  
 gag gct cac aag ctg aac atc cca gtt gtt gcc atc ctg gac acc aac 595  
 Glu Ala His Lys Leu Asn Ile Pro Val Val Ala Ile Leu Asp Thr Asn  
 150 155 160 165  
 tgt gac cca gac gtt gtt gac ttc cca gtt cct ggt aac gac gac gca 643  
 Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro Gly Asn Asp Asp Ala  
 170 175 180  
 atc cgc tcc acc gca ctg ctt tcc cgc gtt atc tcc acc gct gtg gaa 691  
 Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile Ser Thr Ala Val Glu  
 185 190 195  
 gag ggt aag aag gca cgc gag gag cgt cag ctg gca gct gct aag gat 739  
 Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu Ala Ala Ala Lys Asp  
 200 205 210  
 gca gca ggc gac gca aag cct gag gca gag gaa gca cca gca gca gct 787  
 Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu Ala Pro Ala Ala Ala  
 215 220 225  
 gag gct gaa gag gca cct gca gct gag gct gaa gag gca cct gca gct 835  
 Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala  
 230 235 240 245  
 gag taagctgccc ttaactgcag ttt 861  
 Glu

&lt;210&gt; 358

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp  
 1 5 10 15

Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys  
 20 25 30

Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys

ttc acc gag cgt aac ggc atc tac atc att gac ctt cag cag acc ctg 163  
Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp Leu Gln Gln Thr Leu

	10	15	20	
acc tac atc gat cag gct ttc gag ttc gtc aag gaa acc gtt gct cac				211
Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys Glu Thr Val Ala His				
	25	30	35	
ggg ggc acc gtt ctt ttc gtt ggt acc aaa aag cag gct cag gaa gct				259
Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ala				
	40	45	50	
gtt cag gtt gag gca gac cgc gtt ggt atg cct tac gtg aac cac cgt				307
Val Gln Val Glu Ala Asp Arg Val Gly Met Pro Tyr Val Asn His Arg				
	55	60	65	
tgg ctc ggc ggc atg ctg acc aac ttc cag acc gtt tcc aag cgt ctg				355
Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr Val Ser Lys Arg Leu				
	70	75	80	85
aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac				403
Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala Ala Glu Asn Gly Tyr				
	90	95	100	
gag ggt cgc acc aag cgc gaa gtt ctc atg ctg acc cgt gag cgc acc				451
Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu Thr Arg Glu Arg Thr				
	105	110	115	
aag ctg gag cgc gtc ctc ggt ggt atc gca gag atg acc cgc gtg cct				499
Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu Met Thr Arg Val Pro				
	120	125	130	
tcc gca ctg tgg atc att gac acc aac aag gag cac atc gct gtc gct				547
Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu His Ile Ala Val Ala				
	135	140	145	
gag gct cac aag ctg aac atc cca gtt gtt gcc atc ctg gac acc aac				595
Glu Ala His Lys Leu Asn Ile Pro Val Val Ala Ile Leu Asp Thr Asn				
	150	155	160	165
tgt gac cca gac gtt gtt gac ttc cca gtt cct ggt aac gac gac gca				643
Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro Gly Asn Asp Asp Ala				
	170	175	180	
atc cgc tcc acc gca ctg ctt tcc cgc gtt atc tcc acc gct gtg gaa				691
Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile Ser Thr Ala Val Glu				
	185	190	195	
gag ggt aag aag gca cgc gag gag cgt cag ctg gca gct gct aag gat				739
Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu Ala Ala Ala Lys Asp				
	200	205	210	
gca gca ggc gac gca aag cct gag gca gag gaa gca cca gca gca gct				787
Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu Ala Pro Ala Ala Ala				
	215	220	225	
gag gct gaa gag gca cct gca gct gag gct gaa gaa cac ctg cag ctg				835
Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu Glu His Leu Gln Leu				
	230	235	240	245
agt aag ctg ccc tta act gca gtt tct gca gtt agc tgaccaattt				881
Ser Lys Leu Pro Leu Thr Ala Val Ser Ala Val Ser				
	250	255		

aaagccccca cga

894

&lt;210&gt; 360

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 360

Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp  
 1 5 10 15

Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys  
 20 25 30

Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys  
 35 40 45

Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro  
 50 55 60

Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr  
 65 70 75 80

Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala  
 85 90 95

Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu  
 100 105 110

Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu  
 115 120 125

Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu  
 130 135 140

His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala  
 145 150 155 160

Ile Leu Asp Thr Asn Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro  
 165 170 175

Gly Asn Asp Asp Ala Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile  
 180 185 190

Ser Thr Ala Val Glu Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu  
 195 200 205

Ala Ala Ala Lys Asp Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu  
 210 215 220

Ala Pro Ala Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu  
 225 230 235 240

Glu His Leu Gln Leu Ser Lys Leu Pro Leu Thr Ala Val Ser Ala Val  
 245 250 255

Ser



<210> 361  
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 <213> *Corynebacterium glutamicum*

<220>  
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 tct tac gct gac tac gtc gca gaa gac atc aag att cgc gaa ttc ctg 96  
 Ser Tyr Ala Asp Tyr Val Ala Glu Asp Ile Lys Ile Arg Glu Phe Leu  
 20 25 30  
 tcc aag ggc ctc gac cgt gcc ggc atc gcc gac gtc gtc atc gag cgc 144  
 Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg  
 35 40 45  
 acc cgc gac cgc gtt cgc gta gac atc cac acc gct cgc cca ggc atc 192  
 Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile  
 50 55 60  
 gtc att ggt cgt cgt ggc gct gag gct gac cgc atc cgc cgt gag ctc 240  
 Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu  
 65 70 75 80  
 gag aag ctc acc ggc aag cag gtt gcc ctc aac atc ctc gag gtc aag 288  
 Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys  
 85 90 95  
 aac gtc gat gct aac gct aag ctg gtg gca cag tcc atc gct gag cag 336  
 Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln  
 100 105 110  
 ctg acc aac cgc gtg gca ttc cgt cgc gca atg cgc aag gct atc cag 384  
 Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln  
 115 120 125  
 tct gca atg cgt cag cca cag gtt aag ggc atc aag gtc gtg tgc tcc 432  
 Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser  
 130 135 140  
 ggt cgt ctc ggc ggt gcc gag atg tcc cgc acc gag cgc tac cac gaa 480  
 Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu  
 145 150 155 160  
 ggt cgc gtt cca ctg cac acc ctt cgc gca gaa atc gat tac ggc acc 528  
 Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr  
 165 170 175  
 tac gag gct cac acc act ttc gga cgc atc ggc gtc aag gtg tgg atc 576  
 Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile  
 180 185 190  
 tac aag ggt gac gtc gtt ggt gga cgt cgc gag agc gag atc aat gca 624

Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala  
 195 200 205

ccc gca gag cgt cgc ggc cgc ggc gac cgc aac gca cgt ccg cgt cgt 672  
 Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg  
 210 215 220

ggc ggc cag cgt cgt cag cgt gct gag cag aag cag gag ggc 714  
 Gly Gly Gln Arg Arg Gln Arg Ala Glu Gln Lys Gln Glu Gly  
 225 230 235

taaacatgct taticctaag cgc 737

<210> 362

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

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 20 25 30

Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg  
 35 40 45

Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile  
 50 55 60

Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu  
 65 70 75 80

Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys  
 85 90 95

Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln  
 100 105 110

Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln  
 115 120 125

Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser  
 130 135 140

Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu  
 145 150 155 160

Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr  
 165 170 175

Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile  
 180 185 190

Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala  
 195 200 205

Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg  
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Gly Gly Gln Arg Arg Gln Arg Ala Glu Gln Lys Gln Glu Gly  
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 Met Ala Arg Tyr Thr  
 1 5  
 ggc cca gca acc cgt aaa tcc cgt cgt ctg cgc gtc gac ctt gtt ggt 163  
 Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg Val Asp Leu Val Gly  
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 gga gac atg gcg ttt gag cgc cgt cct tac cct cca gga cag gca ggc 211  
 Gly Asp Met Ala Phe Glu Arg Arg Pro Tyr Pro Pro Gly Gln Ala Gly  
 25 30 35  
 cgt gca cgc atc aag gag tcc gag tac ctg ctg cag ctc cag gag aag 259  
 Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu Gln Leu Gln Glu Lys  
 40 45 50  
 cag aag gct cgt ttc atc tac ggc gtc atg gaa aag cag ttc cgt cgt 307  
 Gln Lys Ala Arg Phe Ile Tyr Gly Val Met Glu Lys Gln Phe Arg Arg  
 55 60 65  
 tac tac gcc gag gct aac cgt cgc gca ggc aag acc ggt gag aac ctg 355  
 Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys Thr Gly Glu Asn Leu  
 70 75 80 85  
 gtc gtc ctg ctc gag tcc cgc ctc gac aac gtc gtg tac cgc gca ggt 403  
 Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val Val Tyr Arg Ala Gly  
 90 95 100  
 ctg gca aac acc cgt cgc cag gct cgt cag ctt gtt tcc cac ggt cac 451  
 Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu Val Ser His Gly His  
 105 110 115  
 ttc acc gtg aac ggc aag gca atc gac gtt cca tct ttc cgc gtt tct 499  
 Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro Ser Phe Arg Val Ser  
 120 125 130  
 cag tac gac atc atc aat gtt cgt gag aag tcc cag aag atg aac tgg 547  
 Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser Gln Lys Met Asn Trp  
 135 140 145  
 ttc gaa gag gct cag gac aac ctg gcc gac gca gtc gtc cca gct tgg 595  
 Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala Val Val Pro Ala Trp  
 150 155 160 165

ctc cag gtc gtt cct gag aac ctt cgt atc ctc gtg cac cag ctc cca 643  
 Leu Gln Val Val Pro Glu Asn Leu Arg Ile Leu Val His Gln Leu Pro  
                   170                  175                  180

gag cgc gca cag atc gat atc cca ctg caa gag cag ctc atc gtc gag 691  
 Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu Gln Leu Ile Val Glu  
                   185                  190                  195

ttc tac tcg aag tagtttttgc ttaccgggct gcc 726  
 Phe Tyr Ser Lys  
                   200

<210> 364  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 364  
 Met Ala Arg Tyr Thr Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg  
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Val Asp Leu Val Gly Gly Asp Met Ala Phe Glu Arg Arg Pro Tyr Pro  
                   20                  25                  30

Pro Gly Gln Ala Gly Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu  
                   35                  40                  45

Gln Leu Gln Glu Lys Gln Lys Ala Arg Phe Ile Tyr Gly Val Met Glu  
                   50                  55                  60

Lys Gln Phe Arg Arg Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys  
                   65                  70                  75                  80

Thr Gly Glu Asn Leu Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val  
                   85                  90                  95

Val Tyr Arg Ala Gly Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu  
                   100                  105                  110

Val Ser His Gly His Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro  
                   115                  120                  125

Ser Phe Arg Val Ser Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser  
                   130                  135                  140

Gln Lys Met Asn Trp Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala  
                   145                  150                  155                  160

Val Val Pro Ala Trp Leu Gln Val Val Pro Glu Asn Leu Arg Ile Leu  
                   165                  170                  175

Val His Gln Leu Pro Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu  
                   180                  185                  190

Gln Leu Ile Val Glu Phe Tyr Ser Lys  
                   195                  200

<210> 365

cgc cct gaa gag gtt gca gcc cgc cgt ggc aag acc atc gaa gag gtc 691

Arg Pro Glu Glu Val Ala Ala Arg Arg Gly Lys Thr Ile Glu Glu Val  
 185 190 195

gca cca gca cgt att ctg cgt gca cgc gca ggt cag gag gcg 733  
 Ala Pro Ala Arg Ile Leu Arg Ala Arg Ala Gly Gln Glu Ala  
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taagaaatgg cgctgaagat tac 756

<210> 366

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Met Pro Gly Arg Glu Arg Arg Asp Gly Gly Arg Ser Ala Asp Asp Asn  
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Lys Gln Asn Asp Arg Asn Glu Arg Arg Gly Gly Gly Arg Arg Asp Asp  
 20 25 30

Arg Arg Asn Gln Gln Gln Asp Glu Arg Ser Gln Tyr Ile Glu Arg Val  
 35 40 45

Val Thr Ile Asn Arg Val Ser Lys Val Val Lys Gly Gly Arg Arg Phe  
 50 55 60

Ser Phe Thr Ala Leu Val Ile Val Gly Asp Gly Lys Gly Met Val Gly  
 65 70 75 80

Val Gly Tyr Gly Lys Ala Lys Glu Val Pro Ala Ala Ile Gln Lys Gly  
 85 90 95

Ala Glu Glu Ala Arg Lys Asn Phe Phe Arg Val Pro Met Val Asn Gly  
 100 105 110

Thr Ile Thr His Pro Val Gln Gly Glu Lys Ala Ala Gly Ile Val Met  
 115 120 125

Leu Lys Pro Ala Ala Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Ala  
 130 135 140

Arg Pro Val Leu Glu Cys Ala Gly Ile Gln Asp Ile Leu Ser Lys Ser  
 145 150 155 160

Leu Gly Ser Asp Asn Ala Ile Asn Val Val His Ala Thr Val Asp Gly  
 165 170 175

Leu Lys Gln Leu Val Arg Pro Glu Glu Val Ala Ala Arg Arg Gly Lys  
 180 185 190

Thr Ile Glu Glu Val Ala Pro Ala Arg Ile Leu Arg Ala Arg Ala Gly  
 195 200 205

Gln Glu Ala  
 210

<210> 367

<211> 390

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(367)

&lt;223&gt; RXN00545

&lt;400&gt; 367

gctgacgcaa cgaccctcct gctatgccaa cgacggcatg gccgaaaaaa caattactag 60

accataggag gtgatgaggt ccgtgcgta atacgaactt atg atc att ctc gat 115  
 Met Ile Ile Leu Asp  
 1 5

cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163  
 Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu  
 10 15 20

gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211  
 Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp  
 25 30 35

ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259  
 Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val  
 40 45 50

aac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307  
 Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu  
 55 60 65

gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355  
 Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu  
 70 75 80 85

gga ctc gac aag taaagaactt taaggctcta gag 390  
 Arg Leu Asp Lys

&lt;210&gt; 368

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 368

Met Ile Ile Leu Asp Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser  
 1 5 10 15

Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val  
 20 25 30

Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys  
 35 40 45

Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala  
 50 55 60

Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu  
 65 70 75 80

Arg Thr Lys Val Leu Arg Leu Asp Lys  
85

<210> 369  
<211> 355  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(355)  
<223> FRXA00545

<400> 369  
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accataggag gtgatgaggt ccgtgcgtca atacgaactt atg atc att ctc gat 115  
Met Ile Ile Leu Asp  
1 5  
cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163  
Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu  
10 15 20  
gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211  
Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp  
25 30 35  
ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259  
Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val  
40 45 50  
tac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307  
Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu  
55 60 65  
gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355  
Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu  
70 75 80 85

<210> 370  
<211> 85  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 370  
Met Ile Ile Leu Asp Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser  
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Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val  
20 25 30  
Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys  
35 40 45  
Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala  
50 55 60  
Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu



65

70

75

80

Arg Thr Lys Val Leu  
85

<210> 371  
<211> 588  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(565)  
<223> RXA01279

<400> 371  
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ggctcgttcc cgctacggcg cgaagagggg ataattaaatg cgt aaa tca gca 115  
Met Arg Lys Ser Ala  
1 5  
gct cct aag cgt cca gta gtt cag gac cct gta tac aag tcc gag ctc 163  
Ala Pro Lys Arg Pro Val Val Gln Asp Pro Val Tyr Lys Ser Glu Leu  
10 15 20  
gtt acc cag ctc gta aac aag atc ctc atc ggt ggc aag aag tcc acc 211  
Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly Gly Lys Lys Ser Thr  
25 30 35  
gca gag cgc atc gtc tac ggt gca ctc gag atc tgc cgt gag aag acc 259  
Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile Cys Arg Glu Lys Thr  
40 45 50  
ggc acc gat cca gta gga acc ctc gag aag gct ctc ggc aac gtg cgt 307  
Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala Leu Gly Asn Val Arg  
55 60 65  
cca gac ctc gaa gtt cgt tcc cgc cgt gtt ggt ggc gct acc tac cag 355  
Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly Gly Ala Thr Tyr Gln  
70 75 80 85  
gtg cca gtg gat gtt cgc cca gag cgc gca aac acc ctc gca ctg cgt 403  
Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn Thr Leu Ala Leu Arg  
90 95 100  
tgg ttg gta acc ttc acc cgt cag cgt cgt gag aac acc atg atc gag 451  
Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu Asn Thr Met Ile Glu  
105 110 115  
cgt ctt gca aac gaa ctt ctg gat gca gcc aac ggc ctt ggc gct tcc 499  
Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn Gly Leu Gly Ala Ser  
120 125 130  
gtg aag cgt cgc gaa gac acc cac aag atg gca gag gcc aac cgc gcc 547  
Val Lys Arg Arg Glu Asp Thr His Lys Met Ala Glu Ala Asn Arg Ala  
135 140 145  
ttc gct cac tac cgc tgg tagtactgcc aagacatgaa agc 588  
Phe Ala His Tyr Arg Trp

150

155

&lt;210&gt; 372

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 372

Met Arg Lys Ser Ala Ala Pro Lys Arg Pro Val Val Gln Asp Pro Val  
 1 5 10 15

Tyr Lys Ser Glu Leu Val Thr Gln Leu Val Asn Lys Ile Leu Ile Gly  
 20 25 30

Gly Lys Lys Ser Thr Ala Glu Arg Ile Val Tyr Gly Ala Leu Glu Ile  
 35 40 45

Cys Arg Glu Lys Thr Gly Thr Asp Pro Val Gly Thr Leu Glu Lys Ala  
 50 55 60

Leu Gly Asn Val Arg Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly  
 65 70 75 80

Gly Ala Thr Tyr Gln Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn  
 85 90 95

Thr Leu Ala Leu Arg Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu  
 100 105 110

Asn Thr Met Ile Glu Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn  
 115 120 125

Gly Leu Gly Ala Ser Val Lys Arg Arg Glu Asp Thr His Lys Met Ala  
 130 135 140

Glu Ala Asn Arg Ala Phe Ala His Tyr Arg Trp  
 145 150 155

&lt;210&gt; 373

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(496)

&lt;223&gt; RXA00694

&lt;400&gt; 373

cgactattga gttcgggtgag cggttgagtg ccagaaaaca cacgggttaac gtccaaggtg 60

ggaaggggaac cccaacgaga aaggcatcag gtcgtctcta atg aca atg act gat 115  
 Met Thr Met Thr Asp  
 1 5

cca atc gcc gac atg ctg tcg cgc gtg cgc aat gct agc aat gcg cac 163  
 Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn Ala Ser Asn Ala His  
 10 15 20

cac gac acc gtg tcc atg cca tcc tcc aag atc aag gca aac atc gcc 211  
 His Asp Thr Val Ser Met Pro Ser Ser Lys Ile Lys Ala Asn Ile Ala  
 25 30 35  
 gag atc ttg aag cag gaa ggc tac atc gct aac tac acc gtt gag gat 259  
 Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn Tyr Thr Val Glu Asp  
 40 45 50  
 gca aag gtc ggc aag acc ctg tcc ctc gag ctg aag tac agc aac acc 307  
 Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu Lys Tyr Ser Asn Thr  
 55 60 65  
 cgt gag cgc tcc atc gct ggt ctg cgc cgc gtt tcc aag cct ggt ctg 355  
 Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val Ser Lys Pro Gly Leu  
 70 75 80 85  
 cgt gta tac gct aag tcc acc aat ctg cca cag gtt ctg ggc ggc ctt 403  
 Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln Val Leu Gly Gly Leu  
 90 95 100  
 ggc gtg gct atc att tcc acg tca cag ggc ctc ctg acc gac cgt cag 451  
 Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu Leu Thr Asp Arg Gln  
 105 110 115  
 gct acc gag aag ggc gta ggc gga gaa gtc ctc gcc tac gtc tgg 496  
 Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu Ala Tyr Val Trp  
 120 125 130  
 taatagggag gattgactaa ata 519

&lt;210&gt; 374

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 374

Met Thr Met Thr Asp Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn  
 1 5 10 15  
 Ala Ser Asn Ala His His Asp Thr Val Ser Met Pro Ser Ser Lys Ile  
 20 25 30  
 Lys Ala Asn Ile Ala Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn  
 35 40 45  
 Tyr Thr Val Glu Asp Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu  
 50 55 60  
 Lys Tyr Ser Asn Thr Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val  
 65 70 75 80  
 Ser Lys Pro Gly Leu Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln  
 85 90 95  
 Val Leu Gly Gly Leu Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu  
 100 105 110  
 Leu Thr Asp Arg Gln Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu  
 115 120 125

Ala Tyr Val Trp  
130

<210> 375  
<211> 492  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(469)  
<223> RXN02038

<400> 375  
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agaagcctga ggcctacgag atcaagaagg tggcccagta atg tca gag cct atc 115  
Met Ser Glu Pro Ile  
1 5  
cag aac gag aac gta gag agc aac gtc gca gac gct gct gac atc gct 163  
Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp Ala Ala Asp Ile Ala  
10 15 20  
gca gca acc gct gca acc gag gag ttc acc aac acc atc ggc gat gca 211  
Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn Thr Ile Gly Asp Ala  
25 30 35  
att gct act gct tcc gaa gaa gag acc atc gag gct gca cca gta gta 259  
Ile Ala Thr Ala Ser Glu Glu Thr Ile Glu Ala Ala Pro Val Val  
40 45 50  
ctc gac ggc cca atc cag acc gtt ggt cgc cgt aag cgc gcc atc gtt 307  
Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg Lys Arg Ala Ile Val  
55 60 65  
cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc 355  
Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg  
70 75 80 85  
acc ctg gaa gag tac ttc cct aac aag ctg cac cag cag ctg atc aag 403  
Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His Gln Gln Leu Ile Lys  
90 95 100  
gct cct ttg gtc ctt ctg gac cgc ctg aac caa tgc aac atc gag gct 451  
Ala Pro Leu Val Leu Leu Asp Arg Leu Asn Gln Cys Asn Ile Glu Ala  
105 110 115  
tct ata aag gga cct aaa tagatcggcc aggttatggc aat 492  
Ser Ile Lys Gly Pro Lys  
120

<210> 376  
<211> 123  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 376  
Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp

cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc 355  
 Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg  
 70 75 80 85

gct cct  
Ala Pro

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<400> 378
Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp
   1                               10                          15
Ala Ala Asp Ile Ala Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn
      20                      25                          30
Thr Ile Gly Asp Ala Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu
     35                    40                        45
Ala Ala Pro Val Val Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg
    50                55              60
Lys Arg Ala Ile Val Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe
   65                70              75              80
Lys Cys Asn Gly Arg Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His
      85                    90              95
Gln Gln Leu Ile Lys Ala Pro
      100
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<220>  
<221> CDS  
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<223> RXA01287
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caaaatggaa gatgtgggac gagcggaggaa gaggataagc gtg gcg gga caa aag 115
Val Ala Gly Gln Lys
1 5

atc cgc att agg ctc aag gcc tac gac cac gaa gcg att gat gcg tct 163
Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu Ala Ile Asp Ala Ser
10 15 20

gca cgc aag atc gtt gag acg gtc acc cgt acg ggt gcc cga gtc gtt 211
Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr Gly Ala Arg Val Val
25 30 35

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gga ccg gtg cct ttg cct acc gaa aag aac gta tac gcc gtt att cgt 259  
 Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val Tyr Ala Val Ile Arg  
           40                    45                    50  
  
 tct cca cat aag tac aag gac tct cgc gag cac ttc gag atg cgc act 307  
 Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His Phe Glu Met Arg Thr  
           55                    60                    65  
  
 cac aag cgc ctg atc gac atc ctc gac ccg acg ccg aag act gtt gat 355  
 His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr Pro Lys Thr Val Asp  
           70                    75                    80                    85  
  
 gcc ctt atg cgc atc gac ctt ccg gcc agc gtc gac gtg aac att cag 403  
 Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val Asp Val Asn Ile Gln  
                     90                    95                    100  
  
 tgatcgacgg aatttttggc agc 426

<210> 380  
 <211> 101  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 380  
 Val Ala Gly Gln Lys Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu  
       1                    5                    10                    15  
  
 Ala Ile Asp Ala Ser Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr  
           20                    25                    30  
  
 Gly Ala Arg Val Val Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val  
           35                    40                    45  
  
 Tyr Ala Val Ile Arg Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His  
           50                    55                    60  
  
 Phe Glu Met Arg Thr His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr  
           65                    70                    75                    80  
  
 Pro Lys Thr Val Asp Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val  
                     85                    90                    95  
  
 Asp Val Asn Ile Gln  
           100

<210> 381  
 <211> 113  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(90)  
 <223> RXA00673

<400> 381  
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 Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp Val Thr Pro

1 5 10 15

cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc gtt 90  
 Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val  
 20 25 30

taatagggaa ggaaaggtaa tac 113

<210> 382  
 <211> 30  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 382  
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 1 5 10 15

Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val  
 20 25 30

<210> 383  
 <211> 489  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(466)  
 <223> RXA01280

<400> 383  
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 Met Pro Thr Ile Gln  
 1 5

cag ctg gtc cgt aag gcc cgc cac gat aag tcc gac aag gtg gct acc 163  
 Gln Leu Val Arg Lys Ala Arg His Asp Lys Ser Asp Lys Val Ala Thr  
 10 15 20

gcg gca ctg aag ggt tcc cct cag cgt cgt ggc gta tgc acc cgt gtg 211  
 Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly Val Cys Thr Arg Val  
 25 30 35

tac acc acc acc cct aag aag cct aac tct gct ctt cgt aag gtc gct 259  
 Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala Leu Arg Lys Val Ala  
 40 45 50

cgt gtg cgc ctt acc tcc ggc atc gag gtt tcc gct tac atc cct ggt 307  
 Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly  
 55 60 65

gag ggc cac aac ctg cag gag cac tcc atg gtg ctc gtt cgc ggt ggt 355  
 Glu Gly His Asn Leu Gln Glu His Ser Met Val Leu Val Arg Gly Gly  
 70 75 80 85

cgt gtt aag gac ctc cca ggt gtc cgt tac aag atc gtc cgt ggc gca 403  
 Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys Ile Val Arg Gly Ala



90 95 100  
 ctg gat acc cag ggt gtt aag gac cgc aag cag gct cgt tcc cgc tac 451  
 Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln Ala Arg Ser Arg Tyr  
 105 110 115

ggc gcg aag agg gga taattaaaaa tgcgtaaatac agc 489  
 Gly Ala Lys Arg Gly  
 120

<210> 384  
 <211> 122  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 384  
 Met Pro Thr Ile Gln Gln Leu Val Arg Lys Ala Arg His Asp Lys Ser  
 1 5 10 15  
 Asp Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly  
 20 25 30  
 Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala  
 35 40 45  
 Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser  
 50 55 60  
 Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val  
 65 70 75 80  
 Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys  
 85 90 95  
 Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln  
 100 105 110  
 Ala Arg Ser Arg Tyr Gly Ala Lys Arg Gly  
 115 120

<210> 385  
 <211> 426  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(403)  
 <223> RXA02637

<400> 385  
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 agtcogtaag cacgtcgaat tccgcgagga gcgataatca atg gct aag aag tca 115  
 Met Ala Lys Lys Ser  
 1 5  
 aag atc gcc aag aac gag aag cgc aag gaa atc gtc gcc cgc tac gcg 163  
 Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile Val Ala Arg Tyr Ala

	10	15	20	
gag cgt cgc gct gag ctc aag gca att atc agt aac cca aac acc tct				211
Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser Asn Pro Asn Thr Ser				
	25	30	35	
gac gag gat cgt ctg gat gca cag ttc gaa ctg aac agc cag cca cgt				259
Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu Asn Ser Gln Pro Arg				
	40	45	50	
gat gct gct gct gtc cgc gtt cgt aac cgc gac tca cac gat ggt cgc				307
Asp Ala Ala Ala Val Arg Val Arg Asn Arg Asp Ser His Asp Gly Arg				
	55	60	65	
cca cgc ggc tac ctc cgt aag ttc ggt ctt tcc cgt gtc cgt atg cgc				355
Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser Arg Val Arg Met Arg				
	70	75	80	85
gag atg gct cac cgt ggt gag ctg ccg ggc gtt cgt aag tcc agc tgg				403
Glu Met Ala His Arg Gly Glu Leu Pro Gly Val Arg Lys Ser Ser Trp				
	90	95	100	
taagggagtt ttaccaatg aag				426

&lt;210&gt; 386

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 386

Met	Ala	Lys	Lys	Lys	Lys	Ile	Ala	Lys	Asn	Glu	Lys	Arg	Lys	Glu	Ile
1				5					10					15	

Val	Ala	Arg	Tyr	Ala	Glu	Arg	Arg	Ala	Glu	Leu	Lys	Ala	Ile	Ile	Ser
		20						25					30		

Asn	Pro	Asn	Thr	Ser	Asp	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Phe	Glu	Leu
		35					40					45			

Asn	Ser	Gln	Pro	Arg	Asp	Ala	Ala	Ala	Val	Arg	Val	Arg	Asn	Arg	Asp
	50					55				60					

Ser	His	Asp	Gly	Arg	Pro	Arg	Gly	Tyr	Leu	Arg	Lys	Phe	Gly	Leu	Ser
65					70				75					80	

Arg	Val	Arg	Met	Arg	Glu	Met	Ala	His	Arg	Gly	Glu	Leu	Pro	Gly	Val
			85					90					95		

Arg	Lys	Ser	Ser	Trp
				100

&lt;210&gt; 387

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(367)

[illegible]

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<210> 388
<211> 89
<212> PRT
<213> Corynebacterium glutamicum
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<400> 388
Met Ala Leu Thr Ser Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly
  1                      5                      10                      15
Leu His Glu Thr Asp Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu
          20                      25                      30
Thr Asn Arg Ile Asn Asn Leu Thr Glu His Leu Lys Phe His Lys His
      35                      40                      45
Asp His His Ser Arg Arg Gly Leu Leu Leu Leu Val Gly Arg Arg Arg
    50                      55                      60
Gly Leu Leu Lys Tyr Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp
  65                      70                      75                      80
Leu Ile Ala Arg Leu Gly Leu Arg Arg
          85

```

$\langle 210 \rangle$	389
$\langle 211 \rangle$	618

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(595)

&lt;223&gt; RXA02752

&lt;400&gt; 389

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ccggaggagt cacgcgcagg ttaaacaaga agggctgaac cggctcacca gcacacggtg 60

agtgactgta ctgcccagtg acctagtgag gaaaattcac atg gct gta aag att 115
                               Met Ala Val Lys Ile
                               1 5

aag ctc cag cgc ctc ggc aag atc cgt acc ccg cac tac cgc gtt gtc 163
Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro His Tyr Arg Val Val
                               10 15 20

atc gct gat gca cgc acc aag cgc gac ggc aag gtt atc gag aac atc 211
Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys Val Ile Glu Asn Ile
                               25 30 35

ggt atc tac gag cca aag gct gag cct tcc gta atc aag atc aac tcc 259
Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val Ile Lys Ile Asn Ser
                               40 45 50

gag cgt gcg cag cac tgg ctc tcc gtt ggc gct cag cca acc gag gct 307
Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala Gln Pro Thr Glu Ala
                               55 60 65

gtt gca gcg ctg ctc aag gtg acc ggc gac tgg cag aag ttc aag ggc 355
Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp Gln Lys Phe Lys Gly
                               70 75 80 85

atc gag ggc gca gaa ggc acc ctc cgt gtt gca gag cct aag cca tcc 403
Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala Glu Pro Lys Pro Ser
                               90 95 100

aag ctt gag ctg ttc aac cag gct ctt tct gag gct aac aac ggc cca 451
Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu Ala Asn Asn Gly Pro
                               105 110 115

acc gct gaa gcc atc act gaa aag aag aag aag gct cgc gag gac aag 499
Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys Ala Arg Glu Asp Lys
                               120 125 130

gaa gct aag gaa gca gct gag aag gct gct gct gaa aag gct gcc gct 547
Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala
                               135 140 145

gca gag tcc gaa gag gct cca gct gag gaa gct gct gca gaa gag gca 595
Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala Ala Ala Glu Glu Ala
                               150 155 160 165

taagccactt ttgtttgtac ttc 618

```

&lt;210&gt; 390

&lt;211&gt; 165

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 390

Met Ala Val Lys Ile Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro  
1 5 10 15

His Tyr Arg Val Val Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys  
20 25 30

Val Ile Glu Asn Ile Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val  
35 40 45

Ile Lys Ile Asn Ser Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala  
50 55 60

Gln Pro Thr Glu Ala Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp  
65 70 75 80

Gln Lys Phe Lys Gly Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala  
85 90 95

Glu Pro Lys Pro Ser Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu  
100 105 110

Ala Asn Asn Gly Pro Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys  
115 120 125

Ala Arg Glu Asp Lys Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala  
130 135 140

Glu Lys Ala Ala Ala Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala  
145 150 155 160

Ala Ala Glu Glu Ala  
165

<210> 391

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXA02389

<400> 391

gttgcaacttt atgccaagca gtttatttaa aactgcggga gaaacactcc tcgatggggtt 60

tgtacacaac tttaactaga aagttcaaga ggtatttgcg atg gca aac atc aag 115  
Met Ala Asn Ile Lys  
1 5

tct cag atc aag cgt aac aag acc aac gag aag gct cgt ctg cgt aac 163  
Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys Ala Arg Leu Arg Asn  
10 15 20

cag gca gtt cgc tcc gca gtc cgc acc gag atc cgc aag ttc aac gct 211  
Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile Arg Lys Phe Asn Ala  
25 30 35

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<210> 392
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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<210> 393
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum
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<400> 393
gccccgggtg cacaggaatc tttcgatttt ccaaacatcc ttcatggttt tagaaacctt 60

taccgacgtc aaatagcggg cgctactcaa ggagagttca atg ctc att tca cag 115
                                     Met Leu Ile Ser Gln
                                     1           5

cgc cca acc atc acc gag gaa ttt gtt aat aac gca cgt tcc cgg ttt 163

```

Arg	Pro	Thr	Ile	Thr	Glu	Glu	Phe	Val	Asn	Asn	Ala	Arg	Ser	Arg	Phe		
				10					15					20			
gtc	atc	gag	cca	ctg	gag	cca	ggg	ttt	ggc	tac	acc	ctc	ggg	aac	tcc		211
Val	Ile	Glu	Pro	Leu	Glu	Pro	Gly	Phe	Gly	Tyr	Thr	Leu	Gly	Asn	Ser		
				25				30					35				
ctg	cgc	cgt	acc	ctg	ctg	tcc	tcc	att	cct	gga	gca	gca	gta	acc	agc		259
Leu	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ile	Pro	Gly	Ala	Ala	Val	Thr	Ser		
				40				45					50				
gtc	aag	att	gac	ggg	gta	ctc	cac	gag	ttc	acc	acc	atc	agc	ggg	gtt		307
Val	Lys	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Thr	Thr	Ile	Ser	Gly	Val		
				55			60					65					
aag	gaa	gat	gtc	tct	gac	atc	atc	ttg	aac	atc	aag	gga	ttg	gtt	ttg		355
Lys	Glu	Asp	Val	Ser	Asp	Ile	Ile	Leu	Asn	Ile	Lys	Gly	Leu	Val	Leu		
				70			75			80					85		
tct	tct	gat	tcc	gat	gag	cca	gtt	gtt	atg	cag	ctg	gtc	aag	gaa	ggc		403
Ser	Ser	Asp	Ser	Asp	Glu	Pro	Val	Val	Met	Gln	Leu	Val	Lys	Glu	Gly		
				90					95					100			
cca	gga	gtt	gta	act	gca	ggg	gac	att	cag	cca	cca	gca	ggc	gtg	gag		451
Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Gly	Val	Glu		
				105				110						115			
atc	cac	aac	ccg	gat	ctg	cac	att	gca	acc	ctg	aac	gag	acc	gcc	aag		499
Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu	Asn	Glu	Thr	Ala	Lys		
				120			125					130					
att	gag	atc	gag	ctc	atc	gtc	gag	cgt	gga	cgt	ggc	tac	gtt	ccc	gca		547
Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala		
				135			140					145					
act	gtt	act	gca	acc	ggg	gga	gag	atc	ggc	cgc	att	ccg	gtc	gat	cag		595
Thr	Val	Thr	Ala	Thr	Gly	Gly	Glu	Ile	Gly	Arg	Ile	Pro	Val	Asp	Gln		
				150			155			160					165		
atc	tac	tcc	cca	gta	ctg	aag	gtc	agc	tac	aag	gtt	gaa	gct	act	cgt		643
Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Ser	Tyr	Lys	Val	Glu	Ala	Thr	Arg		
				170				175						180			
gtt	gag	cag	cgc	acc	gac	ttt	gac	aag	ctg	gtc	atc	gac	gtt	gag	acc		691
Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu	Val	Ile	Asp	Val	Glu	Thr		
				185				190					195				
aag	aac	tct	att	acc	gca	cgt	gac	gcc	ctg	gcg	tcg	gca	ggg	aag	acc		739
Lys	Asn	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Leu	Ala	Ser	Ala	Gly	Lys	Thr		
				200			205					210					
ctg	gtt	gag	ctg	ttc	ggc	ctc	gca	cgc	gag	ctg	aac	atc	gca	gcc	gag		787
Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu	Leu	Asn	Ile	Ala	Ala	Glu		
				215			220				225						
ggc	atc	gag	atc	gga	cca	tct	cct	cag	gag	acc	gag	tac	atc	gct	gcc		835
Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Gln	Glu	Thr	Glu	Tyr	Ile	Ala	Ala		
				230			235			240					245		
tac	agc	atg	cca	atc	gag	gat	ctg	gac	ttc	tct	gtc	cgt	tcc	tac	aac		883
Tyr	Ser	Met	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Ser	Val	Arg	Ser	Tyr	Asn		

250	255	260	
tgc ctc aag cgc gaa gac atc cac acc gtg ggt gaa ctc gca gag cgc			931
Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly Glu Leu Ala Glu Arg			
265	270	275	
gct gag tcc gat ttg ctg gat atc cgc aac ttc gga cag aag tcg atc			979
Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe Gly Gln Lys Ser Ile			
280	285	290	
aac gag gta aag atc aag ctt gct ggc ctg ggt ctg acc ctg aag gat			1027
Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly Leu Thr Leu Lys Asp			
295	300	305	
gct cct gaa gac ttc gat cct tca act ctt gaa ggt tat gac gcc gaa			1075
Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu Gly Tyr Asp Ala Glu			
310	315	320	325
act ggt ggc tac atc gat gtc gag gcg gaa gat tcc gag taagtcgcat			1124
Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp Ser Glu			
330	335		
ggtccaattc atg			1137
<210> 394			
<211> 338			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 394			
Met Leu Ile Ser Gln Arg Pro Thr Ile Thr Glu Glu Phe Val Asn Asn			
1	5	10	15
Ala Arg Ser Arg Phe Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr			
20	25	30	
Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly			
35	40	45	
Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr			
50	55	60	
Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile			
65	70	75	80
Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln			
85	90	95	
Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro			
100	105	110	
Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu			
115	120	125	
Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg			
130	135	140	
Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg			
145	150	155	160



Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys  
165 170 175

Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val  
180 185 190

Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala  
195 200 205

Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu  
210 215 220

Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr  
225 230 235 240

Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser  
245 250 255

Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly  
260 265 270

Glu Leu Ala Glu Arg Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe  
275 280 285

Gly Gln Lys Ser Ile Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly  
290 295 300

Leu Thr Leu Lys Asp Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu  
305 310 315 320

Gly Tyr Asp Ala Glu Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp  
325 330 335

Ser Glu

<210> 395

<211> 489

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(466)

<223> RXN02981

<400> 395

aatcacaatc cacctcccgg tttccgtccg gggaaagtat tgcttggcag gggcgattat 60

ggggaaaacc atcgcaacaa ccggaaggg taactgccac atg gca cgt cta gct 115  
Met Ala Arg Leu Ala  
1 5

ggt gtt gac ctc cca cgc aac aag cgt atg gaa gtc gct ctc acc tac 163  
Gly Val Asp Leu Pro Arg Asn Lys Arg Met Glu Val Ala Leu Thr Tyr  
10 15 20

atc tac gga atc ggc cca gcc cgt tcc aag cag ctt ctc gag gag acc 211  
Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln Leu Leu Glu Glu Thr  
25 30 35

gga atc tcc cca gac ctg cgc acc gac aac ctc act gat gag cag atc 259  
 Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu Thr Asp Glu Gln Ile  
 40 45 50  
 gct gct ctt cgt gac gtt att gaa ggc acc tgg aag gtc gag ggt gac 307  
 Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp Lys Val Glu Gly Asp  
 55 60 65  
 ctc cgc cgc cag gta caa gct gac atc cgt cgc aag atc gaa atc ggc 355  
 Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg Lys Ile Glu Ile Gly  
 70 75 80 85  
 tgc tac cag ggt att cgc cac cgc cgt ggc ctg cct gtt cgt ggt cag 403  
 Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu Pro Val Arg Gly Gln  
 90 95 100  
 cgc acc aag acc aat gcg cgt act cgt aag ggt cct aag aag acg atc 451  
 Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro Lys Lys Thr Ile  
 105 110 115  
 gcc gga aag aag aag taaaaatgcc tcctaaagca cgc 489  
 Ala Gly Lys Lys Lys  
 120

<210> 396  
 <211> 122  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 396  
 Met Ala Arg Leu Ala Gly Val Asp Leu Pro Arg Asn Lys Arg Met Glu  
 1 5 10 15  
 Val Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln  
 20 25 30  
 Leu Leu Glu Glu Thr Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu  
 35 40 45  
 Thr Asp Glu Gln Ile Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp  
 50 55 60  
 Lys Val Glu Gly Asp Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg  
 65 70 75 80  
 Lys Ile Glu Ile Gly Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu  
 85 90 95  
 Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly  
 100 105 110  
 Pro Lys Lys Thr Ile Ala Gly Lys Lys Lys  
 115 120

<210> 397  
 <211> 372  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(349)

&lt;223&gt; RXN03139

&lt;400&gt; 397

tccgtaagtt cgggtctttcc cgtgtccgta tgcgcgagat ggctcacctg ggtgagctgc 60

cgggcggttcg taagtccagc tggtaaggga gtttttacca atg aag cag cgt aac 115  
Met Lys Gln Arg Asn  
1 5

aac gct aag cgc gtc cgc ctt gag cag act cgc cgc cca aag aag aac 163  
Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg Arg Pro Lys Lys Asn  
10 15 20

ccg ctg aag gca gcg ggc atc gag aag gtg gac tac aag gac atc aac 211  
Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp Tyr Lys Asp Ile Asn  
25 30 35

acc ctt cgt cag ttc atc tcc gac cgc cac aag atc cgt tca cgt cgt 259  
Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys Ile Arg Ser Arg Arg  
40 45 50

gtc acc ggt ctg acc ccg cag cag cag cgc gag gtt gca acc gcc gtg 307  
Val Thr Gly Leu Thr Pro Gln Gln Gln Arg Glu Val Ala Thr Ala Val  
55 60 65

aag aac gca cgc gaa atg gct ctc ctg ccg ttc acc agc cgc 349  
Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe Thr Ser Arg  
70 75 80

taagactggg aataacgtaa cag 372

&lt;210&gt; 398

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398

Met Lys Gln Arg Asn Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg  
1 5 10 15

Arg Pro Lys Lys Asn Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp  
20 25 30

Tyr Lys Asp Ile Asn Thr Leu Arg Gln Phe Ile Ser Asp Arg His Lys  
35 40 45

Ile Arg Ser Arg Arg Val Thr Gly Leu Thr Pro Gln Gln Gln Arg Glu  
50 55 60

Val Ala Thr Ala Val Lys Asn Ala Arg Glu Met Ala Leu Leu Pro Phe  
65 70 75 80

Thr Ser Arg

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<220>
<221> CDS
<222> (101)..(502)
<223> RXN00673
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[illegible]

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<210> 400
<211> 134
<212> PRT
<213> Corynebacterium glutamicum
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<400> 400  
Met Pro Pro Lys Ala Arg Thr Asn Ala Arg Arg Thr Gly Arg Arg Val

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<210> 401
<211> 684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(661)
<223> RXN00714
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<400> 401																
cgtcaatcaa	gctgtcaaaa	aaaataacaag	ttagggtcaca	aaatgatttc	agtcgtgaga											60
accatcacat					ataagacatc	tcatgatcta	acattttcttc	atg	gct	acg	att	aca				115
								Met	Ala	Thr	Ile	Thr				
								1								5
cgc	acc	gac	aga	ctg	atc	ctc	gta	ccg	ctc	act	gtt	gag	ctc	gaa	gac	163
Arg	Thr	Asp	Arg	Leu	Ile	Leu	Val	Pro	Leu	Thr	Val	Glu	Leu	Glu	Asp	
				10			15					20				
gag	gcc	cac	cag	att	tac	tct	gat	tct	cga	atc	tgg	gaa	cac	cgc	ccc	211
Glu	Ala	His	Gln	Ile	Tyr	Ser	Asp	Ser	Arg	Ile	Trp	Glu	His	Arg	Pro	
				25			30					35				
cag	gcg	cgt	cac	acc	aac	gtg	cgt	gtc	acg	cgc	gac	atc	atc	aag	cgc	259
Gln	Ala	Arg	His	Thr	Asn	Val	Arg	Val	Thr	Arg	Asp	Ile	Ile	Lys	Arg	
				40			45					50				
acc	aat	gaa	agc	tgg	ggc	aag	aaa	gac	ctt	ggc	ccc	tgg	ggt	gtt	tac	307
Thr	Asn	Glu	Ser	Trp	Gly	Lys	Lys	Asp	Leu	Gly	Pro	Trp	Gly	Val	Tyr	
				55			60					65				
ctc	cgt	gac	cgc	cca	tcg	gaa	ttc	gtt	ggc	gtt	ggt	ggc	gtt	gaa	ctc	355

Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu  
 70 75 80 85  
 atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta 403  
 Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu  
 90 95 100  
 tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc 451  
 Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala  
 105 110 115  
 acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc 499  
 Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr  
 120 125 130  
 aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc 547  
 Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro  
 135 140 145  
 gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct 595  
 Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro  
 150 155 160 165  
 gat gtg aga att tat tct gac cgt ccg cta tcg gat gaa att ctt gaa 643  
 Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser Asp Glu Ile Leu Glu  
 170 175 180  
 atg ctc aag caa cga cca tagaccagaa aatctcaccc ctt 684  
 Met Leu Lys Gln Arg Pro  
 185

&lt;210&gt; 402

&lt;211&gt; 187

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 402

Met Ala Thr Ile Thr Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr  
 1 5 10 15  
 Val Glu Leu Glu Asp Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile  
 20 25 30  
 Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg  
 35 40 45  
 Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly  
 50 55 60  
 Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val  
 65 70 75 80  
 Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg  
 85 90 95  
 Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn  
 100 105 110  
 Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr  
 115 120 125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys  
130 135 140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp  
145 150 155 160

Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser  
165 170 175

Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro  
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<210> 403

<211> 1128

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1105)

<223> RXN00897

<400> 403

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ttgacctgga tgccgggtga agatgaggat cctttcgggc atg acg cct agt ctt 115  
Met Thr Pro Ser Leu  
1 5

ccc cgt ttc cgc agc cag aaa cct gcc gtc ggc gat cgt gtt gtt gca 163  
Pro Arg Phe Arg Ser Gln Lys Pro Ala Val Gly Asp Arg Val Val Ala  
10 15 20

cgt cgc cgg att cct ggt gcc aat gtg cat tgg aca gat gtc att ggc 211  
Arg Arg Arg Ile Pro Gly Ala Asn Val His Trp Thr Asp Val Ile Gly  
25 30 35

cat gtg att ggg gtg gat ccg ttg gtg gtt cgc ccg cag tcg gtt ggt 259  
His Val Ile Gly Val Asp Pro Leu Val Val Arg Pro Gln Ser Val Gly  
40 45 50

ggg atg ccg tct gat gcg gaa gaa att gtc att cct gat gat cag ctt 307  
Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile Pro Asp Asp Gln Leu  
55 60 65

gag gtg att aag att ttg tcg ccg cgc acc att agg aat tcg gat att 355  
Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile Arg Asn Ser Asp Ile  
70 75 80 85

cgt gcg gtg gag gtt gcc acg gcg aag gcc ttt ccg ggg ctg gtc aat 403  
Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe Pro Gly Leu Val Asn  
90 95 100

gag tgg cat gat ggt tgg ctg ctg cgt gcc ggt gat ggc att gcg gag 451  
Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly Asp Gly Ile Ala Glu  
105 110 115

cgt tct aat tct gcg tcg cca ctc gcc cca agt gtc ggt tct gag ccg 499  
Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser Val Gly Ser Glu Pro

120	125	130	
gta ccg atg gag gat att tcg cgg ttt tat gca cgt cac gat ctc ccc			547
Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala Arg His Asp Leu Pro			
135	140	145	
gtg aag ctg cac att ccg gag cgg att ggt cgg cct gcg cag aaa gtc			595
Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg Pro Ala Gln Lys Val			
150	155	160	165
att gac gcc gat ccc cag aaa tgg gtg atg ggc ccg gag att ttg gtg			643
Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly Pro Glu Ile Leu Val			
170	175	180	
atg acg aaa tct ttg gac cat gtg gag tcg cac gaa ttg ccc ggt ggc			691
Met Thr Lys Ser Leu Asp His Val Glu Ser His Glu Leu Pro Gly Gly			
185	190	195	
cta gaa ttt agc gtc gat aag cag cct gac cag gag tgg ctg ggc atg			739
Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln Glu Trp Leu Gly Met			
200	205	210	
tac cat ttc cgc gga cag gcg ttg ccc gct cac gcc ctt gag ctt ttg			787
Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His Ala Leu Glu Leu Leu			
215	220	225	
cgc acg caa atc gag ggc cgc atg ggg ttc ggg cgc ctg acc acg ccg			835
Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly Arg Leu Thr Thr Pro			
230	235	240	245
gcg ggg caa acc gtc gcg atc acg cgc gcc acc atc acg gct gcg gag			883
Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr Ile Thr Ala Ala Glu			
250	255	260	
gag cgc ata ttt ttg ggc tat tca gcg gtc gag gtg gat cct gct ttt			931
Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu Val Asp Pro Ala Phe			
265	270	275	
cga cgt cag ggg ctg ggc acc gcg ctc ggc tcg cgc atc cag gag tgg			979
Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser Arg Ile Gln Glu Trp			
280	285	290	
ggc gcc gag caa cac gca cag gag gca tat ctc cag gtt gtc gcc cat			1027
Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu Gln Val Val Ala His			
295	300	305	
aat gaa gca ggt atc ggc ctg tat caa aag ctc ggg ttc agt gaa cac			1075
Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu Gly Phe Ser Glu His			
310	315	320	325
cac cga cac cgg tac gcc gaa cgg aaa ttc taaaatccaa aacagctagg			1125
His Arg His Arg Tyr Ala Glu Arg Lys Phe			
330	335		
gta			1128

&lt;210&gt; 404

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 404

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Met Thr Pro Ser Leu Pro Arg Phe Arg Ser Gln Lys Pro Ala Val Gly
 1              5              10              15

Asp Arg Val Val Ala Arg Arg Arg Ile Pro Gly Ala Asn Val His Trp
      20              25              30

Thr Asp Val Ile Gly His Val Ile Gly Val Asp Pro Leu Val Val Arg
      35              40              45

Pro Gln Ser Val Gly Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile
      50              55              60

Pro Asp Asp Gln Leu Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile
      65              70              75              80

Arg Asn Ser Asp Ile Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe
      85              90              95

Pro Gly Leu Val Asn Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly
      100              105              110

Asp Gly Ile Ala Glu Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser
      115              120              125

Val Gly Ser Glu Pro Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala
      130              135              140

Arg His Asp Leu Pro Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg
      145              150              155              160

Pro Ala Gln Lys Val Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly
      165              170              175

Pro Glu Ile Leu Val Met Thr Lys Ser Leu Asp His Val Glu Ser His
      180              185              190

Glu Leu Pro Gly Gly Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln
      195              200              205

Glu Trp Leu Gly Met Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His
      210              215              220

Ala Leu Glu Leu Leu Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly
      225              230              235              240

Arg Leu Thr Thr Pro Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr
      245              250              255

Ile Thr Ala Ala Glu Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu
      260              265              270

Val Asp Pro Ala Phe Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser
      275              280              285

Arg Ile Gln Glu Trp Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu
      290              295              300

Gln Val Val Ala His Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu
      305              310              315              320

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Gly Phe Ser Glu His His Arg His Arg Tyr Ala Glu Arg Lys Phe  
 325 330 335

<210> 405

<211> 2322

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2299)

<223> RXN01380

<400> 405

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cggcgtcaaaa gatgaacaag tcgaggccgc catcaagctc ttg gat gaa gga aac 115  
 Leu Asp Glu Gly Asn  
 1 5

acc gtt ccg ttc atc gcc agg tac cgc aag gaa atc act ggg gga ctc 163  
 Thr Val Pro Phe Ile Ala Arg Tyr Arg Lys Glu Ile Thr Gly Gly Leu  
 10 15 20

gat gat acc caa ctg cgt gac ctg gaa gaa cgc ctc agt tac ctc cgt 211  
 Asp Asp Thr Gln Leu Arg Asp Leu Glu Glu Arg Leu Ser Tyr Leu Arg  
 25 30 35

gag ctg gag gat cgt aaa caa agc atc ctc gcc gcg att gag gaa caa 259  
 Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala Ala Ile Glu Glu Gln  
 40 45 50

ggc aaa ctc acc gac gat tta cgc tcg ctg att ttg gga tgc gac acc 307  
 Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile Leu Gly Cys Asp Thr  
 55 60 65

aag gct cgc ctg gag gat ctg tac ctg ccg ttc aaa aaa cgg cgc aag 355  
 Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe Lys Lys Arg Arg Lys  
 70 75 80 85

acg aag gcc gat atc gct agg gag gcg gcc ctg gag ggg ctc gtc gat 403  
 Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu Glu Gly Leu Val Asp  
 90 95 100

aag ctt atc gac gcc ccg tcc ctc gac gcc gca gcg cag gca gct gca 451  
 Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala Ala Gln Ala Ala Ala  
 105 110 115

ttt acg act gag gcc ttt gag gat tcc aaa aaa gtt ttg gat gcc gct 499  
 Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys Val Leu Asp Gly Ala  
 120 125 130

cgc gcc att ttg att gac cgc ttc gcg ctc gat gcc gat ttg gtg gcc 547  
 Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp Ala Asp Leu Val Gly  
 135 140 145

gag gtg cgt gag caa atg tat cgc gcg ggt tcc atg gcg gca tcg gtg 595  
 Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser Met Ala Ala Ser Val  
 150 155 160 165

gtg gcg ggc aag gag cag gaa ggc gca aag ttc aag gac tac ttt gag 643  
 Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe Lys Asp Tyr Phe Glu  
 170 175 180

ttt tcc gaa cct ttt gac aag ctt cca tct cac cga att ttg gcg ctg 691  
 Phe Ser Glu Pro Phe Asp Lys Leu Pro Ser His Arg Ile Leu Ala Leu  
 185 190 195

ctg cgc ggt gaa aac gaa ggt gtg ctg agc ctc aac ctc gat gcg ggc 739  
 Leu Arg Gly Glu Asn Glu Gly Val Leu Ser Leu Asn Leu Asp Ala Gly  
 200 205 210

gac gac ata atc tac gaa ggt ttg atc gcc gac cga ttc tcc ctg gac 787  
 Asp Asp Ile Ile Tyr Glu Gly Leu Ile Ala Asp Arg Phe Ser Leu Asp  
 215 220 225

acc cac act tct agc tgg ctg gct gag gct gtg cgc tgg ggt tgg cgc 835  
 Thr His Thr Ser Ser Trp Leu Ala Glu Ala Val Arg Trp Gly Trp Arg  
 230 235 240 245

acc aaa ctg tat gtg tcc tcc gga ttg gat gtg cgc atg cgt ctg aaa 883  
 Thr Lys Leu Tyr Val Ser Ser Gly Leu Asp Val Arg Met Arg Leu Lys  
 250 255 260

gaa aaa gca gag gaa ggc gca ctc gat gtg ttt gcc acc aac ctc cgc 931  
 Glu Lys Ala Glu Glu Gly Ala Leu Asp Val Phe Ala Thr Asn Leu Arg  
 265 270 275

gac gtt ctc ctt gca gct ccc gct ggt cag cgc tcc aca att ggc ctt 979  
 Asp Val Leu Leu Ala Ala Pro Ala Gly Gln Arg Ser Thr Ile Gly Leu  
 280 285 290

gac ccg gga ttc cgc aac ggt gtg aaa gta gct gtc gtg gat tcc acc 1027  
 Asp Pro Gly Phe Arg Asn Gly Val Lys Val Ala Val Val Asp Ser Thr  
 295 300 305

ggt aag gat gtt gcc acc acg atc gtc tac cca cac cag ccc caa aac 1075  
 Gly Lys Asp Val Ala Thr Thr Ile Val Tyr Pro His Gln Pro Gln Asn  
 310 315 320 325

cgc tgg aag gaa gcc gta tcc gaa ctg gct aac ctg tgc gcg acc cac 1123  
 Arg Trp Lys Glu Ala Val Ser Glu Leu Ala Asn Leu Cys Ala Thr His  
 330 335 340

ggt gtg gaa ctc atg gcg atc ggc aac gga acc gcc tcg agg gaa acg 1171  
 Gly Val Glu Leu Met Ala Ile Gly Asn Gly Thr Ala Ser Arg Glu Thr  
 345 350 355

gaa aaa ctc gcc ggc gaa gta gct gac atg atc aaa gcc gca ggt ggc 1219  
 Glu Lys Leu Ala Gly Glu Val Ala Asp Met Ile Lys Ala Ala Gly Gly  
 360 365 370

acg cga cca acc ccc gtg gtg gtc tcc gaa tcg ggc gca tcc gtg tac 1267  
 Thr Arg Pro Thr Pro Val Val Ser Glu Ser Gly Ala Ser Val Tyr  
 375 380 385

tcg gca tca ccg atc gca gcc gaa gaa ttc ccc gac atg gac gtc tcc 1315  
 Ser Ala Ser Pro Ile Ala Ala Glu Glu Phe Pro Asp Met Asp Val Ser  
 390 395 400 405

ctc cgc ggt gca gtt tct atc gcg agg cga ctc cag gat cca ctg gcg 1363  
 Leu Arg Gly Ala Val Ser Ile Ala Arg Arg Leu Gln Asp Pro Leu Ala  
 410 415 420

gag ctc gtc aag att gag ccc aaa gcc atc gga gtc ggc cag tac caa 1411  
 Glu Leu Val Lys Ile Glu Pro Lys Ala Ile Gly Val Gly Gln Tyr Gln  
 425 430 435

cac gat gtc aac cag gtt gca ctt gcc aaa acc ctt gat ggt gtc gtc 1459  
 His Asp Val Asn Gln Val Ala Leu Ala Lys Thr Leu Asp Gly Val Val  
 440 445 450

gaa gac gca gta aac gca gtc gga gtt aac ctc aac acc gca tcc gca 1507  
 Glu Asp Ala Val Asn Ala Val Gly Val Asn Leu Asn Thr Ala Ser Ala  
 455 460 465

cca ctt ctt acc cga gtt gcc gga gtg acc tcc acc ttg gca aac aat 1555  
 Pro Leu Leu Thr Arg Val Ala Gly Val Thr Ser Thr Leu Ala Asn Asn  
 470 475 480 485

atc gtg gcc tac cgc aac gaa aac ggt gga ttc tcc tcc cga aaa gaa 1603  
 Ile Val Ala Tyr Arg Asn Glu Asn Gly Gly Phe Ser Ser Arg Lys Glu  
 490 495 500

ctg aac aaa gtt cct cgc ctg gga ccc aaa gcc ttt gaa cag tgt gct 1651  
 Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala Phe Glu Gln Cys Ala  
 505 510 515

ggc ttc ctc cgc att tct gga tcc acc gac cct ctc gac gcc tcc gct 1699  
 Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro Leu Asp Ala Ser Ala  
 520 525 530

gtt cac ccc gag gcg tac cca gtt gtt cgc aac att gcg aaa gcc aca 1747  
 Val His Pro Glu Ala Tyr Pro Val Val Arg Asn Ile Ala Lys Ala Thr  
 535 540 545

gga ttg gat gtc tcg gga ctg atc gga aac tct gcg gtg ctc acc aaa 1795  
 Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser Ala Val Leu Thr Lys  
 550 555 560 565

ttg aag ccc gct gat ttc gct gat gaa cga ttc ggc atc ccc acc gtc 1843  
 Leu Lys Pro Ala Asp Phe Ala Asp Glu Arg Phe Gly Ile Pro Thr Val  
 570 575 580

acc gac atc atc gcc gag ctg gat aaa ccc gga cgt gac ccc cgc cca 1891  
 Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly Arg Asp Pro Arg Pro  
 585 590 595

gaa ttc aaa acc gcc agc ttc aaa gaa ggc gtg gag aaa atc tcc gac 1939  
 Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val Glu Lys Ile Ser Asp  
 600 605 610

ctc aca ccc ggc atg atc ctg gaa gga act gtc acc aac gtt gcg gcg 1987  
 Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val Thr Asn Val Ala Ala  
 615 620 625

ttc ggc gca ttc gtt gac gtg gga gtg cac cga gat ggc ctc gtt cac 2035  
 Phe Gly Ala Phe Val Asp Val Gly Val His Arg Asp Gly Leu Val His  
 630 635 640 645

gtt tcc gcg atg agc gac aaa ttc atc tcc aac ccc cac gaa gtt gtt 2083

Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn Pro His Glu Val Val  
650 655 660

cgc tct ggt gag gtc gtg aag gta aag gtc atg gaa gtt gac gtc gac 2131  
Arg Ser Gly Glu Val Val Lys Val Lys Val Met Glu Val Asp Val Asp  
665 670 675

cgc aaa cgc atc ggc ctt tcc ctc cgc ttg acc gat gaa ccc ggt gcc 2179  
Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr Asp Glu Pro Gly Ala  
680 685 690

cca gct ccg caa aag cgc gga aac cga cca gcc aaa cag cag cga gct 2227  
Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala Lys Gln Gln Arg Ala  
695 700 705

ccg caa aaa cag tcc gct aag ccc gcc aca ggt tcc atg gca gat gct 2275  
Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly Ser Met Ala Asp Ala  
710 715 720 725

tta cga cgc gcc ggc ctc ggt ggc taaggcaact ttcaaacc aa gcg 2322  
Leu Arg Arg Ala Gly Leu Gly Gly  
730

&lt;210&gt; 406

&lt;211&gt; 733

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 406

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Ile Thr Gly Gly Leu Asp Asp Thr Gln Leu Arg Asp Leu Glu Glu Arg  
20 25 30

Leu Ser Tyr Leu Arg Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala  
35 40 45

Ala Ile Glu Glu Gln Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile  
50 55 60

Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe  
65 70 75 80

Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu  
85 90 95

Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala  
100 105 110

Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys  
115 120 125

Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp  
130 135 140

Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser  
145 150 155 160

Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe

				165					170						175
Lys	Asp	Tyr	Phe	Glu	Phe	Ser	Glu	Pro	Phe	Asp	Lys	Leu	Pro	Ser	His
			180					185					190		
Arg	Ile	Leu	Ala	Leu	Leu	Arg	Gly	Glu	Asn	Glu	Gly	Val	Leu	Ser	Leu
		195					200					205			
Asn	Leu	Asp	Ala	Gly	Asp	Asp	Ile	Ile	Tyr	Glu	Gly	Leu	Ile	Ala	Asp
	210					215					220				
Arg	Phe	Ser	Leu	Asp	Thr	His	Thr	Ser	Ser	Trp	Leu	Ala	Glu	Ala	Val
225					230					235					240
Arg	Trp	Gly	Trp	Arg	Thr	Lys	Leu	Tyr	Val	Ser	Ser	Gly	Leu	Asp	Val
				245					250					255	
Arg	Met	Arg	Leu	Lys	Glu	Lys	Ala	Glu	Glu	Gly	Ala	Leu	Asp	Val	Phe
			260					265					270		
Ala	Thr	Asn	Leu	Arg	Asp	Val	Leu	Leu	Ala	Ala	Pro	Ala	Gly	Gln	Arg
		275					280					285			
Ser	Thr	Ile	Gly	Leu	Asp	Pro	Gly	Phe	Arg	Asn	Gly	Val	Lys	Val	Ala
	290					295					300				
Val	Val	Asp	Ser	Thr	Gly	Lys	Asp	Val	Ala	Thr	Thr	Ile	Val	Tyr	Pro
305					310					315					320
His	Gln	Pro	Gln	Asn	Arg	Trp	Lys	Glu	Ala	Val	Ser	Glu	Leu	Ala	Asn
				325					330					335	
Leu	Cys	Ala	Thr	His	Gly	Val	Glu	Leu	Met	Ala	Ile	Gly	Asn	Gly	Thr
			340					345					350		
Ala	Ser	Arg	Glu	Thr	Glu	Lys	Leu	Ala	Gly	Glu	Val	Ala	Asp	Met	Ile
		355					360					365			
Lys	Ala	Ala	Gly	Gly	Thr	Arg	Pro	Thr	Pro	Val	Val	Val	Ser	Glu	Ser
	370					375					380				
Gly	Ala	Ser	Val	Tyr	Ser	Ala	Ser	Pro	Ile	Ala	Ala	Glu	Glu	Phe	Pro
385					390					395					400
Asp	Met	Asp	Val	Ser	Leu	Arg	Gly	Ala	Val	Ser	Ile	Ala	Arg	Arg	Leu
				405					410					415	
Gln	Asp	Pro	Leu	Ala	Glu	Leu	Val	Lys	Ile	Glu	Pro	Lys	Ala	Ile	Gly
			420					425					430		
Val	Gly	Gln	Tyr	Gln	His	Asp	Val	Asn	Gln	Val	Ala	Leu	Ala	Lys	Thr
			435				440					445			
Leu	Asp	Gly	Val	Val	Glu	Asp	Ala	Val	Asn	Ala	Val	Gly	Val	Asn	Leu
	450					455					460				
Asn	Thr	Ala	Ser	Ala	Pro	Leu	Leu	Thr	Arg	Val	Ala	Gly	Val	Thr	Ser
465					470					475					480
Thr	Leu	Ala	Asn	Asn	Ile	Val	Ala	Tyr	Arg	Asn	Glu	Asn	Gly	Gly	Phe
				485					490					495	

Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala  
500 505 510

Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro  
515 520 525

Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val Val Arg Asn  
530 535 540

Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser  
545 550 555 560

Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp Glu Arg Phe  
565 570 575

Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly  
580 585 590

Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val  
595 600 605

Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val  
610 615 620

Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly Val His Arg  
625 630 635 640

Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn  
645 650 655

Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val Lys Val Met  
660 665 670

Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr  
675 680 685

Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala  
690 695 700

Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly  
705 710 715 720

Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly  
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<210> 407

<211> 1286

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1263)

<223> RXA00157

<400> 407

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1

5

10

15

gtc cag acc gag gct gca att gcc gca aac agc gag cag ctc aat gtc 96  
 Val Gln Thr Glu Ala Ala Ile Ala Ala Asn Ser Glu Gln Leu Asn Val  
 20 25 30

ttg act acc aat cgc agt acc ttg gtt gcc cag cgt gat ggg gct gag 144  
 Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu  
 35 40 45

cgc aac ttg gcc atc gct cgt gcg cag gcg gat aat ctg caa ggt cag 192  
 Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln  
 50 55 60

cgt gct gag tac gag gaa ttc cag cag gca gag cag gct cgc atc cag 240  
 Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln  
 65 70 75 80

gcg gaa gcg gaa gct cag gct gct gcg gag gag aag cgt cgt gcc gat 288  
 Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp  
 85 90 95

gag gct gct gca cag gca gcc gct gaa gct caa gaa gct gcc cag caa 336  
 Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln  
 100 105 110

gct cag gcg gcg gag gaa gcc caa gcc gcg caa gca gct gag aca gca 384  
 Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala  
 115 120 125

caa gcc caa gcc gcg caa gct gcg gaa acc caa gct gca caa gcc gcg 432  
 Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala  
 130 135 140

caa gct cag gca gaa gcg aat gat cgt gcc gcc gcg caa cag cgt gct 480  
 Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala  
 145 150 155 160

gca gag gct caa gca gca gcg gaa cag gcg caa cgt gag gct gac gct 528  
 Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala  
 165 170 175

cag gcg gcc aac gat gcc caa gct cag gca ctg cgt gaa cag gcg ctc 576  
 Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu  
 180 185 190

acc gca gcc tcc atc gct gcg gct gct cta att gcg gcg agc cag tcc 624  
 Thr Ala Ala Ser Ile Ala Ala Ala Ala Leu Ile Ala Ala Ser Gln Ser  
 195 200 205

agc cat gcc act act caa aat cct tac cca act gat gaa gac gcg gat 672  
 Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp  
 210 215 220

ccg acc gat att gcg gac atc caa ggc cca acg cag cca ggt acg ggt 720  
 Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly  
 225 230 235 240

gag tct gga gat tcc cag agc aac tcc agc gac aac gat tcc aca ggc 768  
 Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly  
 245 250 255



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aac gat tcc aca ggc tct gac tct tca gat tca gat tcc tcc ggc aac      816
Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn
      260                      265                      270

gat tct tca gag gtt att tcc ggc gat cgt tcc gct cag att gag act      864
Asp Ser Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr
      275                      280                      285

gtg att gcg cgc gcc atg agc cag ttg ggt gtg cag tac gca tgg ggt      912
Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly
      290                      295                      300

ggc ggt aac gct aat ggc cca act ctg ggt atc cgt gac ggt ggc gtg      960
Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val
      305                      310                      315                      320

gcg gac tct tac ggc gat tac aac aag gtt ggc ttc gac tgc tct gga      1008
Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly
      325                      330                      335

ctg acc ttg tat gcg ttt gcg ggt gtg gga att tca ctt cct cac tac      1056
Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr
      340                      345                      350

acg ggc tac cag tac cag cac ggc acc aag gtg tcg cct tct gag atg      1104
Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met
      355                      360                      365

caa cgt ggc gat ctg atc ttc tat ggt ccg gga gcg tct cag cac gtg      1152
Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val
      370                      375                      380

gca att tac ctc ggt gat ggt cag atg att gag gct ccg aat tcg ggt      1200
Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly
      385                      390                      395                      400

tct gtc gtg aag att tct cct gtt cgc tgg agc gga atg acc gag agc      1248
Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser
      405                      410                      415

gtg gta cgc ctc att tagtttcctc ctatgaatct tga      1286
Val Val Arg Leu Ile
      420

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&lt;210&gt; 408

&lt;211&gt; 421

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

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Ala Arg Ile Val Ala Glu Gln Arg Glu Ala Glu Ala Val Glu Lys Lys
  1             5             10             15

```

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Val Gln Thr Glu Ala Ala Ile Ala Ala Asn Ser Glu Gln Leu Asn Val
      20             25             30

```

```

Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu
      35             40             45

```

Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln

50	55	60
Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln 65 70 75 80		
Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp 85 90 95		
Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln 100 105 110		
Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala 115 120 125		
Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala 130 135 140		
Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala 145 150 155 160		
Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala 165 170 175		
Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu 180 185 190		
Thr Ala Ala Ser Ile Ala Ala Ala Ala Leu Ile Ala Ala Ser Gln Ser 195 200 205		
Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp 210 215 220		
Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly 225 230 235 240		
Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly 245 250 255		
Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn 260 265 270		
Asp Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr 275 280 285		
Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly 290 295 300		
Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val 305 310 315 320		
Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly 325 330 335		
Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr 340 345 350		
Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met 355 360 365		
Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val 370 375 380		

Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly  
385 390 395 400

Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser  
405 410 415

Val Val Arg Leu Ile  
420

<210> 409

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> RXA00208

<400> 409

cggccaattt tttcttttgt ggggggtgcct cttacgcatt tcctgaattt ttgttaggct 60

tgcctaggctc agttaagat atatcgataa gaggttttcc atg aac act cca gcg 115  
Met Asn Thr Pro Ala  
1 5

ccc cgc aaa cga cgc gaa atg aaa atc aag aca gca acc gtc act ggt 163  
Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr Ala Thr Val Thr Gly  
10 15 20

gtg cgt caa att tcc ccc gat ctc atc cgc ttc agc ttc gac tgc cca 211  
Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe Ser Phe Asp Cys Pro  
25 30 35

gaa atc gtt ggc gcc gac ctg ggg ttc acg gac cat tac atc aag atc 259  
Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp His Tyr Ile Lys Ile  
40 45 50

ctc ttc gtg cca gca ggt gcg gat tac tcc tgg cct ttc gac atg gca 307  
Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp Pro Phe Asp Met Ala  
55 60 65

gaa att gcg gaa acc cag ccc cgt gag ctg caa cca gtg cgc cgc acc 355  
Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln Pro Val Arg Arg Thr  
70 75 80 85

tac act ttc cgc acg gtt gac act gtc gca ggc aca ttt gac ata gat 403  
Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly Thr Phe Asp Ile Asp  
90 95 100

ttc gtt gcg cac ggc acc gat ggc ctt gcc ggt cct tgg gcg cag cag 451  
Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly Pro Trp Ala Gln Gln  
105 110 115

gca cag gta ggt gat gtc atc gcg ttc ggc ggc cca ggt ggc gca tgg 499  
Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly Pro Gly Gly Ala Trp  
120 125 130

aag cca gaa acc acc tat gag cac tac gtt ctc gca ggc gat gaa gcc 547

Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu Ala Gly Asp Glu Ala  
 135 140 145  
 gca gca ccc gca att ttc gca gcc tta gaa cac cta ccc gcc ggc acc 595  
 Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His Leu Pro Ala Gly Thr  
 150 155 160 165  
 acc gcc aaa gcc ttc att gaa atc tcc tcc aac gaa gcg cgt ttc aac 643  
 Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn Glu Ala Arg Phe Asn  
 170 175 180  
 gcc cca gcc agc gac aac atc gag gtt gtc tgg gtg ccc cgc gac ggc 691  
 Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp Val Pro Arg Asp Gly  
 185 190 195  
 gcc acc cac ggt aca ttg ctt atc gac gcc ctc cgc cag gac ggc tac 739  
 Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu Arg Gln Asp Gly Tyr  
 200 205 210  
 cca acc aag aaa act tcc tgg ttc atc cac gga gtc gcc gaa atg gtg 787  
 Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly Val Ala Glu Met Val  
 215 220 225  
 aag gaa acc cgc aaa ttc ctc ttc gtg gaa ggc aac gta gac aaa gct 835  
 Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly Asn Val Asp Lys Ala  
 230 235 240 245  
 gat gca tcc att tcc gga tac tgg cgc ctt ggc atg acc gaa gac cag 883  
 Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly Met Thr Glu Asp Gln  
 250 255 260  
 tgg cag gcc tcc aag cgg gag ttc aat gag caa aat gag gca gaa gaa 931  
 Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln Asn Glu Ala Glu Glu  
 265 270 275  
 ctc gcg ctc agc aag gca taagggcaag gggttctaga aag 972  
 Leu Ala Leu Ser Lys Ala  
 280

&lt;210&gt; 410

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 410

Met Asn Thr Pro Ala Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr  
 1 5 10 15

Ala Thr Val Thr Gly Val Arg Gln Ile Ser Pro Asp Leu Ile Arg Phe  
 20 25 30

Ser Phe Asp Cys Pro Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp  
 35 40 45

His Tyr Ile Lys Ile Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp  
 50 55 60

Pro Phe Asp Met Ala Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln  
 65 70 75 80

Pro Val Arg Arg Thr Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly  
                     85                    90                    95  
 Thr Phe Asp Ile Asp Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly  
                     100                    105                    110  
 Pro Trp Ala Gln Gln Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly  
                     115                    120                    125  
 Pro Gly Gly Ala Trp Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu  
                     130                    135                    140  
 Ala Gly Asp Glu Ala Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His  
                     145                    150                    155                    160  
 Leu Pro Ala Gly Thr Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn  
                     165                    170                    175  
 Glu Ala Arg Phe Asn Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp  
                     180                    185                    190  
 Val Pro Arg Asp Gly Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu  
                     195                    200                    205  
 Arg Gln Asp Gly Tyr Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly  
                     210                    215                    220  
 Val Ala Glu Met Val Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly  
                     225                    230                    235                    240  
 Asn Val Asp Lys Ala Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly  
                     245                    250                    255  
 Met Thr Glu Asp Gln Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln  
                     260                    265                    270  
 Asn Glu Ala Glu Glu Leu Ala Leu Ser Lys Ala  
                     275                    280

&lt;210&gt; 411

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26)..(388)

&lt;223&gt; RXA00967

&lt;400&gt; 411

caactagaaa atgactgggg gcgatatg ccg gtg cag gac gca ggc gaa cgc 52  
                                     Met Pro Val Gln Asp Ala Gly Glu Arg  
                                     1                    5

aac aac aat gac cgg cca gtg atg ccg gga gag atc ctc cgt gag gaa 100  
 Asn Asn Asn Asp Arg Pro Val Met Pro Gly Glu Ile Leu Arg Glu Glu  
                     10                    15                    20                    25

ttc atg gag cct ttg ggg ctg tcc caa aac ggc ttg gcg cgg gca ata 148  
 Phe Met Glu Pro Leu Gly Leu Ser Gln Asn Gly Leu Ala Arg Ala Ile

	30	35	40	
gga gtg cca cca cgc agg att aat gag atc gtg cac ggc aaa cgc gca				196
Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ala				
	45	50	55	
atc acg gca gac act gcg ctg cgt tta gct gct tat tta ggt ccc gat				244
Ile Thr Ala Asp Thr Ala Leu Arg Leu Ala Ala Tyr Leu Gly Pro Asp				
	60	65	70	
cca cag ttt tgg ctc aac ttg cag acc cac tac gac ctg tcg gtg acg				292
Pro Gln Phe Trp Leu Asn Leu Gln Thr His Tyr Asp Leu Ser Val Thr				
	75	80	85	
tat tta gat gcg cgc aca ctg ttg gaa gcg atc aag cct tat gat cgt				340
Tyr Leu Asp Ala Arg Thr Leu Leu Glu Ala Ile Lys Pro Tyr Asp Arg				
	90	95	100	105
cag caa aat gtg gct cgg acc ctg aat ccg ctt cag gag agc tcg cag				388
Gln Gln Asn Val Ala Arg Thr Leu Asn Pro Leu Gln Glu Ser Ser Gln				
	110	115	120	
taggagtcgc ctctggtcgg ggc				411

&lt;210&gt; 412

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Met	Pro	Val	Gln	Asp	Ala	Gly	Glu	Arg	Asn	Asn	Asn	Asp	Arg	Pro	Val
1				5					10					15	

Met	Pro	Gly	Glu	Ile	Leu	Arg	Glu	Glu	Phe	Met	Glu	Pro	Leu	Gly	Leu
			20					25					30		

Ser	Gln	Asn	Gly	Leu	Ala	Arg	Ala	Ile	Gly	Val	Pro	Pro	Arg	Arg	Ile
	35					40						45			

Asn	Glu	Ile	Val	His	Gly	Lys	Arg	Ala	Ile	Thr	Ala	Asp	Thr	Ala	Leu
	50					55					60				

Arg	Leu	Ala	Ala	Tyr	Leu	Gly	Pro	Asp	Pro	Gln	Phe	Trp	Leu	Asn	Leu
	65				70					75				80	

Gln	Thr	His	Tyr	Asp	Leu	Ser	Val	Thr	Tyr	Leu	Asp	Ala	Arg	Thr	Leu
			85					90					95		

Leu	Glu	Ala	Ile	Lys	Pro	Tyr	Asp	Arg	Gln	Gln	Asn	Val	Ala	Arg	Thr
		100						105					110		

Leu	Asn	Pro	Leu	Gln	Glu	Ser	Ser	Gln
	115					120		

&lt;210&gt; 413

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<400> 413

<400> 414

Val Val Ala Pro Gln Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu  
1 5 10 15

Ser Glu Arg Phe Leu Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala  
20 25 30

Lys Thr Leu His Ile Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly  
35 40 45

Arg Thr Asp Leu Thr Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe  
50 55 60

Asp Leu Ser Thr Gln Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln  
65 70 75 80

Ala His Arg Arg Ser Ala  
85

<210> 415  
 <211> 1989  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1966)  
 <223> RXA01305

<400> 415  
 ttctcaaggc tccctctcct ttaagttcgt ggccccagcg ccagcttttt tcataaaaac 60

tcaacaggca ctgtgggacc ccttcacttt gaaagacatc atg cgc ccc tct tcc 115  
 Met Arg Pro Ser Ser  
 1 5

cgg cca ctt ggc ctc gtc cta tgc acc gca ctg gca tca acg atc atc 163  
 Arg Pro Leu Gly Leu Val Leu Cys Thr Ala Leu Ala Ser Thr Ile Ile  
 10 15 20

acc gtt ccc gca gcg tcc gcc cag gag cca gcg ctt ctc gat gcc tcc 211  
 Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala Leu Leu Asp Ala Ser  
 25 30 35

gcc atc gcc cca cat acc gcc agc tac gcc tac tac gtt gat gca tgg 259  
 Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr Tyr Val Asp Ala Trp  
 40 45 50

gac acc aac gtt tcc act gat ctg aat cca tca agt aat gca gct gtt 307  
 Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser Ser Asn Ala Ala Val  
 55 60 65

ggc gta ctg gag gaa atg ctt gag ctg tgg acc cca ggc gaa gaa tgg 355  
 Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr Pro Gly Glu Glu Trp  
 70 75 80 85

aac acc ggc gtc aag gtt gac ccc acc gtg ctg gat tcc aac atc gca 403  
 Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu Asp Ser Asn Ile Ala  
 90 95 100

cag tct gtg gca atc tcc cag cag gcg acc gat gct cag caa gaa cgt 451  
 Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp Ala Gln Gln Glu Arg  
 105 110 115

gct tgg gtt att gat cgc cgc aac cag aac tac acc gca acc gac ggt 499  
 Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr Thr Ala Thr Asp Gly  
 120 125 130

ctt ggc gca tac gca gat agt tac cgc gag acc gca cag gtg ggc acc 547  
 Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr Ala Gln Val Gly Thr  
 135 140 145

acc atc cct gac gtt gtt cca gct gat gcc acc acc gtg aag tac aac 595  
 Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr Thr Val Lys Tyr Asn  
 150 155 160 165

gat ggc ggc aat gtg aat ggc aat tgg gca gag acc ggt gga gaa ctc 643  
 Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu Thr Gly Gly Glu Leu  
 170 175 180



gga tcc act gtt gat cta att gaa gct atc cgt cag cat gcc gca acc 691  
 Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg Gln His Ala Ala Thr  
 185 190 195

agc aac aat gcc aag gcg tac tac caa tac cca cgc ccc tac cgc tgg 739  
 Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro Arg Pro Tyr Arg Trp  
 200 205 210

act gaa tcc atc gaa cca gaa gcc tgg ggc gag ggc gtt gac atg cca 787  
 Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu Gly Val Asp Met Pro  
 215 220 225

gag tat gca aac cca ctg cgc aag gat gaa tcc gaa gct gcc agc gat 835  
 Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser Glu Ala Ala Ser Asp  
 230 235 240 245

ggc ggt ttc cct tcc gga cac acc tcc gca ggc ggc atg gca acc aac 883  
 Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly Gly Met Ala Thr Asn  
 250 255 260

ggc ctg gct tac gct ttc cca cag caa tac gat aaa ctg ctc atg act 931  
 Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp Lys Leu Leu Met Thr  
 265 270 275

gca gcg gaa atc ggc gaa agc cgc atc cag ctg ggc atg cac tct ccg 979  
 Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu Gly Met His Ser Pro  
 280 285 290

ctt gat gtt att ggc ggc cgt gtt cta tcc acc gcg att act gca ggt 1027  
 Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr Ala Ile Thr Ala Gly  
 295 300 305

gca ctt aat gat ccg aat ctc gac tcg gtg aag gct gaa gcc ttc gat 1075  
 Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys Ala Glu Ala Phe Asp  
 310 315 320 325

gat gct cag gca tgg atc agt aac cag agc gac atc acc acc aac act 1123  
 Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp Ile Thr Thr Asn Thr  
 330 335 340

cgc gat ttt gat gag caa ctc gcc gag tac acc aac ttc ctc acc ttc 1171  
 Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr Asn Phe Leu Thr Phe  
 345 350 355

ggc ttc gag cag tcc ggc gac acc acc caa gac atg cgc gtg cca aag 1219  
 Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp Met Arg Val Pro Lys  
 360 365 370

gga gct gag gct ctg ctg gaa acc cgc ctt ccg tac ctt gat gac gaa 1267  
 Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro Tyr Leu Asp Asp Glu  
 375 380 385

cag cgc cgt tgg gtt cta cat tcc act ggc ctc gag tcc ggt ttc cca 1315  
 Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu Glu Ser Gly Phe Pro  
 390 395 400 405

gta ctt gat gat gcc gaa ggt tgg ggc cgt ctc aac ctc tac gct gcc 1363  
 Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu Asn Leu Tyr Ala Ala  
 410 415 420

cag gct ggc tac agt gca ttc gat acc aac gtt gac gtc acc atg aat 1411  
 Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val Asp Val Thr Met Asn  
 425 430 435

gcc atc gac ggt ggc tac aac gcc aaa gac aac tgg caa aac gac atc 1459  
 Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn Trp Gln Asn Asp Ile  
 440 445 450

gag ggc gca gga tcc ctg acc aag aac ggt tcc ggt gaa ctc acc ctg 1507  
 Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser Gly Glu Leu Thr Leu  
 455 460 465

tca ggt gac aac tcc tac acc ggt gga acc acc atc acc gcg ggc acc 1555  
 Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr Ile Thr Ala Gly Thr  
 470 475 480 485

ttg gtt gct gca act gag tca gct ctg gga gca ggc gat ctc acc atc 1603  
 Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala Gly Asp Leu Thr Ile  
 490 495 500

aac gat ggt gca acc ttg aag atc acc cag cct gtc acc gtg gat gga 1651  
 Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro Val Thr Val Asp Gly  
 505 510 515

acc gca aac ctg gga gga act ctg cac gtt gcc ctt cct gtt ggc acc 1699  
 Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala Leu Pro Val Gly Thr  
 520 525 530

aac cac gtc acc gtg atc gat gct gca tca att tcc ggt gaa ttt gat 1747  
 Asn His Val Thr Val Ile Asp Ala Ala Ser Ile Ser Gly Glu Phe Asp  
 535 540 545

gag gtt att gtt gat ggc gca gtt gac gct cag gtg agc tac gac aac 1795  
 Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln Val Ser Tyr Asp Asn  
 550 555 560 565

ggc tct gtc gtg att act aca ggc gca cct tct gat gac gta aag gaa 1843  
 Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser Asp Asp Val Lys Glu  
 570 575 580

act ggc tct tct gct ggc gga att ctt gcc atc gtg gca gcc ctg ggt 1891  
 Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile Val Ala Ala Leu Gly  
 585 590 595

ggc att gca gca ctg atc ttc ggt gca ttc acc cag ttt ggt ttc cca 1939  
 Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr Gln Phe Gly Phe Pro  
 600 605 610

cca gca atc aag gaa atg ttc gac ctt taagccttcg ccaacccac 1986  
 Pro Ala Ile Lys Glu Met Phe Asp Leu  
 615 620

ggc 1989

&lt;210&gt; 416

&lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 416

Met Arg Pro Ser Ser Arg Pro Leu Gly Leu Val Leu Cys Thr Ala Leu  
 1 5 10 15  
 Ala Ser Thr Ile Ile Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala  
 20 25 30  
 Leu Leu Asp Ala Ser Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr  
 35 40 45  
 Tyr Val Asp Ala Trp Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser  
 50 55 60  
 Ser Asn Ala Ala Val Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr  
 65 70 75 80  
 Pro Gly Glu Glu Trp Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu  
 85 90 95  
 Asp Ser Asn Ile Ala Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp  
 100 105 110  
 Ala Gln Gln Glu Arg Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr  
 115 120 125  
 Thr Ala Thr Asp Gly Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr  
 130 135 140  
 Ala Gln Val Gly Thr Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr  
 145 150 155 160  
 Thr Val Lys Tyr Asn Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu  
 165 170 175  
 Thr Gly Gly Glu Leu Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg  
 180 185 190  
 Gln His Ala Ala Thr Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro  
 195 200 205  
 Arg Pro Tyr Arg Trp Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu  
 210 215 220  
 Gly Val Asp Met Pro Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser  
 225 230 235 240  
 Glu Ala Ala Ser Asp Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly  
 245 250 255  
 Gly Met Ala Thr Asn Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp  
 260 265 270  
 Lys Leu Leu Met Thr Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu  
 275 280 285  
 Gly Met His Ser Pro Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr  
 290 295 300  
 Ala Ile Thr Ala Gly Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys  
 305 310 315 320  
 Ala Glu Ala Phe Asp Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp

325	330	335
Ile Thr Thr Asn Thr Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr 340	345	350
Asn Phe Leu Thr Phe Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp 355	360	365
Met Arg Val Pro Lys Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro 370	375	380
Tyr Leu Asp Asp Glu Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu 385	390	395 400
Glu Ser Gly Phe Pro Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu 405	410	415
Asn Leu Tyr Ala Ala Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val 420	425	430
Asp Val Thr Met Asn Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn 435	440	445
Trp Gln Asn Asp Ile Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser 450	455	460
Gly Glu Leu Thr Leu Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr 465	470	475 480
Ile Thr Ala Gly Thr Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala 485	490	495
Gly Asp Leu Thr Ile Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro 500	505	510
Val Thr Val Asp Gly Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala 515	520	525
Leu Pro Val Gly Thr Asn His Val Thr Val Ile Asp Ala Ala Ser Ile 530	535	540
Ser Gly Glu Phe Asp Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln 545	550	555 560
Val Ser Tyr Asp Asn Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser 565	570	575
Asp Asp Val Lys Glu Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile 580	585	590
Val Ala Ala Leu Gly Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr 595	600	605
Gln Phe Gly Phe Pro Pro Ala Ile Lys Glu Met Phe Asp Leu 610	615	620

&lt;210&gt; 417

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(397)

&lt;223&gt; RXA01453

&lt;400&gt; 417

tacagcattc gagtcaacga ccagtggcgg atctgcttcc gttggaacga ctccgggcccc 60

gaaaacgtcg agatcgtgga ttatcactga ggaggagacg atg gct cag aag ctc 115  
Met Ala Gln Lys Leu  
1 5

tac ccg ccg att cac cct ggt gag att ctc atg gag gac ttc atc aag 163  
Tyr Pro Pro Ile His Pro Gly Glu Ile Leu Met Glu Asp Phe Ile Lys  
10 15 20

ggc ttc ggc ctc aca cag aac aag gtc gcc gta tcg atc ggg gtg cct 211  
Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val Ser Ile Gly Val Pro  
25 30 35

ccg cga cgc atc aac gag atc gtg cac ggc aag cga tcc atc acg gcc 259  
Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ser Ile Thr Ala  
40 45 50

gat acg gct ctg cgt ctc ggg cgg tac ttc ggt atc gac ccg cag ttc 307  
Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly Ile Asp Pro Gln Phe  
55 60 65

tgg ctg agc ctt cag act cag tac gag ttg gag ctc gat cgc gac gcc 355  
Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu Leu Asp Arg Asp Ala  
70 75 80 85

ggt gca gcg act tac gca cag atc acg ccg ctg aag gtc gcg 397  
Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu Lys Val Ala  
90 95

tgagctcggt ggccagaaaa cat 420

&lt;210&gt; 418

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 418

Met Ala Gln Lys Leu Tyr Pro Pro Ile His Pro Gly Glu Ile Leu Met  
1 5 10 15

Glu Asp Phe Ile Lys Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val  
20 25 30

Ser Ile Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys  
35 40 45

Arg Ser Ile Thr Ala Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly  
50 55 60

Ile Asp Pro Gln Phe Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu  
65 70 75 80

Leu Asp Arg Asp Ala Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu  
                   85                                  90                                  95

Lys Val Ala

<210> 419

<211> 945

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(922)

<223> RXA01824

<400> 419

ctaaagcgct gctcaaagaa gtttttgacc tcgacgcact catcctcaaa gaccccaaca 60

acggccgacc actcatcggtg cccacagaca ggagaaactc atg aaa gaa acc gac 115  
   Met Lys Glu Thr Asp  
   1                  5

aac cta ctg cgc gaa aac tcc cac gac cgc gac atc tct gaa atc gtc 163  
   Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp Ile Ser Glu Ile Val  
                                   10                                  15                                  20

gcc acc atc act gcc ctt gac cac cca tca ccc tca ctt ctg cga ttc 211  
   Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro Ser Leu Leu Arg Phe  
                                   25                                  30                                  35

aca gct ttt gtt cca gga tca gca aac aac cca gtg tgg gca gaa gcc 259  
   Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro Val Trp Ala Glu Ala  
                                   40                                  45                                  50

aac gtg gca atc agg ctt tac ctc agc gaa gaa ttc gac gac gcc acc 307  
   Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu Phe Asp Asp Ala Thr  
                                   55                                  60                                  65

cgc gtc tac acc gtc cga tcc ttt gat gcc gca act gaa agc atc gtg 355  
   Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala Thr Glu Ser Ile Val  
                                   70                                  75                                  80                                  85

gtg gat gtg gtt caa cac cac cac gaa agc ccc atg atg cgc tgg tca 403  
   Val Asp Val Val Gln His His His Glu Ser Pro Met Met Arg Trp Ser  
                                   90                                  95                                  100

gac acc gta aaa atc aac gac acc ctc gtg ctc acc gga ccc cgc cca 451  
   Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu Thr Gly Pro Arg Pro  
                                   105                                  110                                  115

cac ttt gtc atc ccc gaa ggc gaa caa gca gca ctc ttc ctt gat gac 499  
   His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala Leu Phe Leu Asp Asp  
                                   120                                  125                                  130

acc gcc atc ccc gct ctc gcc gct att ttg gat caa tgg cca aca gat 547  
   Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp Gln Trp Pro Thr Asp  
                                   135                                  140                                  145

ctt cgt ggc aaa gga tgg gtt gtc act gac gat ccc gca gcc ttc gat 595

Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp Pro Ala Ala Phe Asp  
 150 155 160 165  
 gaa cta ccc agc atc gac gga ctg gaa ctg aac ctg ctc gcg ccg gga 643  
 Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn Leu Leu Ala Pro Gly  
 170 175 180  
 tca gat cca act gtt cag cca ctt gcc caa cag gca tat gac ctg gaa 691  
 Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln Ala Tyr Asp Leu Glu  
 185 190 195  
 aac cca gaa act tac gtg gtg tgg gca gcc ggc gag cga gat gaa ata 739  
 Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly Glu Arg Asp Glu Ile  
 200 205 210  
 aaa tcc atc cgc agg cac ttc cgc aag cag gtg gga ttg gaa aaa gat 787  
 Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val Gly Leu Glu Lys Asp  
 215 220 225  
 gca gtg gcc gtg ttt ggg tac tgg aaa tac aac acc acc aac act cag 835  
 Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn Thr Thr Asn Thr Gln  
 230 235 240 245  
 atc gat gca gtc cgc aaa gaa aac tac atg aag atg ctc tct gaa ggg 883  
 Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys Met Leu Ser Glu Gly  
 250 255 260  
 cta cag ctg gaa aac ttc gac gac ctc tca ttg gag att taaggggtcg 932  
 Leu Gln Leu Glu Asn Phe Asp Asp Leu Ser Leu Glu Ile  
 265 270  
 agtttttaga atg 945  
 <210> 420  
 <211> 274  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 420  
 Met Lys Glu Thr Asp Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp  
 1 5 10 15  
 Ile Ser Glu Ile Val Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro  
 20 25 30  
 Ser Leu Leu Arg Phe Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro  
 35 40 45  
 Val Trp Ala Glu Ala Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu  
 50 55 60  
 Phe Asp Asp Ala Thr Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala  
 65 70 75 80  
 Thr Glu Ser Ile Val Val Asp Val Val Gln His His His Glu Ser Pro  
 85 90 95  
 Met Met Arg Trp Ser Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu  
 100 105 110

Thr Gly Pro Arg Pro His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala  
 115 120 125  
 Leu Phe Leu Asp Asp Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp  
 130 135 140  
 Gln Trp Pro Thr Asp Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp  
 145 150 155 160  
 Pro Ala Ala Phe Asp Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn  
 165 170 175  
 Leu Leu Ala Pro Gly Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln  
 180 185 190  
 Ala Tyr Asp Leu Glu Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly  
 195 200 205  
 Glu Arg Asp Glu Ile Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val  
 210 215 220  
 Gly Leu Glu Lys Asp Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn  
 225 230 235 240  
 Thr Thr Asn Thr Gln Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys  
 245 250 255  
 Met Leu Ser Glu Gly Leu Gln Leu Glu Asn Phe Asp Asp Leu Ser Leu  
 260 265 270  
 Glu Ile

<210> 421  
 <211> 1017  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(994)  
 <223> RXA01832

<400> 421  
 tttcagtcac agggagggac aaagccatgc ccttaggcgt tttctaggag aagacactta 60  
 tggaacacccc aacttattga gaaaaggagg tcgcaaagtt atg gct act tcg aat 115  
 Met Ala Thr Ser Asn  
 1 5  
 cgg ata gct aat gct atg aac agt ttg gcc aag ctg gac agt tct atg 163  
 Arg Ile Ala Asn Ala Met Asn Ser Leu Ala Lys Leu Asp Ser Ser Met  
 10 15 20  
 caa cgc ggc ctt gat aat gcg ttg gcg ttt gtt ttc cgt ggt cgc gtt 211  
 Gln Arg Gly Leu Asp Asn Ala Leu Ala Phe Val Phe Arg Gly Arg Val  
 25 30 35  
 gtt ccg gct gag ctt gag gag ctt ttg aag caa gag gct gag gac aat 259  
 Val Pro Ala Glu Leu Glu Glu Leu Leu Lys Gln Glu Ala Glu Asp Asn



40	45	50	
gtg gtt cat act gag ttt ggc tat gtt gag gcg ccg aat gtt ttt aag			307
Val Val His Thr Glu Phe Gly Tyr Val Glu Ala Pro Asn Val Phe Lys			
55	60	65	
gtt tcg gtg agc ccg aac gat ttt agt aat ctt gtc gat cgt ttt cct			355
Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu Val Asp Arg Phe Pro			
70	75	80	85
gat cag ccg gct cgt ttt ggt gat cag atg atg agg ttc tgc agg aac			403
Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met Arg Phe Cys Arg Asn			
90	95	100	
agt ggc tgg acg ttg gtt ggg ccg gtg att gtg ttg att gaa gag gat			451
Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val Leu Ile Glu Glu Asp			
105	110	115	
tct tcg ttg cac acg ggc cag ttg aag tcg gtt tcg gag aag gat ccg			499
Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val Ser Glu Lys Asp Pro			
120	125	130	
gat ccg gag tta agt agc ggt tat ctg cct ttg gaa ggc gac ggc atc			547
Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu Glu Gly Asp Gly Ile			
135	140	145	
ctg cct gtc gca gaa agt gag tct aag aac gtg tct gac agt tcc cct			595
Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val Ser Asp Ser Ser Pro			
150	155	160	165
tac act ggt acg gag ttt ttg ccg gcg caa tca gcg gat cgc cct ttg			643
Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser Ala Asp Arg Pro Leu			
170	175	180	
gtt cag ggt gtg ccg cag tct cag gtt gat gcg aat cgc cag gct gcg			691
Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala Asn Arg Gln Ala Ala			
185	190	195	
atg aag ccc gcg ggc cct acg gtg act ttg ctg ctg cag gat ggt tcg			739
Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu Leu Gln Asp Gly Ser			
200	205	210	
agc cgg act tat ttg gtt cgg gag ggt tcg aac atc att ggt cgt agt			787
Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn Ile Ile Gly Arg Ser			
215	220	225	
aat gat gcg gat ctt cgt ttg ccg gat act ggt gtg tct cgt cag cat			835
Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly Val Ser Arg Gln His			
230	235	240	245
gtg gag atc acg tgg gat ggc cgg gat gcc att ttg gtt gat ttg aag			883
Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile Leu Val Asp Leu Lys			
250	255	260	
tcg act aat ggc acc acg gtg aat gac act cct gtg gat aat tgg ttg			931
Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro Val Asp Asn Trp Leu			
265	270	275	
ttg gct gat ggt gat gtc att acg gtg ggt cat tcc aat atc gaa gtt			979
Leu Ala Asp Gly Asp Val Ile Thr Val Gly His Ser Asn Ile Glu Val			
280	285	290	

cgt att gtt agt ccc tagagggaga ggttgatcaa tgg  
 Arg Ile Val Ser Pro  
 295

1017

<210> 422  
 <211> 298  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 422  
 Met Ala Thr Ser Asn Arg Ile Ala Asn Ala Met Asn Ser Leu Ala Lys  
 1 5 10 15  
 Leu Asp Ser Ser Met Gln Arg Gly Leu Asp Asn Ala Leu Ala Phe Val  
 20 25 30  
 Phe Arg Gly Arg Val Val Pro Ala Glu Leu Glu Glu Leu Leu Lys Gln  
 35 40 45  
 Glu Ala Glu Asp Asn Val Val His Thr Glu Phe Gly Tyr Val Glu Ala  
 50 55 60  
 Pro Asn Val Phe Lys Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu  
 65 70 75 80  
 Val Asp Arg Phe Pro Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met  
 85 90 95  
 Arg Phe Cys Arg Asn Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val  
 100 105 110  
 Leu Ile Glu Glu Asp Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val  
 115 120 125  
 Ser Glu Lys Asp Pro Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu  
 130 135 140  
 Glu Gly Asp Gly Ile Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val  
 145 150 155 160  
 Ser Asp Ser Ser Pro Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser  
 165 170 175  
 Ala Asp Arg Pro Leu Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala  
 180 185 190  
 Asn Arg Gln Ala Ala Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu  
 195 200 205  
 Leu Gln Asp Gly Ser Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn  
 210 215 220  
 Ile Ile Gly Arg Ser Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly  
 225 230 235 240  
 Val Ser Arg Gln His Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile  
 245 250 255  
 Leu Val Asp Leu Lys Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro

260

265

270

Val Asp Asn Trp Leu Leu Ala Asp Gly Asp Val Ile Thr Val Gly His  
 275 280 285

Ser Asn Ile Glu Val Arg Ile Val Ser Pro  
 290 295

&lt;210&gt; 423

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(667)

&lt;223&gt; RXA02533

&lt;400&gt; 423

gtttgtgtgca atccaatgct actccacag agcgggctac tttctctaaa aatgttctca 60

tagtagataa aattgttctt aaagcgacat tattgtctgc atg gaa gac gat ctc 115  
 Met Glu Asp Asp Leu  
 1 5

agt gct gct ctc gtc aaa gcg ctt ttc gac gcg cga acc caa cgc agg 163  
 Ser Ala Ala Leu Val Lys Ala Leu Phe Asp Ala Arg Thr Gln Arg Arg  
 10 15 20

ctc tct atc tcg gcg tta gct gaa tcc tcc ggt gtg tcg cga gca atg 211  
 Leu Ser Ile Ser Ala Leu Ala Glu Ser Ser Gly Val Ser Arg Ala Met  
 25 30 35

att tcc cgc gtg gaa aac gca gag gcg caa cca agc gct gca tta ctt 259  
 Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro Ser Ala Ala Leu Leu  
 40 45 50

gga cgc ctt tcc ggt gca ttg ggt atg acg ctt tcg gag ctc att gca 307  
 Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu Ser Glu Leu Ile Ala  
 55 60 65

cag gct gaa ggt ggc tat gac cgg ggc gct cgg cgg tca aag cag tct 355  
 Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg Arg Ser Lys Gln Ser  
 70 75 80 85

gta tgg aca gat cca gct acc ggt tac aca cgg cgt gca gtg tca cag 403  
 Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg Arg Ala Val Ser Gln  
 90 95 100

ccg tca gaa tcc cca cta gaa cta gtg gaa gta atg ctg cct cct ggg 451  
 Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val Met Leu Pro Pro Gly  
 105 110 115

gcg gaa gtt ggc tac cca gct gat gct tat cgt ttc atg gat cag gtg 499  
 Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg Phe Met Asp Gln Val  
 120 125 130

gtc tgg gta ctc gaa ggg gcc gtt cgt att act gaa ggt gaa gag gtc 547  
 Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr Glu Gly Glu Glu Val  
 135 140 145

cac gaa ctt tca acg ggg gat tgt cta cgg ttt ggg cct ccg cga gat 595  
 His Glu Leu Ser Thr Gly Asp Cys Leu Arg Phe Gly Pro Pro Arg Asp  
 150 155 160 165  
 acc gac ttt gct aat ccc acc acc gta gcc act agg tat tta gtt gcc 643  
 Thr Asp Phe Ala Asn Pro Thr Thr Val Ala Thr Arg Tyr Leu Val Ala  
 170 175 180  
 ttg gac aag cgt gta cct cgt gct tgatataaca agtaaggaag cct 690  
 Leu Asp Lys Arg Val Pro Arg Ala  
 185

&lt;210&gt; 424

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 424

Met Glu Asp Asp Leu Ser Ala Ala Leu Val Lys Ala Leu Phe Asp Ala  
 1 5 10 15  
 Arg Thr Gln Arg Arg Leu Ser Ile Ser Ala Leu Ala Glu Ser Ser Gly  
 20 25 30  
 Val Ser Arg Ala Met Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro  
 35 40 45  
 Ser Ala Ala Leu Leu Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu  
 50 55 60  
 Ser Glu Leu Ile Ala Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg  
 65 70 75 80  
 Arg Ser Lys Gln Ser Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg  
 85 90 95  
 Arg Ala Val Ser Gln Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val  
 100 105 110  
 Met Leu Pro Pro Gly Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg  
 115 120 125  
 Phe Met Asp Gln Val Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr  
 130 135 140  
 Glu Gly Glu Glu Val His Glu Leu Ser Thr Gly Asp Cys Leu Arg Phe  
 145 150 155 160  
 Gly Pro Pro Arg Asp Thr Asp Phe Ala Asn Pro Thr Thr Val Ala Thr  
 165 170 175  
 Arg Tyr Leu Val Ala Leu Asp Lys Arg Val Pro Arg Ala  
 180 185

&lt;210&gt; 425

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1012)

&lt;223&gt; RXN02727

&lt;400&gt; 425

gatcagttcc tagatctcgt tgaggacgcc ctcgttcagt tccaagagga aaacgaagac 60

ctaaagcagc aggtcgaaga gctagaggcg caggttgccg gtg gtc ctt ctt ccg 115  
 Val Val Leu Leu Pro  
 1 5

ctg cta gtt cct caa ctg cag gtg cag cca cag ttg cag ctt cca agt 163  
 Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln Leu Gln Leu Pro Ser  
 10 15 20

ctg ttg acg agg cag cgc tgc gca agg aaa tca aag aga agc tgc gct 211  
 Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser Lys Arg Ser Cys Ala  
 25 30 35

ccg aat acg gca tcc aag ctc gat gat gcc tcc aag gcc gct cag aag 259  
 Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser Lys Ala Ala Gln Lys  
 40 45 50

gct caa aac gat gcg aag tcc gct caa gat cag cta cag cgt gca caa 307  
 Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln Leu Gln Arg Ala Gln  
 55 60 65

gct gac gca aag gca gct cgc gac gaa gct gaa aag gcc aag gct gaa 355  
 Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu Lys Ala Lys Ala Glu  
 70 75 80 85

gct aag tca gca gca tcc tcc agc acc act aag gca gca gcg gtt ggc 403  
 Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys Ala Ala Ala Val Gly  
 90 95 100

gct gtc ggc gct ggc acc gga gca gca gtt gct aca ggt gct gca aat 451  
 Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala Thr Gly Ala Ala Asn  
 105 110 115

gtg gac acc cac atg cag gca gcg aag gtt ctg gga ctc gca cag gaa 499  
 Val Asp Thr His Met Gln Ala Ala Lys Val Leu Gly Leu Ala Gln Glu  
 120 125 130

atg gca gac cgc ctg acc tca gag gct cgc tcc gaa tcc aag tcc atg 547  
 Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser Glu Ser Lys Ser Met  
 135 140 145

ctg gac gag gct cgc gaa gca gca gag aag cag atc gag gaa gca aac 595  
 Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln Ile Glu Glu Ala Asn  
 150 155 160 165

agc acc tcc aac cgc act ctg gaa gat gct cgc gca aac gct gag aag 643  
 Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg Ala Asn Ala Glu Lys  
 170 175 180

cag atc gct gaa gcg cag aac cgc gct gac act ctg gtc aac gaa gct 691  
 Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr Leu Val Asn Glu Ala  
 185 190 195

gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca 739  
 Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala  
 200 205 210

gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa 787  
 Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln  
 215 220 225

gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac 835  
 Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His  
 230 235 240 245

acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc 883  
 Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln Asn Ala Leu Glu Thr  
 250 255 260

cgc atc gcg gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg 931  
 Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu  
 265 270 275

aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc 979  
 Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser  
 280 285 290

tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032  
 Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu  
 295 300

ctt 1035

<210> 426  
 <211> 304  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 426  
 Val Val Leu Leu Pro Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln  
 1 5 10 15  
 Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser  
 20 25 30  
 Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser  
 35 40 45  
 Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln  
 50 55 60  
 Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu  
 65 70 75 80  
 Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys  
 85 90 95  
 Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala  
 100 105 110  
 Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu  
 115 120 125

Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser  
 130 135 140  
 Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln  
 145 150 155 160  
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## APPENDIX A: DNA SEQUENCES

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>RXA00407

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>RXA00414  
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>RXA00415-upstream  
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>RXA00415

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>RXA00460

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>RXA00538

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>RXA00542

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>RXA00543-upstream

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>RXA00543-downstream

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>RXA00544-upstream

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>RXA00544

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>RXA00670  
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>RXA00671  
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>RXA00697  
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&gt;RXA01238-upstream

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&gt;RXA01238

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>RXA01279  
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>RXA01286  
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>RXA01374

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>RXA01423-upstream

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>RXA01423

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>RXA01423-downstream

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>RXA01424-upstream

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>RXA01424

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>RXA01424-downstream

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>RXA01453-upstream

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>RXA01453

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>RXA01453-downstream

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>RXA01480-upstream

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>RXA01480

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>RXA01481-upstream

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>RXA01481

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>RXA01581  
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>RXA01661  
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>RXA01683-upstream  
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>RXA01683  
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>RXA01688

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>RXA01689

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>RXA01713

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>RXA01718-upstream

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>RXA01718

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>RXA01735-upstream

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>RXA01735

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>RXA01736

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>RXA02037  
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>RXA02043

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>RXA02370

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>RXA02533-upstream

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>RXA02533

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AGTCAATTAGGAATTACGCTAACCGGTTTGATCATCGGGTGGGTGCGTGAAGGATCTGTC  
GCGGCTTTACTAGAACCAGTGATCGGTAAACTACCTTTTAGTTCGGCTATTAGCAGTACA  
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>RXN03148-downstream  
TAAGAGCTATAGTATCGTCAATA

>RXN03163-upstream  
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>RXN03163  
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TCGCCGATCGTGGTGATCCACCTCAAACAGCAAAGCTAATTGAGCAACTCAGTGATCGC  
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GAAGAGGCAGATACCTCCACGTCGTGGGAGTCATTGGGTGAGGTAAAGAACCCGATTTA  
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 GGCTACGTGCCAACCTTGGCGTGTGGAAACTGCCGCACCCAGCGCGGTGCCGGCACTGT  
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 GCTGTGGTGCTGGGAACGGAACGCACAGCAGAAGAACTGGGCGCGCGTTCCCGTCTGTG  
 CGGGTAATTACCTCTGGTGGCAACAAGGTGGTGGATTGGGTGGAAAACCGAGCCAGCATT  
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>RXN03166-upstream

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>RXN03166

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 GTGCAGCGCTTCCGATTGAGAACATTTCCCAGGCCAGCGCAAACCAGCGTTCTGGTCGT  
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 TCCCGTGATGGTGAGAGCAAAGAATTCAGTGGAGCCAGAGGTACCAAATTCCTGGTCTTT  
 CCTGGTTCTGCGCTAACCAAGAAGCCGCCACAGTTTCATCATGGCTGGCCAAATTGGTAGAA  
 ACCTCACGTTTGTGGGCTCGCGATGTAGCCAAGATTGAACCAGAGTGGGTGGAAAAAGCA  
 GCCGGCCCATTTGCTCAAGCACCAATACTCTGAACCGTATTGGTCTTCAAAGCGTGGCGGC  
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 TCCCTACCACACGGT

>RXN03166-downstream

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>RXN03175

GTCCGCGCAAGCGAAAAAGACACCGCCACCGCACTGCAACCCGCCTTAGATAACGGATGG



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CATGAACTTGAAGATGTGAACATCGGTTTTGGATCTTTCCTTGACTCCGGCCGCTACATT  
GAAGCAACCATCAAAGACACCACCCTGGATGTGCCAGTAACCGTGGCATCTCTTTACCTC  
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GACGGCCCCCTACACTTGGTGGACCTACCGCGGAAAAGCCTTCGACACCGGCGCCGGATGG  
CGCATCGACTACCAAGCAGCAACCGCAGCGATGCTCGAACGCGCAGAACGCTCCTGGGTA  
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TCC

>RXN03175-downstream  
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>RXN01389tr  
CAGGACGGCGATAAGCTCGCTGGCCGCCACGGTAACAAGGGTGTGTGCGGTAAAATTTTG  
CCTCAGAAAGATATGCCATTTCCTTCCAGACGGCACTCCTGTTGACATCATCTTGAACACC  
CACGGTGTTCACGTCGTATGAACATTGGTCAGGTTCTTGAGACCCACCTTGGCTGGCTG  
GCATCTGCTGGTTGGTCCGTGGATCCTGAAGATCCTGAGAACGCTGAGCTCGTCAAGACT  
CTGCCTGCAGACCTCCTCGAGGTTCTTGCTGGTTTCCTTGACTGCAACTCCTGTGTTTCGAC  
GGTGCCTCAAACGAAGAGCTCGCAGGCCTGCTCGCTAATTCACGTCCAAACCGCGACGGC  
GACGTCATGGTTAACGCGGATGGTAAAGCAACGCTTATCGACGTCGCTCCGGTGAGCCT  
TACCCGTACCCGGTTTCCATCGGCTACATGTACATGCTGAAGCTGCACCACCTCGTTGAC  
GAGAAGATCCACGCACGTTCCACTGGTCTTACTCCATGATTACCCAGCAGCCACTGGGT  
GGTAAAGCACAGTTTCGGTGGACAGCGTTTCGGCGAAATGGAGGTGTGGGCAATGCAGGCA  
TACGGCGCTGCCTACACACTTCAGGAGCTGCTGNCCA

## APPENDIX B: AMINO ACID SEQUENCES

&gt; RXA00050 (1-2196, translated) 732 residues

MSNTENVNGD VEQPNNVISS ESQETPQGDS ASADFALETP TNTVEDAPAS EGSEEITRVA  
 DTSEDADSAD ADNASNVINE NEDSSEGANQ PSNESSSTEAL KSGFDALGLP ERVLDVARKV  
 GYETPSPIQA QTIPILMGQ DVVGLAQTGT GKTAAFALPI LARIDKSVRS PQALVLAPTR  
 ELALQVADSF QSFADHVGGGL NVLPYGGQA YGIQLSGLRR GAHIVVGTPG RIIDHLEKGS  
 LDISGLRFLV LDEADEMLNM GFQEDVERIL EDTPDEKQVA LFSATMPNGI RRLSKQYLLN  
 PAEITVKSET RTNTNITQRF LNVHRNKMD ALTRILEVTE FEAMIMFVRT KHETEEVAEK  
 LRARGFSAAA INGDIQAQR ERTVDQLKDG RLDILVATDV AARGLDVERI SHVLNFDIPN  
 DTESYVHRIG RTGRAGRTGE AILFVTFRER RMLRSIERAT NAPLHEMELP TVDQVNDFRK  
 VKFADSITKS LEDKQMDLFR TLVKEYSQAN DVPLEDIAAA LATQAQSGDF LLKELPPERR  
 ERNDRRRDRD FDDRGGRGRD RDRGDRGRG SRFDREDDENL ATYRLAVGKR QHIRPGAIVG  
 ALANEGGLNS KDFGRITIAA DHTLVLPKD LPQSVLDNLR DTRISGQLIN IERDSGGRPP  
 RRFRDDRGG RGGFRGDRDD RGGGRGRDRD RGSRGGRGG RDRDRGGRG GFRGRDRGD  
 RGGRGGRGG RD

&gt; RXA00060 (1-2457, translated) 819 residues

VTEKTDQTLN LIDGHSMAFR AFFALPAENF STSGGQATNA VYGFLSMLST LLKDEQPTHV  
 AVAFDVGRKT FRDMFPAYK AQREATPPEF KGQVEILKEV LSTLGITTIE KIDFEADDVI  
 ATLSVAAKPL GFKTLIVTGD RDSFQLVNDT TTVLYPMKGV SVLHRTPEA VEEKYGLTPR  
 QYPEFAALRG DPSDNLPNIP GVGEKTATKW IAQYETLDNL LDHADEIKGK VGASLRERIE  
 QVRMNRKLTE MVKDLELPLG PDDFEMKPVQ VAEVAAKFDD LEFGTNLRER VLAVVKAEGS  
 AAPVEEVEAE QVVVDTSQSLA QWLPARAGQA LALALAGVAK PAAGDTYALA IADTKRHAVL  
 VDVADISAED EKALATWLAS EDPKMLHGAK AAYHMLAGRG FELHGVVHDT AIAAYLLRPG  
 QRTYELADVY QRHLQRQLST NDNGGQLTLL DAADDQSLVD DVIAILELSE ELTKQLQEIQ  
 AFELYHDLEI PLSGILARME AIGIAVDVAT LEEQLKTFIG QVAQEEEAAR ELAEDPTLNL  
 SSPKQLQVVL FETFGMPKTK KTKTGYSTAA AEIEALAIKN PHPFLDHLA HRQYQMKMTT  
 LEGLIREVAP DGRITHTFNQ TVASTGRLLS TDPNLQNIPI RTEAGRKIRS GFVVGEGYET  
 LLTADYSQIE MRVMAHLSQD PGLIEAYREG EDLHNYVGSK VFNVPIDGVT PELRRQVKAM  
 SYGLVYGLSA FGLSQQLSIP AGEAKQIMES YFERFQGVQR YLREIVEEAR KAGYTETLFG  
 RRRYLPELTS DNRVARENAE RAALNAPIRE LPQTSSRWP

&gt; RXA00061 (1-210, translated) 70 residues

MIRVDRSLKE AAVKSRVLLQ VHDELVVEVA AGELEQVREI LEREMDNAIK LSVPLEVSAG  
 DGVNWDAAAH

&gt; RXA00066 (1-813, translated) 271 residues

VTDPLSAALD SGRINHAYLF SGPRGCGKTS SARILARSLN CVEGPTSTPC GVCNSCVALA  
 PGGPGTLDVT ELDAASNGV DDMRELRELA NYAPAESRYR VFIIDEAHMI STQGFNALLK  
 IVEEPPAHLI FIFATTEPDK MIGTIRSRTH NYPFRLTPG DMRKVLKNAV DGEGVHVDDS  
 VYPLVIRAGG GSPRDSLSIL DQLIAGSGPE GLTYERALPL LGVTSFTLID DSIHALASKD  
 NASMFTTIDN VIEEGLEPRR FTIDLPSDPL R

&gt; RXA00095 (1-2289, translated) 763 residues

MNTSPFTPGS PDLIDGLNEQ QRAAVEHIGS PLLIVAGAGS GKTAVLTRRI AYLMRYRGVH  
 PQQILAITFT NKAAMERER VSQLVGPVAV RMWVATFHSV CVRILRQQAQ LVEGLNTNFT  
 IYDSDSRRL LTMIADLEL DIKKFSARTL LGAISNLKNE LVTPQEALAD AERTHNPHYET  
 VVARAFSEYQ SRLRRANAVD FDDLIGETVR IFREHPPVAE YYRRFRHVL IDEYQDTNHA  
 QYELISTLVG KPDQDPSELV VVGDSQSIY AFRGATIRNI EFERDFSNA RTILLEQNYR  
 STQTILSAAN AVISQENRR PKNLWTALGE GEQIIGYVAD NEHDEARFIA SEIDNLVDHG  
 MSYSDIAIMY RTNNSRALE DVFMRTGVPY KVVGGTKFYE RKEIRDIIAY LRVLENPDDT  
 VNLRIINTP KRGIGDRAQA FIALHSENNQ ISFGQALLDA ALGKVDLLGA RGKNAIKFN  
 ELFDALRSEL PTMVNEVTGL PDIGQVISRI LDITGYKAE EASNDPQDGA RLDNLNELVS  
 VAREFSSDAA NRMVNEVPEG EAQPGSLQAF LERVSIVADA DQIPDSNGV VTLMTLHTAK  
 GLEFFIVFLT GWEDGQFPHL RSLGDAKELA EERRLAYVGI TRARKLYMT RAMLRSSWGN  
 PVTNPPSRFL QEVPAELIDW RREEPQMSSA WAPRPTRSIP TKTRTNKQL DLSVGDRVNH  
 DKYGLGTVLS SDGSGPRATV TIDFGSSGKV RLMLLGGVPM EKL

&gt; RXA00103 (1-4560, translated) 1520 residues

MAKSILSRFR PQVAEWFDRV FASPTPVQEG TWEAVSKGKN ALVVAPTGS KTLAAFLWAL

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DSLTEQTGQQ VLDTGTPVPV RGGKVKVLYI SPLKALGVDV ENNLRAPLTG IARTASRMGL
DVPNITVAVR SGTTPSAERA RQVRKPAHIL ITTPESAYLM LTSKAGATLS DVDVVIIDEI
HAMAGTKRGV HLAALTLELE KLVGRPVQRV GLSATVRPLE TVAGFLGGGR PVEIVAPPAE
KKWDLTVTVP VEDMSDLPVQ EPGSTIGELV MDDPLGITGE SALPTQGSIW PHIEQQVYNQ
VMSAKSTIVF VNSRRSAERL TSRLNEIWAM EHDPELSLPQ LRRDPAQIMS SADVAGKAPQ
VIARAHHSV SKDERATTET MLKEGRLRAV ISTSSLELGI DMGAVDLVIQ VESPPSVASG
LQRVGRAGHT VGATSIGSFY PKHRSDLVQT AVTVQRMKEG LIEEIHVPKN ALDVLAQQTV
AAVSIKDVQV DEWYETIRKA YPYRDLAREV FDSVIDLVSG VYPSTDFAEI KPRVVYDRVS
GVLEGRPGSQ RVAVTSGGTI PDRGMFGVFL VGDGPRRVGE LDEEMVYESR VGDVFTLGAS
SWRIEEITRD QVLVTPAPGH TGRLPFWTGD AAGRPAELGK ALGAFRRSTL TDPSSSGLEG
WAHDNLI AFL QEQEESTGVL PDEKTLVLER FKDELGDWRI VLHTPYGRGV NAAWALAVGA
KIAEETGMDA QAVAGDDGIV LRLPEGDEDP SAALFMFEAE EIETLVTEQV GNSALFASRF
RECAARALLL PRNPGKRAP LWQQRQRAAQ LLDVARKYPS FPIILETVRE CLQDVYDLPA
LKNLIEDLQL RKVRIAEVTT QQPSPFASAL LFNYTGAFMY EGDSPLAEKR AAALALDPAL
LAKLLGEVEL RQLLDPDIIA EVHQQLRRQG DRAARNNEEL ADLRLILGPI PLDELGEHIT
FENPDLEDRA MTRVINGREH LAQVLDAPLL RDALGVPVPP GVPAQVETIT DALEQLVNRW
VRTRGPFTAN DLAEAFGLGI ATAITALQSA PVIEGRYRQG VDVQEYCATI VLSIIRRRSL
AAARKQTRPV SOSAFARFLL DWQQIAPVGA TPELRGVDGT YTVIEQLAGV RLPASAWEDL
VLPRRVADYS PIHLDELTSN GEVLIVGAGQ AGSRDPWISL LPVDYAAQLV GEASTSMSPL
QDAVLDQLRA GGAFLLFSDIL EENFGYTAAQ LQEA MWGLVE AGLVSPDSFA PIRARLASGT
TAHRAKRRPA RSRLRTRTSF ASDVPPDMRG RWTLSVQPAD ATSRVAHGE GWLDRYGVLT
RGSVVAEDIV GGFALAYKVL SGFEESGKAM RGYFIEGLGA AQFSTPAIID RLRGHDDSPD
VEGWPSGATD PDVYLIAAAD PANPYGAALP WPEQGPSRAA GAMVVLCDGL LLAHLTRGGR
TLTVFSDNIP KIATALITYE RLTVEKINGD NVFDSPLLEQ FRKHGATITP KGMRFRPPVA
RETPSDTLPT RTFRGGFGRR

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> RXA00157 (1-1263, translated) 421 residues

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ARIVAEQREA EAVEKKVQTE AAIAANSEQL NVLTTNRSTL VAQRDGAERN LAIARAQADN
LQGQRAEYEE FQQAEEQARIQ AEAEAEQAAAE EKRRADEAAA QAAAEAEQEA QQAQAAEEAQ
AAQAAETAQA QAAQAAETQA AQAAQAQAEA NDRAAAQORA AEAEQAAAEQA QREADAQAAN
DAQAALREQ ALTAASIAAA ALIAASQSSH ATTQNPYPTD EDADPTDIAD IQGPTQPGTG
ESGDSQSNS DNDSTGNDST GSDSSSDSDSS GNDSSSEVISG DRSAQIETVI ARAMSQGLVQ
YAWGGGNANG PTLGIRDGGV ADSYGDYNKV GFDCSGLTLY AFAGVGISLP HYTGYYQYQH
TKVSPSEMQR GDLIFYGPGA SQHVAIYLGD GQMIEAPNSG SVVKISPVRW SGMTESVVRL
I

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> RXA00163 (1-561, translated) 187 residues

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LDQAGLDSVE LLALRDVEAY DEPIEDGRTF ADNAQIKARA GVTHGTGIATI ADDSGIAVEE
LNGMPGVLSA RWSGAHGNDT ANNELLQAQM EHVDPERRNA AFVSVCVLAL PDGQEFVQEG
RWEGQLLRGP KGENGFYDYP LFIPAEEDIG QGRSSAELSA EEKDALSHRG QALRGLVEKI
AQVAAAS

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> RXA00208 (1-849, translated) 283 residues

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MNTAPPRKRR EMKIKTATVT GVRQISPDLI RFSFDCPEIV GADLGFTDHY IKILFVPAGA
DYSWPFDMAE IAETQPRELQ PVRRTYTFRT VDTVAGTFDI DFVAHGTDGL AGPWAQQAQV
GDVIAFGGPG GAWKPETTYE HYVLAGEDEAA APAIFAALAH LPAGTTAKAF IEISSNEARF
NAPASDNIEV VVWVRDGAH GTLLIDALRQ DGYPTKKT SW FIHGVAEMVK ETRKFLFVEG
NVDKADASIS GYWRLGMTED QWQASKREFN EQNEAEELAL SKA

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> RXA00212 (1-1560, translated) 520 residues

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MNILCLLCWK FAVRCSSLWR ISQEVNAQRI ADGGKPFANP RNAAAGSLRQ KNIEDVKKRR
LRMISHGIGF TEGFSPASQH DAYLALAANG LPTSPYTEAV TDPEDVVKKV SYWADHRHDA
LHEMDGLVIK VDDIASQRL GSTSRAPRWA IAYKYPPEEV TTKLLDIQVG VGRTRGVTPF
AVMEPVLVAG STVSMATLHN QSEVKRKGVL IGDTVVIRKA GEVIPEVLGP VVELRDGTER
EYIFPTLCPE CGTRLAPAKA DDVDWRCPNM QSCPGQLSTR LTYLAGRGAF DIEALGEKGA
EDLIRTGILL DESGLFDL TE DLLSSNVYT TNAGKVNASG KKLLDNLQKS KQTDLWRVVLV
ALSIRHVGP AARALAGRYH SIQALIDAPL EELSETDGVG TIIAQSFKDW FEVDWHKAIV
DKWAAAGVTM EEEVGEVAEQ TLEGLTIVVT GGLEGFTRDS VKEAIIISRG KASGSVSKKT
DYVVIGENAG SKATKAEELG LRILDEAGFV RLLNTGSADE

```

> RXA00213 (1-573, translated) 191 residues

VTEDNAQLRR TWNDLAEKVR YHRDRYYNEQ PEIPDADFDA LFKQLQQLEE DHPELAVPDS  
PTMVVGAPVA EQSSFDNVEH LERMLSLDNV FDEQELRDWL GRTPAKQYLT ELKIDGLSID  
LVYRNGQLER AATRGDGRVG EDITANARVI EDIPHQLQGT DEYPVPAVLE IRGEVFITVE  
DFPGGQRAAH C

> RXA00214 (1-711, translated) 237 residues  
MNSPSNPSPT VPSLDTTKML SFDLETTGVN PFDTRIVTSA MVTITSKGAE PIELLADPGI  
EIPAAATAVH GITTEHARAN GRPHDEVLA E TISRLRAGWQ AGLSVIVFNA SYDLTVLRNH  
DPSFTIDGLV YDPFVIDKVK DRYRKGKRTL TDMCAHYDVQ LGNAHEATSD ALAAARIAWK  
QVRLWPELTK MTGEELMEFQ AVNYEQQKS FRSYLIGQGR DASDVNTSWP VQTDPAS

> RXA00313 (1-939, translated) 313 residues  
MAGNDSRRGG LRKTNKKGAT KSGGQVRRG LKKGKPTPKA EDRTYHAAHK RKVERDRRDR  
GRHQREMPPEL VVGRNPVLEC L HARVPATAL YVAEGAANDE RLSEAVHTAA GRNLPVLEVN  
KLELDRMTGN GMHQGIGLAI PPYAYADVHD LIANAAASKK PGMFVILDNI TDPRNLGAVI  
RSVGAFFGNG VIIIPERRSAS VTAVAWRTSA GTAARVPVAK ETNMTRVVKE FQONGYQVVG  
LDAGGDHTLD TYDGTDNVVI VVGSEGGKGIS RLVRENC DTI MSIPTEGWVE SLNASVAAGV  
VLSEFSRQRR IKG

> RXA00341 (1-1407, translated) 469 residues  
MKLYAAVLDF EPVAQEFVGE RGFDPHIHDE AASSVDRYAQ EREDLLHMPF VTIDPVGSRD  
LDQAVLIEEI DSGFRVHYAI ADVAAFVEPG SELEKISLHR GQTIYLPDSP ARLHPEELSE  
DAASLLEGQT RPAVVWSIDL DERGEVTATK VRRGLVKSR RLDYDQAQID AENGR LHPSI  
SLLPKVGQLR QESALRREAV NLSIPSQRVV KVPND DAGEH YEIVIEPRPH IMDYNSEISL  
LTGMVAGEMM VKAGHGILLRT LAPATKESEA TFRSEAQALG FEIAPEQPIG EFLQSVDPNT  
PKGMAIQREA QKLLRGSGYA SVKNGDSEVH SGVGGYYAHV TAPLRRLIDR FATEHCLAIA  
SGTDVPEWVT RVEEQVLD TM KYSSILASQV DNACLDL TEA TVLKYWEGQN FNAV VVASEP  
EKNSARLFVY KPPVLAKCIG APEQGTNQDV TLVTANLKKR EVLFAWPAD

> RXA00361 (1-1848, translated) 616 residues  
MTTSETAPSK ASLYELLEGV SLSDERTFRR RLSKARAPKA LGAIKADIDK ARLLIDEKSQ  
LIPSITYPEN LPVSSRRDDI AEAIRDNQVQ I IAGETGSGK TTQIPKICLD LGRGRRLIG  
HTQPRRLAAR TVAERIADEL GQDIGESVGY AIRFDDRVS HTSVKLM TDG ILLAEMQRDR  
FLNAYDTIII DEAHERSLNI DFILGYLRQL LPKRPDLKVI ITSATIDPER FAEHFADASG  
KPAPIIEVSG RTFPVEIRYR PLEVLDGDKI IDTDPLDGLC SALEELMAEG DGDILCFFAG  
ERDIRDAMEA IEARRWKGV E VTPLEFGRLSN QEQRHVFSPH SGRRIVLSTN IAETSLTVPG  
IHYVVD TGTA RISRYSVRTK VQRLPIENIS QASANQRSGR CGRVADGIAI RLYSEDDFNS  
RPEFTDPEIL RTNLSAVILR MASRLGDIN DFPPVQAPEQ RSIRDGILL HELGALTD DT  
QADGSPQLTQ IGKDLANIPV DPRMARMLVE ANTLGCLHSV MVIVSALTIQ DVRERPLEFQ  
AQADQAHARF KDTTSDFLGF LKLWEYIADQ RNQSSGNSFR QQMKKEFLHY MRIREWWDLV  
RQLEQIGQQL GWAKKE

> RXA00407 (1-576, translated) 192 residues  
LNVAQVEALA RAGAVDCLGV GRRQALWQAG VAAATEKPGML PGLSVIEAPA LPGMSAFELM  
ATNISATGVT ADYQPMALIR ERMEELGIVP ADRLLEVEDG TRLRIAGIVT HRQRPQTASG  
LTFLGMEDET GLMNMVMSVG LWQRQVRLAR NAKALIIRGI VQNAQGVATV VADRLEPLDM  
GEFLSRGSRD FR

> RXA00414 (1-420, translated) 140 residues  
MQGEASVPFA ELHATSSYNF LTGASDPSDV VVQAKKLGLA ALSVMDRDGF YGAVRFAEAA  
AEAGMHTVYG AELS LQEGVL TVLCKNPEGY KKLSHLISDA KMARGEKGF AIRRCQWLLN  
MLQGIGWSLQ VFSGWTKSTM

> RXA00415 (1-1962, translated) 654 residues  
MVAEHAAGDW VVLAGFQWLD KIDYVIDCFK PENIVLEFGS TMTPEDADR N EYLRRTQAKF  
QLRGILSTNP ESAARGSVRL AGAKQALARK MPLADAESEL HPMGTTWMRS GDTLLKAHPD  
YADLIATTVE LAAECAFTLD LVAPNLPKWD TPGEHTEMSW LAHLVSTRID TRYVGRSADI  
KARAATQIDY ELGVIEKLGF PGYFLVNDL VEFCDRSNIL CQGRGSAANS AVCFVLGITN  
AEPISAGLLF ERFLSPDRDG PPDIDIDIES GRREEVIQYV YEKYGRDNAA QVANVITYRT  
KGAMRDAARA LGYPQGAADA WAKGTSEPPD DVLELAAQFK GQPRHLGIHS GGMVICDRPI  
ADVVPVEWAR MDNRSVVQWD KDDCATAGLV KFDLLGLGML EAIHHMLDLV AEHRGKKINL

WELDLAEPEV YDMLCKADAV GVQVESRAQ LSTLPRLKPR TFFDLVVEVA LIRPGPIQGG  
SVHPYLRRRA GEEAITYDHP VLEKSLGKTL GIPLFQEQLM QVAVDAAGFS GGEADSLRRA  
MGSKRSPERM AALRSRFFQG LKDTNGIVGE TAEKLWNKIV AFAAYGFPES HSQSFAVLVY  
FSAWFKYHYP AEFCVGLLRA QPMGFYSPQS LISDARRHGV SILPITVNDG GVEA

> RXA00460 (1-378, translated) 126 residues  
MPEHPLHVIF DNPVIPPNTG NAIRMCAGTG AHLHLVEPLG FELTEKHLRR AGLDYHDLAD  
VTVHATFDEA MAAVPGRVFA FTTTANTRFT DIAFEPGDAL LFGTEPTGLP QEHEVHSRIT  
SELRIL

> RXA00538 (1-1269, translated) 423 residues  
MSRISARTLA IALAGATAAS LAVVPAATAN PAGTAPVINE IYEGGGNSGS LFSNDFIELY  
NPTSGDISLD GWSVTTYAAN GNSGGTTNLT GNIPANGYYL IQQRAGSNNT GALPTPDATG  
NLAMGASQGS VALTDNSGLT ADLVGFGGTS MFEGTAAAPE TSNKLSVQRK EVGADSDNNS  
VDFETGAPTP TSSGGSAPVD PGEPETPVNP GETVSIAQIQ GTGLATPLEG QTVTTEGIVT  
AVYAEGGFNG YYIQTPGSGT APKVAGDASD GIFVYVGSNG SYPELGASVT VTGKATEHYE  
MTQLGNSSFT VSDTAFEPVT PLELDTVPTG DDIREAYEGM LLKPTGAHTV TNNYATNTFG  
EIALAPGNEP LYQATQMVAP GAEAIAYEAE NVAKQITLDD GRSGNYTRGD SSTPMAWLVO  
DGG

> RXA00542 (1-519, translated) 173 residues  
ALFLTVNVWR QAAENVAESL SKGMRVIVTG RLKQRSYETR EGEKRSVFV EADEVGPSLT  
FAKADVQRTG RGGNSGGNYG GGNQGGGLGG NQGNQGGGFS NQNSGGFGGN QGNQQQSNQG  
GFGGNQNSQ GNNFNQGGFG GGSPQAAPDN DPWNSAPPAG SGGFGGADDE PPF

> RXA00543 (1-426, translated) 142 residues  
MKLILTAAVE NLGVAGDIVE VKNGYGRNLL LPRGLAIVAT PGAEKQIEGI KRAQEAREIR  
DLDHAREVKV ALEALEGVTI AVRTSESGKL FGSVKTDDIV DAVKAAGGPN LDKRAIVLPK  
NLVKTITGKYQ VEAKLTDGIV SA

> RXA00544 (1-1530, translated) 510 residues  
MATDTHAASF DDDYVPPQEP SDSFADDAHV DVPAPAFEDF SPAQAFGQGT RGGDSQGFKK  
RGRKDESREY RDFRQPPYDN DAEMGVLGAM LLSPTTVIDI LDILTPEDFY RPSHQLIFQA  
IIDLFSDNRD IDPVIVSGRL DRTNDLDRVG GGAYLHDLIQ SVPTAANARY YAEIVSEKAV  
LRLVDAGTR VVQLGYEGDE GAEIDAVDR AQQEVFAVSQ KNQSEDYAVL ADILDETMAE  
LEMLNDGGIA TGIPTGFKDL DDLTNGLRGG QMIIVAARPG VGKSTIALDF MRSASIKNNM  
ASVIFSLEMS KSEIVMRLLS AETEIRLADM RGGKMDTAW EKMVQKLDKV AQAPLFIDDS  
ANLTMMEIRS KARKLKQKHD LKMIVVDYLQ LMSSGKRVES RQQEVSEFSR QLKLLAKELD  
VPLIAISQLN RGPESRTDKR POLADLRESG SLEQDADIVM LLYRPDSQDK DDERAGEADI  
ILAKHRGGPI DTVQVAHQLH YSRFVDMARG

> RXA00545 (1-255, translated) 85 residues  
MIILDPSQDE RTVAPSLDKF LEVVRKDKGD VVKVDVWGKR RLAYPIDKKE EGVYAVVDLK  
CESATVLELD RVLNLNDGVL RTKVL

> RXA00562 (1-630, translated) 210 residues  
MDADPLIEDD VSGAEVKDSS DEPLLALTRY VFDRGERPVT RGLFHQVAAI LSIVSGSVLS  
TYAWMELVWW QALGVMVYAL AMLGLFAVSA AYHRGPWRRL HTVAWWRKAD HSTIAVFIAA  
TYTPLCLIVL EPGTAAWMLG IAWVGAIDSV IMNMVWINHP RWLSVLVYLA LGWLIVPLVP  
QLWSGAGPTV VWLLLAEGIV YSVGALVYGF

> RXA00625 (1-339, translated) 113 residues  
SDHDPIKVG F NLSETTEPTI PVEPTDPAEP TDPTTPVKPT DPVETTDPS PTDPAEPTDP  
AEPTDPEETK KPEEPKNPGS SNGSSQYATI AAIIAAILGA IALAFQFFHS SSN

> RXA00670 (1-489, translated) 163 residues  
MPTPKKGARL GGSASHQKKI LSNLAASLFE HGAIKTTDAK AKALRPYAEK LITKAKSGSV  
ADRRNVLLALV PNKEIVAYLF NELAPKFENR PGGYTRIIKL ENRKGDNAPM SQISLVLEET  
VSAEASRATR ASASKKAAEE AETEEVVEAP AEETATEEAA EEK

> RXA00671 (1-1014, translated) 338 residues

MLISQRPTIT EEFVNNARS FVIEPLEPGF GYTLGNSLRR TLLSSIPGAA VTSVKIDGVL  
 HEFTTISGVK EDVSDIILNI KGLVLSSDSD EPVVMQLVKE GPGVVTAGDI QPPAGVEIHN  
 PDLHIATLNE TAKIEIELIV ERGRGYVPAT VTATGGEIGR IPVDQIYSPV LKVSYKVEAT  
 RVEQRTDFDK LVIDVETKNS ITARDALASA GKTLLVELFGL ARELNIAAEG IEIGPSPQET  
 EYIAAYSMPT EDLDFSRSY NCLKREDIHT VGELAERAES DLLDIRNFGQ KSINEVKIKL  
 AGLGLTLKDA PEDFDPSTLE GYDAETGGYI DVEAEDSE

> RXA00672 (1-603, translated) 201 residues  
 MARYTGPATR KSRRLRVDLV GGDMAFERRP YPPGQAGRAR IKESYLLQL QEKQKARFIY  
 GVMEKQFRRY YAEANRRAGK TGENLVVLE SRLDNVYRA GLANTRRQAR QLVSHGHFTV  
 NGKAIDVPSF RVSQYDIINV REKSQKMNWF EEAQDNLADA VVPAWLQVVP ENLRILVHQL  
 PERAQIDIPL QEQLIVEFYFYS K

> RXA00673 (1-90, translated) 30 residues  
 LQAAGLEIGS ISDVTPQPHN GCRPPKRRRV

> RXA00694 (1-396, translated) 132 residues  
 MTMTDPIADM LSRVRNASNA HHDTVSMPS KIKANIAEIL KQEGYIANYT VEDAKVGKTL  
 SLELKYSNTR ERSIAGLRRV SKPGLRVYAK STNLPQVLGG LGVAIISTSQ GLLTDRQATE  
 KGVGGEVLAY VW

> RXA00695 (1-534, translated) 178 residues  
 MSRIGKEPIT IPSGVETKID GQLVEVKGPK GTLNVNVPPEP ISVAVEDGKI VVTRPDDHRT  
 NRSLHGLSRS LVNNLVVGVV EGYTIKMEIF GVGYRVALKG KDLEFSLGYS HPVLIASEG  
 ITFAVDGNTK LSVSGIDKQK VGQVAIVIRR LRKDDPYKKG GIRYEGEQIR RKVGKTGK

> RXA00696 (1-402, translated) 134 residues  
 MSNTENKQKR VSVGKDIATR RRVARARRHF RIRKNLRGTP EAPRLVVHRS SRMHVQIID  
 DVAGHTLAAA SSIEAEVRAT EGDKKAKGAK VGQLIAERAK AAGIEQVVFD RAGYKYHGRV  
 AALADAAREG GLKF

> RXA00697 (1-633, translated) 211 residues  
 MPGRERRDGG RSADDNKQND RNERRGGRR DDRRNQQQDE RSQYIERVVT INRVSKVVKG  
 GRRFSFTALV IVGDGKGMVG VGYGKAKEVP AAIQKGAEAA RKNFFRVPMV NGTITHPVQG  
 EKAAGIVMLK PAAPGTGVIA GGAARPVLEC AGIQDILSKS LGSDNAINVV HATVDGLKQL  
 VRPEEVAARR GKTIEEVAPA RILRARAGQE A

> RXA00698 (1-183, translated) 61 residues  
 MALKITQIKG TVGTPKPHRE NLRSLGLKRI RHTVIRPDTP EVRGMILAVR HLIVVEEVAG  
 E

> RXA00699 (1-444, translated) 148 residues  
 MSEPIKLHDL RPAAGSNKAK TRVGRGEASK GKTAGRGTKG TKARKQVSAA FEGGQMPLQM  
 RLPKLKGFKN PNKVDYQVVN IADLAEKFPQ GGDVSIADIV AAGLVRKNEL VKVLGNGDIS  
 VKLNVNTANKF SGSAAKEIEA AGGSATVA

> RXA00706 (1-267, translated) 89 residues  
 EFLDRLLTVA LPRIRDFRGL SDQQFDGHGN YTFGLTEQTM FYEIDVDKID RPRGMDITVV  
 TTAVTDDAGR SLLRELGPFF KGEDGNRQQ

> RXA00709 (1-339, translated) 113 residues  
 VADNTGAREI LCIRVLGGST RRFAGIGDVI VATVKEATPG GNVKSGEIVK AVIVRTKKT  
 RRADGSYISF DENAAVIAIK DNEPRGTRIF GPVARELREK KFMKIVSLAP EVI

> RXA00710 (1-312, translated) 104 residues  
 MKVHKGDMVL VISGPDKGAK GQVIAAFPKT EKVLVEGVNR IKKHVANSAP ERGAESGGIV  
 TQEAPIHVS NVMVIDSDGNP TRVGYRFDEN GKKVRVSRN GKDI

> RXA00711 (1-156, translated) 52 residues  
 MTENYIPRLK TRYQDEIRTK LQGEFEFENV MQIPGVTKIV VNMVGDAAR DS

> RXA00717 (1-960, translated) 320 residues

VTPPARRDGT PDKKQSNRSG GYRSSVRGYK PGSSRPNTRQ QPQKKDEILL SNAKPAKKQN  
VKSDDDWSMG FLNRNDSGV RLQKVLAAQAG VASRRHAEIL IDQGRVEVND RIVTTQGVVRV  
DPNNDVIRVD GVRIHINEDL EYFVLNKPGRG MHSTMSDELG RPCVGDLVSE KTASGQRLFH  
VGRLDADTEG LLLLTNDGEL ANRLMHPKYE VSKTYLATVR GEATNKLVSAL LRDGVELEDG  
PAKADFAQII DVFQGKSLLR IEIHEGRKHI VRRLFDELGF PVERLVRTKL HTVQLGDQKP  
GSLRALNSSE LTSLYKVVQL

> RXA00789 (1-243, translated) 81 residues

MTNPDIIVGSG QGNDSFEPVA QLSYERARDE LVEIVKILEL QMGGLDESLK YWERGEALAK  
RCEEHLGAS ARVEQALNQA E

> RXA00790 (1-1026, translated) 342 residues

RNRPTPLKDG DRVIVYGKPA FYAGRGTFSL WVTDIRPVGI GELLARIEEL RKRLAAEGLF  
DPARKKRLPF LPNRVGLITG RGSAAERDVL SVAKDRWPEV QFEVINTAVQ GASAVPEIIE  
ALRVLDQDPR VDVIIIARGG GSVEDLLPFS EEALQRAVAA AQTPVVSAG HEPDTPVLND  
VADLRAATPT DAAKRVVPDV AEERMLINQL RSRSAALRG WVQREQQALA AIRTRPVLAD  
PMTPINRRRD EIAQAVGLIR RDVTHLV RTE QALVASLRAQ VSALGPSATL ARGYSVVQVI  
PRDGSAPPEV TTIEQSPPGS QLRIRVADGS ITAASMGTOQ AN

> RXA00798 (1-2355, translated) 785 residues

DYWDLSAEFN ARENGKADSD NPSSFTARLS TIDGNRVAQG RDFNDRGELT SEAVVVDKQR  
AEALAEALEG QEMAVVGVEE KPYTRRPYAP FMTSTLQOES GRKLHYTSE TMRIAQRLYE  
NGHITYMRTD STSLSEQGMK AARDQALELY GAIEYVSPSPR TYDRKVKNSQ EAHEAIRPAG  
ETFATPGQLH QGLDAEEFKL YELIWQRTVA SQMADAKGTS MKVTIGGTAK TGEKTEFNAT  
GRTLTFPGFL RAYVETTRTA DGRDVADNAE KRLPLLSEGD LLKVLSEAD GHSTNPPARY  
TEASLVKKME DLGIGRPSTY ASIIKTIQDR GYVYSRGNAL VPSWVAFVAV GLLEANFTSL  
VDYDFTSSME DELDNIAAGR EGRTWLNLF YFGDAEADQS MAESVARQGG LKALVDANLE  
HIDARSVNSL KLFDDAEGRA VNVVRVGRYP YIERIVGTTA EGEPEFQRAN LPEETTPDEL  
TLEVAEKLFA TPQGGRELGI NPANGRMVVA KEGRFGPYVI EQVTDSEERAG AEAQAEVVVA  
AERKAEDQOR ATDGMRPKNW ETKTAANQKE KRINQLVEEN LKPATASLFS GMEPAAVTLE  
EALKLLSLPR EVGVDPDSNE VITAQNGRYG PYLKKGSDSR SLNSEEQIFT VTLDEARRIY  
AEPKRRGRAA AQPPKQLGD NDVSGKPMVT KDGRFGPYVT DGTTNASLRK GDVPESLTD  
RANELLSEER AKEAADGGAP AKKTSTKKTAK AKKTAKKT AKKTVRKAPP KTTKNVVKAG  
AKKKS

> RXA00807 (1-1119, translated) 373 residues

VFDLAGSKT VSKTLFDAAS SARALVRART TERARARAEH QNPAMIHDSG FAQSWLFTGP  
PGSGRSVAAK VFAATLVCSN PDVVGCGQCE DCRAAMGGSH PDIEHIVPQQ LSIQVDAARE  
VIKAAVSPV AGNWRVVIFE NADRLTMQAA NALLKTVEEP TESTVMILCA PTTDPRDIAI  
TLRSRCRHLY IPTPSIAEVA RILVAEGNVS QADAELAAAA SGAHIGRARY LAHNNAQRR  
RASILNLAEL IFHGDVAFRS VNTLVKVMET EAKDSNKEKE EGDLEAVRIS LGMAAKGKGV  
HKAVERGAGD FKALEDQQKL RRTFLRDSL DLALVDLAGI YRDIIISSQ AQVGLTHPDM  
EGLSQELATK VSQ

> RXA00809 (1-510, translated) 170 residues

LTPDFESEK TQAMRPSFGE ELAAIVSKRY SESTLTHMVT LPASKAKYVD WPSWVPASLR  
DALVNRGINK LFSHQEQTAH LAWNGQHVVV ATGTSSGKSL GYQLPILSAL GTDPTACALY  
LTPTKALGSD QLTSTSTLLR DIPDFHPINP APYDGDTPSE ARSGIRDLR

> RXA00817 (1-1710, translated) 570 residues

FYGSHTPVIL ASATSSDPEI HASRLLAGPV KAVTEDGAPT GERTVLLWEP GFIEGAEGEN  
GAPVRRRAST EAANIMATLI SEGARTLTFV RSRRQAEIVA LRAQEELSTL GRPDFARRVA  
SYRAGYLAED RRRLERLLDD GTLLGVASTN ALELGIDVGG LDAVVTAGFP GTVASFWQQA  
GRAGRRGQGS LVVLVARDEP MDTYLVHHPA ALLEKPVAA VFDPTNPHVI RGHVYCAAVE  
KPLTEAEVAA FGAQKVVEKL EIEGLLRKRP RGWFAVEKPM SEDPDELSPD SAHQQVSLRG  
GSGSEFMIVD ITDGRLLGTI DSAKAMSQTH PGAVYLHQGE SFVIDELDL ENLALARPEL  
PDYTTYARSD TDIRITSAPL EDEVFDAGG LWVANVEVQV TDRVTGYVTR LSDGTTLDAT  
PLYLPPQILQ TRAVAYTIDP LALEAMGIPA ADIPGALHAA EHAAIGMLPL LATCDRWDIG  
GVSTALHADT GYPTVFVYDG MDGGAGFADT GFRRFAQWIE ATFEVVRSCS CESGCPSCVQ  
SPKCGNGNNP LDKAGAIKLL GAMVTLLGTS

> RXA00823 (1-780, translated) 260 residues

MGSIPTQKRP RVGSHIANKG QETDIGRKRR ARRINRTLTV AYPDAHCELD FTNPLELTV  
TILSAQCTDV RVNQVTPALF KRYPTATDYA NADRTELEEF IRPTGFYRNK ATSLIGLGEA  
LISLHDGQVP GTLEQLVELP GVGRKTANVV LGNAFGVPGI TVDTHFGRLV RRLKLTDEED  
PVKVEKVMNE LIEKPEWTMF SHRLIFHGRR ICHSRRAACG ACMLAADCPG FGLEGPSDPF  
EAQKLIKSDD REHLLKMAGM

> RXA00890 (1-1275, translated) 425 residues

LSIATVVALL FSGLLGAVES ALSSVSRARV EQMLKDEASG SASLLRVIDE RALHINMLIM  
LRTLLDASAA VFAGAIAVNV MDSWANGIVL AIVVVSLLTF AVVGVFGRTV GRKNPYSVML  
RSVVLSGLA KILGPIARGL IWIGNIAPG PGFRNGPYAT EVELREMVDI AQEHGIVEIE  
ERRMIQSVFD LASTTVRQVM VPRPEMIWIE SGKTAGQATA LCVRSRHSRI PVIGENVDDI  
IGIVYLKDLV QKTYATDGG KSVLVDEVMR EATFVPDSKS LDALLQEMQE DHKHIAILVD  
EYGGVAGLIS IEDILEEIVG EIADEYDARE VAPIEKIGDR TYRVVSRLSL EDLKDHIIEE  
LDLEIEFGDE IEDQVDTVGG LIAFELGRVP LPGATVETCG LKLTAEGAKN RRGRLRMHSA  
VVEVG

> RXA00898 (1-789, translated) 263 residues

MRIVNWNVNS ARTRVDRMVD FLLRHVDVVL AVQETKCKDE QFPTERFTEI GYEVAFHGLN  
QWNGVAIISR VGIENVETHF PAQPGFNKDI TKEQSIEARA IGARCGGVQV WSLYVPNGRE  
IADPHYDYKL RWFSLRNVY IDTLEYRPEE KLVLLGDFNI APTDIDVWDI AAFEGKTHVT  
EPERAAFDGL IEAGLKETTP GPGTYTYWDY KGARFLKGE MRIDFQLASP ALAATAGETP  
VDVEERSGTG ASDHAPVIVD YKV

> RXA00967 (1-363, translated) 121 residues

MPVQDAGERN NNDRPVMPGE ILREEFMEPL GLSQNGLARA IGVPRRRINE IVHGKRAITA  
DTALRLAAYL GPDPQFWLNL QTHYDLSTY LDARTLLEAI KPYDRQQNVA RTLNPLQESS  
Q

> RXA00990 (1-453, translated) 151 residues

VATDIAARGI DVDDVSLVVH VDPPAEHKAY LHRAGRTARA GTSGTVVTLV MDEQIKEVRE  
LFQKAGVTAA EVKVNENSPE LAKITGARRP SGVALPAPGQ QQPKREQKNT HNRSDSRGSS  
RNPRRRGQSG SRSTGRSNPR RQTSRKDGPK S

> RXA00994 (1-342, translated) 114 residues

MTTFLELKL DPVRELRSQ GITEAFPIQE AAIPDALAGK DVLGRGPTGS GKTFTFGLPM  
ITRLARSGAS KPGRRPGLVL VPTRELAAQV RERLDDPARV MGLRVLEVVG GVNI

> RXA01030 (1-1176, translated) 392 residues

MTSTTQPGTT PELSADTHSE PWDVVIENTL EPFQKVVRQF IIDRPYSGIF LTMGGGKTLT  
TSLATYIQP PGHILVVAPL NISRLTWPEE VRKWNIPVNA ISLITNERGT KLTRAKRLKL  
YEETATTPPT LYYITINLLE DIVNYFGDRW PFWTVIIDE QTISSDISSK TRALFSVRPY  
IGRLILLTGT PSANKFDSIY AQVAVLDYGA SLGDNIDVER ARWCAPDIIT DKQVRRWKPA  
NKQAEAEVYR TISHLVMSAV NTDIKLPLH FVDHEVHMSD DEHRDYELFK KDAVLAALLD  
MAEENEGGEG ADDTDAADSA TTPPASSQF TNPAIPAGLL QAIQQTQDTN GRAIAPVTTA  
ELDHFDLPLV QRQEDLGLTV VISAVHASDS AA

> RXA01064 (1-636, translated) 212 residues

MSLSISFHKI ALSATTLGA VAISACALVT QAPPINAAPV TGSSSLSFLL DLGTTTPTSI  
DTVKLTTQQAQ NQAAPRVAAS LVRVVDGDTI VVNYQGAQKT VRMIGIDSPE TKHPTKPVGF  
YGPSSQNLT TMLRGATITL EFDSTQARED QYGRLLAYVW YTKGDSGLKL ANLEQIASGS  
AAEYSFDTRY NHRNIFLRAQ TLAASSLGM WG

> RXA01149 (1-258, translated) 86 residues

VVAPQSRKPQ HPGEILSERF LEPRGISHYD LAKTLHITEA TIANFVEGRT DLTIGLAVRL  
SRSFDLSTQE WIALQRTFDQ AHRRSA

> RXA01157 (1-1605, translated) 535 residues

MSFSAEKGTH LSEFIADLGF DLDEFQIKGC HAVEEDHGVL VCAPTGAGKT IVGEFAVSLA  
LSRGTKCFYT TPIKALSNQK YHDLVAKHGS DAVGLLTGDV SINHDADIVV MTTEVLRNMI



YAGSFALERL SHVVMDEIHF LADASRGAVW EEVILNLDD S VNIIGLSATV SNSEEFGEWL  
 TTVRGDTRVI VTDHRPVPLD QYMMVQRKVM PLFEPGTGDR VNKELEATID RLNSKQSEQG  
 RAAYSRSGEGF RARSKGDKQD SRTGKPREQD RHRPLGRPEV LSILKGINML PAITFIFSR A  
 GCDGALYQCL RSKLVLTQDA ESEETARIVD AGVVGIPEED LQVLNFKQWR AALMRGFAAH  
 HAGMLPAFRH IVEELFVKGL VRAVFATETL ALGINMPART VVLEKMKVFD GEGHVDLTPG  
 QYTQLTGRAG RRGIDVLGNA VVQWSPALDP RWVAGLASTR TYPLISTFQP GYNMSVNLLK  
 TIGYEPSLRL LEKSFAQFQA DGSVVGDVRE IERAEAKVAE LRAQLNKEIA ATNPA

> RXA01238 (1-1401, translated) 467 residues

VIAAYGASIS LDDSTLTISY SPLLAALSKS SAQSESVDLT QVSGVSVQDP TAFTHGFLNL  
 EGVDKSIAFA PNSSADLAAL AADIDAVLKG EKPQHLGGGA FVVPAPSTV AGLNFVGFVDV  
 ETANDDWGSI CQIGLVKYVD GVEESSESWL CTPPESLNFF NEINIGIHGI TPEMVADQPR  
 FADLVPMVE FVGDLPLVAH NAQFDFLTALS RACAASGIDV PEMIYGCSLT LARNEKLQVE  
 NHKLPTVASH LGFELKNHHD AAEDARACAA ITIALAKRHS FECSFVDFVH SRGFTMGTV D  
 NARVYPVLKD RSGANVALQR RNFGLDAGKT EVPVQPAVDP AWETPKAEPK KQSGRRAPWD  
 KVATPEVIPD PNPADAPSSI LYGQNVTLTG DFEPYEKGAL WQRIADQ GAL IGKNVTKKT T  
 ILVAGPWATI TSKQKRAEEL KEKGQDIQIW DEKQLFTALG LDEQPPF

> RXA01255 (1-1080, translated) 360 residues

MSTTSSEQDH AARIEAERQE AIEAAPFVS S SIQSSGIHPS TSRMVTIDLV TLSPNLEPVE  
 TFHAVLDSKT DPGPFHLHGV TEEEFASAKR FGQILKSLDR LIDGRTLLIH NAARSWGFI V  
 SEAKRAMNDA ARANRNSNRG NRRGGRGRRR QRVGHIKPL VIVDTLASAR RQAIALDDVR  
 IRGVAHTLGL DAPAAEASVE RAQVSHRQLC REETLLVARL YGALKQSGPL AEIDPQSLRA  
 DKFGLQRSII RVQAQEA SPT LVNPGTYEPG KTLIAGMEV V VAPEIEMDPD IIIQACVDAD  
 LSYSEKLTRQ TSVVVCNQTR DIDGKAMHAQ RKGIPLLSDV AFLAAVKRVK EGKKVDVEKR

> RXA01279 (1-465, translated) 155 residues

MRKSAAPKRP VVQDPVYKSE LVTQLVNKIL IGGKKSTAER IVYGALEICR EKTGTDPVGT  
 LEKALGNVRP DLEVRSRVVG GATYQVPVDV RPERANTLAL RWLVTFTRQR RENTMIERLA  
 NELLDAANGL GASVKRREDT HKMAEANRAF AHYRW

> RXA01280 (1-366, translated) 122 residues

MPTIQQLVRK ARHDKSDKVA TAALKGSPQR RGVCTRYTT TPKKPNSALR KVARVRLTSG  
 IEVSAYIPGE GHNLQEHSMV LVRGGRVKDL PGVRYKIVRG ALDTQGVKDR KQARSRYGAK  
 RG

> RXA01286 (1-654, translated) 218 residues

MSENEIKGIL GTKLGMTQIF DEENRVIPT VVEAGPCVVS QIRTVETDGY NAIQIAYGEI  
 DPRKVNQPLT GHFKKAGVTP RRHVTEIRMD DVSGYEVGQD VTVEIFNDIK FVDVTGTTKG  
 KGYAGAMKRH GFAGQGAGHG NQAAHRRVGG IGAAATPGRI FKGKRMAGRM GNDRVTTQNL  
 KVQKIDADAN IILIKGAIPG NRGGIVTVKT AVKGGAHA

> RXA01287 (1-303, translated) 101 residues

VAGQKIRIRL KAYDHEAIDA SARKIVETVT RTGARVVGPV PLPTEKNVYA VIRSPHKYKD  
 SREHFEMRTH KRLIDILDPT PKTVDALMRI DLPASVDVNI Q

> RXA01305 (1-1866, translated) 622 residues

MRPSSRPLGL VLCTALASTI ITVPAASAE PALLDASAIA PHTASYGYV DAWDTINVSTD  
 LNPSSNAAVG VLEEMLELWT PGEWNTGVK VDPTVLDSNI AQSVAISQQA TDAQQERAWV  
 IDRRNQNYTA TDGLGAYADS YRETAQVGT IPDVVPADAT TVKYNDGGNV NGNWAETGGE  
 LGSTVDLIEA IRQHAATSNN AKAYYQYPRP YRWTESIEPE AWGEGVDMPE YANPLRKDES  
 EAASDGGFPS GHTSAGGMAT NGLAYAFPQQ YDKLLMTAAE IGESRIQLGM HSPLDVIGGR  
 VLSTAITAGA LNDPNLDSVK AEAFFDDAQW ISNQSDITTN TRDFDEQLAE YTNFLTFGFE  
 QSGDITQDMR VPKGAEEAL E TRLPYLDDEQ RRWVLHSTGL ESGFPVLDDA EGWGRNLNLYA  
 AQAGYSAFDT NVDVTMNAID GGYNAKDNWQ NDIEGAGSLT KNGSGELTSL GDNSYTGTT  
 ITAGTLVAAT ESALGAGDLT INDGATLKIT QPVTVDGTAN LGGTLHVALP VGTNHVTVID  
 AASISGEFDE VIVDGAVDQA VSYDNGSVVI TTGAPSDDVK ETGSSAGGIL AIVAALGGIA  
 ALIFGAFTQF GFPPAIKEMF DL

> RXA01334 (1-384, translated) 128 residues

MAKLTKDELI EAFKEMTLIE LSEFVKEFEE VFDVTAAAPV AVAAAGAAGG EAAAAEEKDE

FDVVLEDAGA KKIGVIKAVR ELVSGGLKE AKELVEGAPK AILEGANKDD AEA AKALEE  
AGAKVTLK

> RXA01335 (1-513, translated) 171 residues  
MANPRNEAAL AELKARFAET DTVVLTEYRG LTVAQTTELK KALGFDVQYS VAKNTLVKIA  
ANEAGVEGLD DLLTGPTAVA FIKGEAVDTA KVLKKFGEEN KAFVVKGGYM DGNALTAEQV  
NAIAELDNRE TTLAKLAGAM KGLAKAAGL FNAPASQVAR LAVALQDKKD A

> RXA01343 (1-651, translated) 217 residues  
IYSPLEAANL VKETSSKNYD ASIDVAIRLG VDPKADQLV RGTVSLPNGT GKTVRVAVFA  
QGEKATEAEA AGADFGTDE LVEKIQGGWT DFDVAIATPD QMAKIGRIAR VLGPRGLMPN  
PKTGTVTNDV AKAIEEVKGG KISFRVDKAS NLHAAIGKAS FDAKLAENY GALLDEIIRI  
KPSSAKGIYV KRVTLSTTG PGVEVDTHVT KNYAEEA

> RXA01353 (1-339, translated) 113 residues  
MNILDKIDAA SLRDDVPAFR AGDTLDVHVK VIEGTTTRTQ LFKGVVIRRO GGGIRETFTV  
RKVSFGIGVE RTFPVHSPNI EKIEVIRRGD VRAKLYYLRL ELRGKAARIK EKR

> RXA01356 (1-627, translated) 209 residues  
LSRNLGPVA GVDEAGRGAC CGPISIAACI LPDKPIQELA ALTDSSKLSA STREKLMPLI  
KKHALAWSVI VISAQDIDRF GIQHANISGM RRAVAALGTQ PGYVLTDAMK VPGFTVPYLP  
IIGGDASARC IAAASVLAKQ TRDDIMTDMA NDYPHYGLEI HKGYSTKIHM DAVRHHGASP  
EHRYSYANVA KAHQEWLHAA DNDTTEGGA

> RXA01363 (1-699, translated) 233 residues  
MSSLIPIVHAA GSIQEGITEY LTTSFSLADK QVATELKRFL GHGDSGMFHG PYVRARLPYA  
QAQEWENVLS WLPENFVPHY HQKAAFQRLS SLDNRGKDRR PDPTLVVTGT GSGKTESFLY  
PILDHALRLR KRGQQGIKAL LLYPMNALAN DQADRLARLI HNNPALKGVT AGIYTGEAKG  
NRTQMGEREL INDPQAMRVS PPDILLTNYK MLDQLLLRVS DREMWOQSAT SLQ

> RXA01374 (1-882, translated) 294 residues  
MSESGALSST DSLSPGVITIE VRDEIWLVT VTRSTDGFRV KARGLSDYVR DHEATFF TAL  
DKDLKVIDPT QVTVSLDDSS NYRRLRLWLE ATMRKTPVPL YQESLSVADQ MLADPLEYQL  
AAVRKTLSSA NLRPRVLIAD AVGLGKTLEM GMILAELIRR GRGERILVVT PRHIMEQFQQ  
EMWTRFAIPL VRLDSVGIQQ VRQKLPASRN PFTYFPRVIV SMDTLKSPKY RAQLEKVHWD  
AVVIDEIHNA TNAGTQNNEL ARTLAPTAEA LILASATPHN GDPESFKEIL RLLD

> RXA01423 (1-141, translated) 47 residues  
MAKGKRTFQP NNRRRARVHG FRLRMTRTAG RAIVAARRRK GRAKLT A

> RXA01424 (1-309, translated) 103 residues  
VHLWDSAESL DGTEKQGEVA SFGGPRFGLV VSKAVGNAV V RHRTSRRLRH ICASIAEKSP  
ELLSPTHVHV IRALAGAGNA TSAELERDIR YGLGKASRVR TNK

> RXA01453 (1-297, translated) 99 residues  
MAQKLYPPIH PGEILMEDFI KGFGLTQNKV AVSIGVPPRR INEIVHGKRS ITADTALRLG  
RYFGIDPQFW LSLQTQYELE LDRDAGAATY AQITPLKVA

> RXA01480 (1-1893, translated) 631 residues  
MAKGRIPESD IQAIRERTPI EEIVGDYVQL KSAGADSLKG LSPFKDEKTP SFHVRPNRGY  
YHCFSTGKGG DVFSFLMEME HISFPEAVEV CAEKIGYQIN YQGGGPGRRE EPGTRQRLIL  
ANKAAHQFYR EQLETPEAQF GREFLLQRFQ GQHHYHFEC GYAPAGWDTL TKHLLKKGFE  
FKELEAAGLS KMGKRGPIDQ FORLLWPIK NLSGDVIGFG ARKLFDDDKM GKYMNTPETL  
LYKSKSVLFG LDSAKKAIAA GHQAVVVEGY TDVMAMHAAG IDTAVASCGT AFGEHLQML  
RRLMLDDNYF RGEIYTFDG DEAGQKAAMR AFEGDQKFTG QSFVSVAPNG MDPCDLRLER  
GDAAVRDLVA RRIPMFEFVI QSIISEYTLD TVEGRLAALR RAVPIVADIR DKTQLQSEYAR  
LLSGWVGWSD PSEVLQVHE EARRPKRDKK PVRAKRFDQP LEDQSLRPTM ALPNRPNPVL  
WQERESLKIA LQYPELAGSY FDGLPTDSFT NPAYRMVRDA ISAAGGCERA LDGTDWLPVAV  
SENMTDILGT SLVSELAMEP IEVEAQDLES YTDGVLSRLQ ETRVGNQIAI LKGQLQMRMP  
SEDEQAYNSL FSDLVALEQA RRELLARAFA G

> RXA01481 (1-492, translated) 164 residues  
 MQNSKKTLLGG VLGVIIVLAA AWFGIDLSTS GEATSQASSS ATTTTITSSN TPTSESISSN  
 SDDLGDSCSM SELPQEADEV VDDILAGGPF DYPDNDGVRF GNYEGVLPKE SSNNYYREYTV  
 ETPGLSHRGP LRIVTGGSNP TDPEVWYYTS DHYETFCAIT DAEN

> RXA01487 (1-267, translated) 89 residues  
 MALTSEQKKS ILSEFGLHET DTGSPEAQIA LLTNRINNLT EHLKFHKHDH HSRRGLLLLL  
 GRRRGLLLKYL ADNNDVDRYD LIARLGLRR

> RXA01495 (1-447, translated) 149 residues  
 MADNARAARM AKRIQTIVAS AIERDIKDRR LEFVTITDVT MTGDLHDAKV FYTVRGASIE  
 EEPDLEAAAE ALHRARGQLR KIVGQQLGVR FTPTLTYSID TVPEASAHME ALLDRARKRD  
 EELAKLREGA APAGDADPYK TSSKSESEE

> RXA01563 (1-810, translated) 270 residues  
 QIFDLHLLKG HGSEDWSKRP LPESWLNLYAA LDVEMLLELA DVMAEILDQQ GKLPWAEQEF  
 VHIVDQFATM TEPSETSWQD LKGLSTLKRQ DQLVVAREMW LERDSFAASR DLAPGKVLSN  
 KVIVEVARVL PRTPAELAQV KGFPGRSQGA TKRWFRIITR ALKSPRRNWP KPQQRKDGIP  
 DRRWASYYP EEHEVLQEUR ALIDDLAADI NVPGENILQP STLRVAVWMA KHTGEIHNAE  
 TLNAVLRDYG ARQWQIDQTF PILSANLLKL

> RXA01568 (1-435, translated) 145 residues  
 WDNITYLMRA ARKGTIVPMV IELDGRFVGQ LTIGNIQHGG ISDAWIGYVW SSAVTGRGIA  
 TAACALGVDH AFRRIGLHRL TATYLPNSPA SGKVLGHS GF RPEGYLIRNL HIDQWMDHH  
 FVALLADEYS ITAVERLTRE GRLRR

> RXA01581 (1-813, translated) 271 residues  
 MALDFNEAFT ERTPRIVNAA KLHRAAQRKK DKRFLVEGEN SVEAAVATGA ATDLFVTESA  
 AERFEEIVRT AGYMNVTYTHA ITDKAAKHL S DTVTTTGIFA LCDDVLWSVG KAITGQPRLV  
 SVPVETREPG NAGTLIRVSD AVGADAVVFA GESVDPLGAK AVRSSAGSLF HIPVARNNNI  
 ADVLGQLRSK GLQILATSAD GEVDLDDADE LLAKPTAWLF GNEAHGLDES LLAQADHRVR  
 IPIRGRAESL NLATAASICL YESSKALFAG E

> RXA01594 (1-744, translated) 248 residues  
 MIRGRRVFVA GMLALKPATV VEPEVSIRVE EDASEDWASR GAHKLLGALE SFEPLGLKVK  
 GRRVLDAGAS TGGFTDVLLR REASEVAVD VGYGQLIWRL QNDDRVRVVD RTNIRYMTLE  
 DTGGECDDMV GDLSFISLKL TLPAAIAKVL S DGADLLPMVK PQFEVGKDRL GSGGVRSPE  
 LRAEVTADVA KFAATLGLSL KHVVASPLPG PSGNVEYFLW LVKDGGASMP DDQQLSAMID  
 TAVKEGPQ

> RXA01637 (1-309, translated) 103 residues  
 VREASVEKQP ASSDPLETIR SRWSELNRIV EKQSVRTSIM LTEARVLGLR GDTLVLGHST  
 GALAARLNAA DHNGILVKVL AEETGLQLKV ECIVGTNP AE AGF

> RXA01661 (1-666, translated) 222 residues  
 LDSTNTPGPT EWGESRVGKG PWEENPGVP RPTSPLFDVT LLNEGDRNV VDAYRYWTRE  
 AIVEDI DTRR HSLHVAIENF ENDANIGTVV RTANAFVNT VHIVGRRRWN RRGAMVTDYR  
 QHLMHHEDVD SLLAWAIAER LTIVAIDNTP GSVPLETAE L PKNCLLLFGQ EGPVTEAAR  
 AGALMTCSIA QFGSTRSINA GVAAGIAMHA WIRQHADLSQ AW

> RXA01682 (1-234, translated) 78 residues  
 RTKVDAYKSQ KRGGKGVCGA ELKQDDIVRH FVSSSTHDWI LFLHQLRSRV PPQGIRTSRG  
 IPHRTWTARG QPSGIPTW

> RXA01683 (1-750, translated) 250 residues  
 VYRLKAFELP EASRTARGQH VANLLEFQPG EQIAQVIQLE SYNDFPYLV L ATAHGRVKKS  
 RLLDYESARS GGLIAINLNE DDRLIGAALC GEEDDLLLV S EFGQSIRFTA DDEQLRPMGR  
 ATAGVKGMRF RDNDQLLSMS VVRDGEFLV ATSGGYGKRT PLEDYSTQGR GGLGVVTFKY  
 TPKRGRLVSA IAVEEDEIF AITSAGGVVR TEVKQIRPSS RATMGVRLVN LEEGVELLAI  
 DKNVEDQGEA

> RXA01684 (1-873, translated) 291 residues

GDTAIYDTLV RMAQPWSMRY PLVDGQGNFG SRGNDGPAAM RYTECRMTPPL AMEMVRDIRE  
 NTVNFSPNYD GKTLEPDVLP SRVPNLLMNG SGGIAVGMAT NIPPHNLNEL ADAIFWLLN  
 PDAAESEALE ACMKFVKGPD FPTAGLIIGD KGIHDAYTTG RGSIRMRGVT SIEEEGNRTV  
 IVITELPYQV NPDNLISNIA EQVRDQKLVG ISKIEDESSD RVGMRIVVTL KRDAVARVVL  
 >NNLKFHSQLQ ANFGANMLSI VDGVPRTLRL DQMLRYYVAH QIEVIVRRTQ Y

> RXA01688 (1-564, translated) 188 residues

QFEGQTKTKL GNTEIKSFVQ RMANEHIGHW LEANPAEAKV IINKAVGSAQ ARLAARKARD  
 LVRKRSATDL GGLPGKLADC RSKDPEKSEL YIVEGDSAGG SAKSGRDSMF QAILPLRGKI  
 LNVEKARLDK VLKNAEVQAI ITALGTGIHD EFDINKLRYH KIVLMADADV DGQHIATLLL  
 TLLFRFMP

> RXA01689 (1-726, translated) 242 residues

FSDSYAVSG GLHGVGISVV NALSTRVEAD IKLHGKHWYQ NFEKSVPEL IEGGNARGTG  
 TTIRFWPDAE IFETTEFDFE TISRRLQEMA FLNKGLTITL TDNRATDEEL ELEALAEQGE  
 TATELSLDEI DNETELVEET TDAPKKPKKR EKKKIFHYPN GLEDYVHYLN RSKTNIHPSI  
 VSFEAKGDDH EVEVAMQWNS SYKESVHTFA NTINTREGGT HEEGFRSALT SLMNYAREH  
 KL

> RXA01713 (1-354, translated) 118 residues

MVSDLLQPRD GIPPLLSTPG EFTAAADLLA SGTGPFAIDT ERASGFRYDD RAFLIQIRRR  
 GSGTLLFDPE QFRPELTQAL KPVLNGQEWI IHAASDLP S LAWLDLHPGL LFDTELAG

> RXA01718 (1-486, translated) 162 residues

LLTAVLSLIA GLVVIGVIIV LNGYFVAQEF AYMSVDRNEL RALADSGDKK ARRALSITKR  
 TSFMLSQAQL GITVTGLLVG FVAEPLVGNA LGVLLGGVGV PAAVSISVGT VLALAISTVV  
 QMIFGELFPK NYTLATPLKS ALALAPSTTW YLKPRWLVDH IL

> RXA01735 (1-282, translated) 94 residues

VANTEHNYDA SSITILEGLE AVRKRPGMYI GSTGPRGLHH LIWEVVDNSV DEAMAGHATK  
 VEVTLLEDGG VQVVDDGRGI PVDMPHSGAP TVQV

> RXA01736 (1-2868, translated) 956 residues

TVSTYDSYAG TLIREYGLLL PVEPSARLIT QTELYHIARN VVNNYDGELT ATQTPATVTE  
 YLLKLVSMD NHMVTAEDIR EESDPFIKLF DELPKGKGQR DNLNAEMTKW RDTQVARLQY  
 LPLVKALKEE LHNQAVVTFG EQMSKAAHLA STHPQVGYSQ RRRFRVVMLD EYQDTSHSQR  
 VLLSSILFGGT DPGLTVNAV G DPMQAIYGWR GATAANLENF VDDFPVIHLD GKTRAPKNEL  
 TTSWRNPPEV LTLANAVSRE VLGSPDAPTR TVQPLQPREG APTGEVSLGW FGTAQEREF  
 VADEMVKHWN AREEKGTFTA AVLVRKKRHS APMAEELTKR GIPVEIVGLS GLLDIPEIAD  
 LISLATMLVR PHDNRAALRI LAGPHVGLGV ADLQRLQGRA RNIAGRVSRE RREKNPDPLA  
 ELDAIIEEAT AIEPEAVVGL ADAVADLGE G DRFSEEGLSR LKRLATQLRY LRKYSLGRSV  
 ADIFADIETV FNIRTEVLSR QDPHADGAAG TVHLDKF AEE VASHGGIGLP ELLDYFELAK  
 DQEEGLEPGE VTVRSRDRVQI LTVHKAKGLE WDIVSVLHAD ASTYDAKAST WLKNVTMIPS  
 SLRGDAGTGA PEMDTSEADD RKALED SGKE YTSEVREGLR EENSRLFYVG ITRSERVLLV  
 TGSALDESGT KAKVPYGHLE ILRDKAPECV VSWWEGEEGD VEKQKPAEGV FPQLLAADSS  
 GADLVRGPRA EPNNEGGLES LWKEVSALI DEHRRLSNPI VEVETPRELT ATDLVSMKNN  
 PEQFARRMRR PVPFKPNTYA KRGTLFHQWL EDRFGSTALL DETELPGIDE DYSDDAFIEL  
 RDAFLGSTWE NRTPEFVEHP FEVTIGEHVI RGRMDAVFHT DGTWMVVDWK TGRTPTGPEM  
 DAAIIQLAVY RLAWARLKG L EPEEVRAAFH YVAHDHTFEP NDLPTQEELA RLLSQE

> RXA01739 (1-597, translated) 199 residues

VINLQDLDED QRIAASAPRG PVCILAGAGT GKTRTITYRI AHLIDQGFVS PNRVLAVTFT  
 SRAAGEMRHR LNLMGIGGVQ ARTFHAAARK QLLYFWPQVA GNLPWRLLDN KFQLVGRAVR  
 GARLESQTEK VRDILGEIEW AKASLITPEQ YPDRLGTRTP PAPAEEKIAEV YQRYENMKAT  
 PEGMLLD FDD LLLHTAGAL

> RXA01740 (1-1422, translated) 474 residues

VAEEFRQQYR SFVVDEYQDV TPLQQRVLDA WLGDRDDLT VGDANQTIYS FTGATPEFLL  
 NFSRKYPEAT VVKLQRDYRS TPQVTALANT VIGQARGRVA GTRLELQGMR IAGPEPEFSA  
 FDDEPTEARE VAGRILTLLK NGVQASEIAV LYRINAQSAV FEQALADAGI VYQVRGEGEF

FTRPEIRQAL SQLIRTSQRD VDESDLVRLT QRTLVPPLGLS SEEPSGAQER ERWQSLNALV  
 DLVKDLVKAT PDLDLTGLLL KLRERQEAH PPTVEGVTLA SLHAAKGLEW DAVFLVGLVD  
 STLPISHAIK SGDEAIEEER RLFYVGVTRA REHLHCSWAL ARQEGGRKSR KRSRFLDGIV  
 VEMASESGTP RSNRPKNCRV CGSVLSSPAE KAVGRCASCP IQADERVFEQ LRTWRNDTAK  
 RENKAAYMVF SNATLMAIAE MNPTNENELL SVPGVGPMKI ENYGDDVLAI LGAL

> RXA01772 (1-2364, translated) 788 residues  
 FKKAFFKQSE ALGIVYTPVE IVDFILRAAD DVSKKHFGRG LSDKDVHVLD PFTGTGTFMV  
 RLLQSGLIKP EDLARKYANE LHATEIMLLA YYVAAVNIET TYFGLEGERA LRNGEDAPVY  
 EPFDGIVLGD TFQMYEDDDK LDLDVFTANN DRMERQRLTP VQVIVGNPPY SVGQSSANDN  
 NANLKYPTLD RRIEDSYAKY STATNKNSLY DSYLRAFRWA TDRIHTQGVV AFVSNNGWVD  
 GNTADGVRLS LAQDFSEIYV FNLRGNSRTG GDIAKREGGN VFNVRVGTQI IVAVKNPQLS  
 GCRILYKDIG DNLSADAKLN EIAVATIEGA EWQTISPNEY GDWISQRSVD FDTWPLVLDK  
 KNKSALKVFQ TFSAGLKTGR DAWCYGPTSA QVKTNITRLL ETYEQAAQRF NSWVVDNGVT  
 SPKEADVNFQ LKQNPDLADS KKISWDSNLK MSLSRGDTFS FDPSSIQMSL YRPFPPQOTY  
 FHVSLNQRRY QLPSMFPTPE HDNQGFYIVN PGSAPFSTL ATNLLPDLAM WGSNAGQFFT  
 RWTWEPIETR EGELDFGNGL FSTTPKKGVE GEILDGYRRV DNITDEILKL YQSSLGEDVT  
 KDDIFYFYVA QLHDPAYREA YAADLKKMLP HIETPTDRAR FDHFVTAGKE LMDLHINYED  
 VEPWDVEVKV KEKADPTDRE TWRVTMKMWA KVRDPETKKL VEDHTTILIYN SSITISGIPE  
 EAENYQLGSR SAIWLIDRY QVKKDKASGI VNDPNDWADE VGNPRYIVEL IAKVTRVAVE  
 TMRIVEEL

> RXA01786 (1-441, translated) 147 residues  
 MRAAKITRGF TSNPAGSVLV EFGNTRVMCT ASVELGVPRF KRDSGEGWLT AEYAMLPAAT  
 AERNRRESMA GKVKGRTHEI SRLIGRSLRA AVDLSQLGEN TIAIDCDVLQ ADGGTRTASI  
 TGAYVALADA IKVLQERGUV PGSPLLA

> RXA01797 (1-708, translated) 236 residues  
 GSIWIWDLTP EDRSAYDDQV RQGSWMGMRR SAMLSPTPRL TSAKMQRILE LFEEAEEHGR  
 KALIFTYFLD VLDELEKHLG ERVIGRISGD VPATKRQLLV DALSHSKPGS ALIAQITAGG  
 VGLNIQSASL CIICEPQVKP TIEQQAVARV HRMGQTATVQ VHRLIGDETA DERMLEILAG  
 KTHVFDVYAR LSETAEIPDA VDITESQLAA RVIDEERARL GLTESTGPKD EETALS

> RXA01824 (1-822, translated) 274 residues  
 MKETDNLLRE NSHARDISEI VATITALDHP SPSLLRFTAF VPGSANNPVW AEANVAIRLY  
 LSEEFDDATR VYTVRSFDAA TESIVVDVVQ HHESPMRWR SDTVKINDTL VLTGPRPHFV  
 IPEGEQAALF LDDTAIPALA AILDQWPTDL RGKGWVVTDD PAAFDLPSI DGLELNLLAP  
 GSDPTVQPLA QQAYDLENPE TYVWVAAGER DEIKSIRRHF RKQVGLEKDA VAVFGYWKYN  
 TTNTQIDAVR KENYMKMLSE GLQLENFDDL SLEI

> RXA01832 (1-894, translated) 298 residues  
 MATSNRIANA MNSLAKLDSS MQRGLDNALA FVFRGRVPA ELEELLKQEA EDNVVHTEFG  
 YVEAPNVFKV SVSPNDFSNI VDRFPDQPAR FGDQMMRFCR NSGWTLVGPV IVLIEEDSSL  
 HTGQLKSVSE KDPDPPELSSG YLPLEGDGIL PVAESESKNV SDSSPYTGTE FLPAQSADRP  
 LVQGVPSQV DANRQAAMKP AGPTVTLILQ DGSSRTYLVR EGSNIIGRSN DADLRLPDTG  
 VSRQHVETIW DGRDAILVDL KSTNGTTVND TPVDNWLLAD GDVITVGHNS IEVRIVSP

> RXA01866 (1-321, translated) 107 residues  
 LKPGHRDDGV TVLIPIPVLG GLDTEGFDWL VPGLRLDLVT ELIRTMPKAL RRTVVPAPDF  
 AERVLPLLRP YMTPLTTQLA DALHTLGGQG INASDFDPAK LPDHLRI

> RXA01867 (1-492, translated) 164 residues  
 PEWVEKAAGP LLKHQYSEPY WSSKRGAAAM HRKSTLFGVT IVAVKVVPYH TVDFVAARDM  
 FIRHALIEGD WSTHHRFYHD NVAKLEAIGE LEAKARRRDI VVDEDTLFDY YDAKLPSNAT  
 TTRNFDSSWK KTSRVTPDLL DFDPDSLIKE DAGALRRSLR RQVD

> RXA01876 (1-1473, translated) 491 residues  
 IIGPNKTFLE YISHVLPELG ETGVVLSTVG ELFPGIVPTG SEDTLTREIK GSEEMASILA  
 EAVKAYQVLP EKTIVVSVDG IEISIDEKTV AKSRTRARRA RQSHNSARPI FREHLVEQLA  
 HQMAQTIGAD PLGGKNLLSA ADIDQLHDDL LDDAALQSVI DDFWPELRPQ DVLHDLILSE  
 ERINVAAGY DEETKSALLR GELDPWAPSD AALLDELALL IGLPDPEEAR EKAEAKWREQ

IDDAQEVLVDV LSSSQSSDID DVTEAEVLSA FDVIDAETLA QRQTVTDNRT TAERAQADHK  
 WAYGHVIVDE AQELSPMEWR MVFRRSPSRW MTLVGDIQOT GWPAGVDDWA ESLWPFVEKR  
 FRHHELTVNY RTPAEIMSA NELLTQINPD IAPAMAIRES GREVVNLPLD ADLSAVMDSL  
 REEDSQRTIA VISSRRHHES DFYLVDDIKG LEFDHVIVVD PAGIVEESPQ GLQDLYAVT  
 RATQSLTILG E

> RXA01893 (1-555, translated) 185 residues  
 MIDEILFEAE ERMTATVEHT REDLTTIRTG RANPAMFNGV MAEYYGVPTP ITQMSGITVP  
 EPRMLLIKPY EMSSMQVIEN AIRNSDLGVN PTNDGQVLRV TIPQLTEERR KDMVKLAKGK  
 GEDGKIAIRN IRRKGMQDLK KLQKDG DAGE DEVQAAEKEL DKVTAGFVAQ VDEVVARKEK  
 ELMEV

> RXA01912 (1-771, translated) 257 residues  
 MRRFIFTERN GIYIIDLQQT LTYIDQAFEF VKETVAHGGT VLFVGTKKQA QEAVQVEADR  
 VGMPYVNHWR LGGMLTNFQT VSKRLNRMKE LQAMDAAENG YEGRTKREVL MLTRERTKLE  
 RVLGGIAEMT RVPSALWIID TNKEHIAVAE AHKLNIPVVA ILDTNCDPDV VDFPVPGNDD  
 AIRSTALLSR VISTAVEEGK KAREERQLAA AKDAAGDAKP EAEAPAAAE AEEAPAAEAE  
 EHLQSLKLPL TAVSAVS

> RXA01948 (1-603, translated) 201 residues  
 SVELPAEIFD REVSVALLHQ VVNAQLAAAR QGTHSTKTRG EVRGGGRKPF RQKGTGRARQ  
 GSIRAPHFTG GGISHGPKPR DYSQRTPKKM IKAALYGALS DRARNARIHV VSELVPGQTP  
 STKSAKAFIE RLTERKSVLL VVSREDINAQ KSANNLPGVH ILAADQLNTY DVLKSDDVVF  
 SVEALHTFIN RASGAAQEEQ N

> RXA01949 (1-303, translated) 101 residues  
 MATIANPRDI IIPVSEKS YGLMEQNVYT FFVSTDANKT QIKIAIEEIF GVKVASVNTV  
 NRAGKRKRSR TGFGTRKATK RAYVTLREGS DSIDIFSGSV A

> RXA01950 (1-384, translated) 128 residues  
 MAIRKYKPTT PGRRASSVSM FTEITRSTPE KSLLRPLSKT GGRNSHGHT TRHRGGGHKR  
 RYRVIDFRNN DKDGV LAKVA HIEYDPNRTA NIALASLLRW REALHPRTEG PDPGHRYRVR  
 RCSRHQGW

> RXA02037 (1-330, translated) 110 residues  
 GKKGPLYAPN VDCGDHVIVI NADKVAVTSN KREREMRYRH SGYPGGLKSM TLGRSLDLHP  
 ERTIEDSIVG MMPHNKLTA SAKKLHVFSG SEHPYAAQKP EAYEIKKVAQ

> RXA02038 (1-309, translated) 103 residues  
 MSEPIQENV ESNVADAADI AAATAATEEF TNTIGDAIAT ASEEETIEAA PVVLDGPIQT  
 VGRRKRAIVR VRLVAGSGEF KCNGRTLEEY FPNKLHQQLI KAP

> RXA02041 (1-714, translated) 238 residues  
 RLGITSDWKS HWYADKSYAD YVAEDIKIRE FLSKGLDRAG IADVVIERT DRVRVDIHTA  
 RPGIVIGRRG AEADRIRREL EKLTGKQVAL NILEVKNVDA NAKLVAQSLA EQLTNRVAFR  
 RAMRKAIQSA MRQPQVKGK VVCSGRLGGA EMSRTERYHE GRVPLHTLRA EIDYGTIEAH  
 TTFGRIGVKV WIYKGDVVG RRESEINAPA ERRGRGDRNA RPRRGQRRQ RAEQKQEG

> RXA02042 (1-414, translated) 138 residues  
 MLIPKRVKYR RQHRPTRSGI SKGGNRVTFG EYGIQALEPA YITNRQIESA RIAINRHVRR  
 GGKVINIFP DRPLTQKPLG VRMSGSGKGPV EKWVANIKPG RILFEMSYPD EATALEALRR  
 AGQKLPCVKR IVKREDQL

> RXA02043 (1-141, translated) 47 residues  
 MAIGTPAHEF RELNEEELVT RLNEAKEELF NLRFLATGQ LTNNRRL

> RXA02077 (1-396, translated) 132 residues  
 MLGKGELLTE GRSKDSILAD TTEALFGAIF RQHGFTARD VILRLFAYKI DNASARGIHQ  
 DWKTTLQEEL AQRKRPMAY SATSVGPDHD LVFTAIVTLE GEEMGRGEGP NKKLAEQEEA  
 HQAFRLRES RA

> RXA02145 (1-1617, translated) 539 residues

MSLATVGNL DSRVTMASGI RRQINKVFPT HWSFMLGEIA LYSFIVLLLT GVYLTFFDP  
SITKVIYDGG YLPLNGVEMS RAYATALDIS FEVRGGLFIR QMHHWAALLF VVSMVLHMLR  
IFFTGAFRRP REANWIIGVV LIILGMAEGF MGYSLPDDL SGVGLRIMS IIVGLPIIGT  
WMHWLIFGGD FPSDLMLDRF YIAHVLIIPA ILLGLIAAHL ALVWYQKHTQ FPGAGRTENN  
VIGIRIMPLF AVKAVAFGLI VEGFLALLAG VTTINAIWNL GPYNPSQVSA GSQPDVYMLW  
TDGAARVMPA WELYLGNYTI PAVFWVAVML GILVLLVLT PFIERKFTGD DAHNNLLQRP  
RDVPVRTSLG VMALVFYILL TVSGGNDVYA MQFHVSLNAM TWIGRIGLIV GPAIAYFITY  
RLCIGLQRSD REVLEHGIET GIIKQMPNGA FIEVHQPLGP VDDHGHPIPL PYAGAAVPKQ  
MNQLGYAEVE TRGGFFGPD EDIRAKAKEI EHANHIEAN TLRALNEANI ERDKNEGKN

> RXA02179 (1-828, translated) 276 residues

MTTRTVISDP ADPRLDVDRD LNHSDSRPDL PGGKGLVVAE GPLVVGRLLS SRYPVRAIVG  
FKNKLDSELD SIDASLVEGI PVYEVSRELL AEVAGFDMHR GLLATADRTE EASVAQVLEN  
ARTVVVLEGV GDHENIGSMF RNAAGMGVDA ILFGNGCADP LYRRVVRVSM GHVLRPLFAH  
LEGTYTTWQR SLEQLKEAGF HLVSLTPDPE AEHLEDALAG KDKVALLVGA EGPGLTEHAM  
RATDVRRARIP MAPGTDSLNL ATSAIAFYE RDRSQ

> RXA02190 (1-1458, translated) 486 residues

MPTNNAPQVA INDIGSAEDF LAIDATIKY FNDGDIVEGT VVKVDRDEV LLDIGYKTEGV  
IPSRRELSIKH DVPDDEVVEV GDQIDALVLT KEDKEGRLL SKKRAQYERA WGAIEELKEK  
DEPVTGTVIE VVKGGLIIDI GLRGFLPASL VEMRRVRDL PYIGQELEAK IELDKNRNN  
VVLRRRAFL QTQSEVRSEF LHQLQKGQVR KGVVSSIVNF GAFVDLGGVD GLVHVSELSW  
KHIDHPSEVV TVGDEVTVEV LEVDLDRERV SLSLKATQED PWRVFARHTA VGQIVPGKVT  
KLVPFGAFVR VEEGIEGLVH ISELAQRHVE VPDQVAVGE EVMVKVIDID LERRRISLSL  
KQADEDYTEE FDPSPKGMAD SYDEQGNIFY PEGFDAETNE WLEGFDEQRQ AWEARYAESE  
RRFTAHTAQI ERRRQQAEEA AAEPAGNYS TDSAEDAPAA EAVESAGSL ASDEQLAALR  
EKLGN

> RXA02241 (1-2028, translated) 676 residues

VARVLPLGL PHLDRDFDYR ISEDQHDDVQ PGVRVRVRF GRLVDAIVMS RTAQTSHCK  
LMWLDRLVISP IVVYPPQTAK LIEQLSDRYG GVRSDLRISA LPARHAGAE ADTSTSWESL  
GEVKEPDLSS WSAYQHQS F VDAVLGTTA RASWQIAPGD DWALALASLA VKVVKDGGGA  
LLVVPDQDL DRLEAALRGL VAAKQITVLN SGLGPQARYR RFLSVLSGQG RLIIGTRSA  
FAPVKDLKLA VILNDGDDNL VDPRAPYAH REVLTTRSSL EASSLIAGH ARTAETQLLV  
ESGWMHNLIA PRDTIRTRMP RIQAVGDSDF QMERDPMARS ARLPGIAFHA VRSALERDQP  
ALIQVPRKGY VPTLACGNCR TPACRHCNG PVGLPQSSD LAGVPTCRWC GRPDSRFKQC  
NCGSPKLRAV VLGTERTAE LGRAFPSPRV ITSGGNKVVD SVENRASIV STPGAEPFVA  
NSPERPEKSE KPEHKGAYGA LLLLDTWALM GRQDLRAME ALHKWAAAT LVHSHLHQGQ  
VIVVADPSFP AVQSLIRWDM AGAAAQELAS RREVMFPSPV HMAAIDGATA ALESFLDLAE  
LPDHAENVLP VDLPPGVSLP GEYDEQRF GPRLIRTP L GPRSELGRAL RSAQVARAVR  
KNDLPLRIQM DPHIG

> RXA02293 (1-2388, translated) 796 residues

MSSRIGNFLI NRISTGLPVE NIIPHLQEA SAGPKNLVIQ APPGTGKTTL LPPLVANILC  
NEGAGNATPT KVLVTAPRRV AVRAAARRLA QLDDSQLGTK VGFSVRGEHI SGSHVQFMTF  
GVLRQLLNN PELPGIGAVI IDEVHERQLD SDLLLGMLAE LSQLRDDFSL IAMSATLDSD  
KFANLLDAQV LSVEAPIFPL DISYAPARAP RLNAKGVDWD FLDHMAQKTH DAVTHSEHSA  
LIFVPGVREI DRVMSTLKS L GHNNVFPLHG QLSPTQDRA LAPSQQORII VSTPVAESSL  
TVPGVIRIGVD SGLSRSPKRD SARGMTGLIT SSCAQASAGQ RAGRAGREGP GOIIRCYSEE  
DFSHPREFVT PEISSADLTQ AALWLAQWGT SPADLPLLDQ PPHAAWTAAQ QILRLIGALE  
GDAITSLGHR LSTLPLCPQL SASLLRFGEQ SAKILAVVSE NPQGDVEKQQ PDKREVERLR  
RLAPASVGKA SAGQIVGAFF PQLIGRKIDN GEYLLASGTR ARLMDSLDKD AEWISVAAIN  
RQNSAIIIRA AARISDDAI DIIGVVEETR AIFVNGKVQA RKVKAAGAIE LSSTPTKPTF  
AEASEIATA LAKGGIDLFI FSDKAASLRD RLKFIHEHRG EPWPDIEDAD PHLWLSPEIE  
ALSHGTRLNN IDMPALQRL LPWPEATNFE EFAPSHLSVP SGNQHRLDYS SGRPVIRVKL  
QECFGLLESP QLCGIPVQFH LLSPAGRPLA VTDDLRSFWS GPYSQVRAEM RGRYPKHPWP  
EDPWTAPATA RTKNRM

> RXA02357 (1-1203, translated) 401 residues

NSSRPEEITD LSAVPDWTFL EKRPELTLGS QLELRFRVML RRALKNRHAK LVDRVNGSNS

YVDIEMSSGV RWRMSEQVDR GYTRPDFWFE PLNGNYPTVA VFTDGAAFHI SSANYRLDGD  
 IQKRMKLALD PDNLPWNIT SLDLDRFSNP AAQGEPAWF SPIGRQLSKA NLILDPOSTA  
 LLAATPMDQL LAFLDNPAAS SWKEFAHIAA AHMLGHNPQK NGDGIVGTFR NKISLRATMV  
 NRELRARQLW LAPTTPEELE VDTWTAFNL ANLMWLAPES VYVSTNGSPH KIDIVPAPAA  
 PLVVEVPPELW APILDGFTAD EDEEAEGALQ ILAKEHALVP ETTGDELSSI PTIATWPSVK  
 IALLYESDPD EPLEDDLKAE GWTLLEFANDL ETS DIPAAALR P

> RXA02359 (1-1869, translated) 623 residues

VELPSPGEAL AHAGHTPEVL EAELGIDPAA TRIVLELASE DDIAAALPSS PTWEKDALIG  
 LVAGLSIEDI RESLAIPAPS TEPDTRSED TRLIAGLKTPA AQMDFAYLDT PNSNDLRRVI  
 ETEGFDGSRV YIDPSQORSLV TRNFSGSGRV FGGAGTGKTV VVVHRANRLV TSDGHLETDD  
 KTPRVLLTTY TRGLADALKS SMNALNPTFP EAEKPGSPGL WISGIDALAN KVVVALANTAE  
 REAATTAILG RAAGRITPFI GNGEQEFWID AIISADPGDL SEEISNTEFL AQEFETVILA  
 RGITQEKDYL RAPRPGRGTP LNRVQRKKVW AIIQQFMTSC AREGKMSWPA LSSIAANILE  
 QRAAAGQGRL FDHVLIDEAQ DFHAGHWLLL RAAVAEGPND IFLAEDSHQR IYGQHHVLSR  
 FGISTRGRAS KRLTLNYRTT AENLSYALGM LTGEWTDAG ETDTIEHYRS ARKGPKPHLY  
 QFESETDEFE AIAELIKVWQ DRTTDVIRIGI LARTRPLINR VVNALSEQGI DAVKTQNAEL  
 AAHETVSVMT MHGAKGMEFT HVILIGMGRD LIPLQYTMQG LGAEARNDQA QRRSLLLYVA  
 ASRARDALVL THTPESELL PRV

> RXA02363 (1-4800, translated) 1600 residues

MSNAPKKSFS DFFSPLATET ETTITLSAIE VEKVNKTEV TRNIDPVEAA EQISRDRYRY  
 LKTLISPSNK TIAAEFNREI DESENLYVGP ILQLTPPYAP GKSPAQLIDE GVLSPNFSRL  
 DAALPKDRPL YQHQEDALRK IASGRNLIVS TGTGSGKTES FLIPIFDQLL RQQQAGELNP  
 GVRALLLYPM NALANDQEKRL RELLEADTPE ITFGRYTGDT KQTREEAEKY FKLINGRNAT  
 PLPNELISRD EMQENPPHIL LTNYAMLEYL LLRPADNAFF DDAYSNNWKFL LVLDEAHVYA  
 GAQGTEVGML MRRLKDRVQR GNPLQCIATS ASLEGTKEAI MTFGQDLFGE PFEFVNEDPS  
 RQDLVSAHR KLPKFTFTWSL PDELFDQPLE SDGLFQALQE RGGDQYEELS KEEHIVKLRE  
 LSQSSSTRVE DIGKGLWPNV TDKASMRTH MLVNLGSGVL SHDGVPAISA RYHMFVRAVE  
 GAFLGYTEQG KPIVSLDRQV TLGDTARPMY EMGACIKCGT VHISAHNDSG FLVPPENSSN  
 FDEQQLKWV LTDDFETADI DEDDLETDAD ENVKVLELQK LCTACGKLNG KNSLLCSGCS  
 SHHDQFIDVK ILEPRNGSQL TCTRCGGREK NLIRRLRTDS NAAPSVLTTS LFQLLPESAD  
 QDTSRKIGAG RKLLTFSDSR QAAAYAAPYL QASYTRLLER RILIELTRDE EFTEGASIER  
 WISRASEVAK NNRVLANNLN PRETLEQTGN WVFADLASTV RSSSTEGLGL AKIELTPEAL  
 SQLSFRKPLG EMFGDPDAAD AFFNLFAQEF RHKGAINCPD YVNLEDERFG PRRGQHFFTK  
 DGGKRSTRRL YSWIPQRGTN NRKDFITKVL NRIGQAGDEG ENITTLHLHL WNDYTNSEIL  
 KVPGEKAEGY TLNYSNLQVS PGKQHSWYEC DTCRNTPFN VLGLCPHGFC KGKLKEIDTF  
 LPEYATNHYR KLATSLEILP LSAKEHTAQW TPTEAAEVQK EFIEGKINVL SCSTTFELGV  
 DVGDLQSVMM RNVPPRTANY VQRAGRAGRR SGSAAFVLTF AKRSSHD LAV FKNPTQMIDG  
 EMTVPFLHIN NARIARRHTY SIALAAFFRE QAAQNRFWKK AGEFFLGTD APLYRPAVAE  
 QEATEILEEF LSPVPNYITE ALRRVPESL HEDLDIENQG WVKQFLEIFD TTRQEISEDF  
 QTLKKMQGRA LGSEQGKKAD AFKRTITTLM DQDLLGYLAK KNMLPKYSFP VDTVDLQTNF  
 SEAGNKVSLS RDLQLAITDY APGAELVAGG KLWKSAGIRH LAGKKVETFY WTTCTECKHT  
 ETSRFGFTSE DVCSQCSAPI SLGKENKFLI PRFGFVADPN PTEVGTAPPV RSSNRLEFVK  
 QFGVKDDSEE FSNSDGTATA QVLTSSWSRT EMGALETGPN KNGFWYCQTC GFGTPNGAEI  
 PKSHRNPRTK QCGTYYLEP HSLGHTYQTD IATVAVPSYT NLD FEGWRS MYAIEAAAE  
 CLEINRDDL N GTMAKHDRP TMVLFDTVP GAGITRKVRE NFPQVLEAAI RRVETCSCGI  
 DTSCYACLR FSNQRFHLDL RRDIALDLLH HMAVAMPKSE

> RXA02369 (1-2289, translated) 763 residues

VPNNKAVEAE ISPSAVLAAE FDRDSLSEKT RVHQLAKRLG MVSKDVVVAL DGIGLVKVAQ  
 SNLSKEEVEK LLDALSQPVL NAAPAAVPDV EPVEKIRRRV EKNVENEIHQ IEKVERELA  
 AVAQPTDFEA AAREEATAEL LEDIVPEITP APVEASVYTP IFVAPAVVPT ENVQDTDEQ  
 VRERTARKRR GRRGTGRGRG AEAETVTEVS EEASTSEVEE VNEPIGIGKS TRLEAQRERR  
 TEMREENKKR RHVVSTQEFM ERRESMERRM IVRERQRHDH PGLVTQVGVL EDDQLVEQFV  
 TSDAQMSMVG NIYLGRVQNV LPSMEAAFID IGKGRNGVLY AGEVDWKAAG LGGRGRRIEQ  
 ALKAGDQVLV QVSKDPLGHK GARLTTOISL AGRYLVVYVP GRSAGISRKL PGPERRKLE  
 ILGRVPAQG GTIIRTAAG VSEENIAADV NRLHTLWEQI KERTAEKKS RGSKPITMYE  
 EPDMLVKVIR DLFNEDFTSL IVDGDRAWNT VRAYIQSVAP DLVSRVEHFN RADFDGKDAF  
 EAFDLNTQLE EALSARKVNL SGGSLIIDRT EAMTVIDVNT GRGTGKGGGN LEETVTLLNI  
 EAAEEIVRQM RLRDLGGMIV VDFIDMVLPE NQELVLRRLN EALENDRTRH QVSEVTSLGL



VQMTRKRIGA GLLETFSSPC EHCEGRGIIV HVDPVDTVDE RVEAKAEERS RRHQRSNSTN  
KAAAHEHPMVV AMRDLVESDE HDLDQEFEEL AASMIVLDDS DLL

> RXA02370 (1-792, translated) 264 residues  
MTPIYYDVND DKLDEPERIL AESTVEPEEG PRMRARRQRQ ESAADDIAAI AAAAVDIASE  
EDPDEPSGSS YVSDFEAEPI APVVEKAAEP VAEPTADYEK ARAEFEASPR RRRKTRGNSR  
SDHAPKPEDF APVVEEVAET PVKTPARKAP RNRNPSELSS GAPSSAPSTR NRRRAVRRQL  
VEAPETVVEI APEAAPEQVA EPQVEFDQPD NRRKRRRAVR VTAAPVEKKV ASTSNARAPK  
KEPQAASTTN PGRRRRATRR GPRS

> RXA02371 (1-270, translated) 90 residues  
MYAIVKTGGK QYKVAEGDLV KVEKIEGEPG ASVALTPVLL VDGADVTTAA DKLASVSVNT  
EIVEHTKGP KILKYKNKT GYKKRQGHRO

> RXA02389 (1-261, translated) 87 residues  
MANIKSQIKR NKTNEKARLR NQAVRSVRT EIRKFNAIE AGDKDAAQAO LRTASRALDK  
AVTKGVFHIN NAANKKSMA TAFNKL

> RXA02419 (1-192, translated) 64 residues  
MKNKTHKGTA KRVKVTGSGK LVREQANRRH LLEGKSSTRT RRLKGIVEVD KADTKRMKRL  
LGKA

> RXA02420 (1-381, translated) 127 residues  
VARVKRSVNA KKKRREILKS AKGYRGQSR LYRKAKEQWL HSMTYSYRDR RARKSEFRKL  
WIQRINAAAR MNGITYNRLI QGLRLAEIEV DRKILADLAV NDFATFSAIC EAKAALPED  
VNAPKAA

> RXA02463 (1-114, translated) 38 residues  
MTYVHCXGRT GRAGHNGTAV TLVGFXETXK WTXDXNEX

> RXA02468 (1-531, translated) 177 residues  
VEITDALEAL GINRTFAIQE YTLPIALDGH DFIGQARTGM GKTYGFGVPL LDRVFDSDADV  
AETDGTPRAL VIVPTRELAV QVGDDLQRAA TNLPLKIFTF YGGTPYEEQI DALKVGVDDV  
VGTPGRLLDL HKRGALSLDK VAILVLDEAD EMLDLGLPLD IEKILRALTH QHQTMLF

> RXA02522 (1-543, translated) 181 residues  
MWARDINFLY MSTEQELQIG KVKSHGIRG EVVVELSTDD PDIRFAIGEV LNGKQAGKEH  
SLTIDAARMH QGRLLVKFAE VPDRTAADSL RGTRFFAAPL EDEDEDGDFY DHELEGLRVI  
HEGEDIGEV GVMHGPAIEI LEVRLTSGKE TLIPFVHAIV PEVDLEEGTA TITPPEGLLD  
L

> RXA02533 (1-567, translated) 189 residues  
MEDDLAALV KALFDARTQR RLSISALAES SGVSRAMISR VENAEQPSA ALLGRLSGAL  
GMTLSLIAQ AEGGYDRGAR RSKQSVWTD P ATGYTTRAVS QPSESPLLV EVMLPPGAEV  
GYPADAYRFM DQVVVWLEGA VRITGEEVH ELSTGDCLRF GPRDRTDFAN PTTVATRYLV  
ALDKRVPRA

> RXA02615 (1-636, translated) 212 residues  
MQFAQNPRLT NDAVILEPLS HQWTQDLQEA VASQELWRHW FVALPTPEGM AEEIDRRLAE  
HADGLCAPWA IISAATGRAV GMTSFHTLDH ANKRLEIGRT WMAAHVQGTG INPSVKFLQL  
QRAFEDLGVN AVEFRTNWHN HRSRAAIERL GAKQDGVLRK HRIHPDGTVR DTVIYSITND  
EWPAVKLTLM ERLYRHMQVP IIPNEASLFD AS

> RXA02633 (1-264, translated) 88 residues  
MKKDIHPDYH AVVFQDAGTG FQFLTSTAS SDRTVSWEDG NEYPLIVVDV TSESHPFWTG  
AQRVMDTAGR VEKFERRFEGG MARRKKKA

> RXA02635 (1-234, translated) 78 residues  
MSAHCQVTGR KPSFGKSVSH SHRRTSRRWN PNVQRRKFYV PSEGRTITLT VSTKGLKVID  
RDGIEAVVAQ IRARGEKI

> RXA02636 (1-162, translated) 54 residues  
MARNDIRPII KLKSTAGTGY TYVTRKNKRN NPDRISLMKY DPVVRKHVEF REER

> RXA02637 (1-303, translated) 101 residues  
MAKKSIAKN EKRKEIVARY AERRAELKAI ISNPNTSDED RLDAQFELNS QPRDAAAVRV  
RNRDSDHGRP RGYLRKFGLS RVRMREMAHR GELPGVRKSS W

> RXA02657 (1-3582, translated) 1194 residues  
MARLSHMAKQ SSFVHLHNHT EFSMLDGMK IDMLADEVKA QGMPAVGITD HGNMYGSNPF  
YRKMTFMGIK PIIGIETMYA PESRFKKERV RWGEPHQKSD DVSGSGAYLH QTMLAENTTG  
LRNLFYLLSSM ASYEGQLGKW PRMDADIIE HAEGIIATTG CPSGDVQTRL RLGQFDEALE  
AAAMWQDIYG RDNYFLELMD HGLDIETRVR SELLEIGRKL NLPPLVTNDC HYVLESQAQA  
HEAMLCVQTG KTLHDEDRFK FGGTGYVVK AEQMRALWDD MVPDGCNTL WIAERVQSYD  
EIWEEHSHDR MPIADVPEGY TPTTWLHHEV MAGLEDREFSG QQVPEDYIER AEYEISVIDM  
KGYPSYFLIV AEIHKHARS GIRVGPGRGS AAGALVAYAL TITNIDPMEH GLLFERFLNP  
ERPSAPDIDI DFDDRRRGEM IRYAADRWGE DKIAQVITFG TVKTKQALKD SARVQMGQPG  
YQIADRVIKE LPPAIMAKDI PLSGITDPDH PRFNEAGAVR QLIETDPDVK RIYDTARGLE  
GVVRQSGVHA CAVIMSSVPL LDCIPMWKRP ADGALITGWD YPACEAIGLL KMDFLGLRNL  
TVIGDAIENI KANRDGEVLD LENLAIIEDE TYKLLGRGET LGVFQLDGGG MQELLKRMQP  
TGFNDIVAAL ALYRPGPMGV NAHWYADRK NGRKPITPIH PELEEALIEI LGETYGLIVY  
QEQIMRISQK VANYTAGQAD GFRKAMGKKK PEVLEKEFAN FEGGMKANGY SDAAIKTLWD  
TILPFAGYAF NKSHAAGYGL VSFWTAYLKA HYAPEYMAAL LTVSGDNKDK SAIYLSDCRH  
LGIRVLSPDI NESSLNPLPV GTDIRYGLGA IRNVGAEVVD SILDTRKEKG LFKDFSDYLD  
KIDTLPCNKR ITESLIKGGG FDSLGHARKG LMLVFEDAVID SVIATKKAAD KGQFDLFAAF  
DSDNNDDVAS FFQITVPDDE WDRKHELALE REMGLYVSG HPLDGYEDAI AAQVDTALT  
IVAGELKHGA EVTVGGIISG VDRRFSSKDG SPWAIVTIED HNGASVELLV FNKVYSIVGS  
MIVEDNIILA KAHISIRDDR MSFLCDDLRLV PELGPGNGQG LPLRLSMRTD QCTMSNIAKL  
KQVLVDNKE SDVYLNLDIG DNSTVMILGD HLRVNRSASL MGDLKATMGP GILG

> RXA02682 (1-327, translated) 109 residues  
MSYHDHSDIE YLKKIGANSP DAFKAFVHFD EAALRGPNKK IPRNYTEMIA LAVAFTTQCA  
YCIDIHTAA KKEGVTTTEL AEVALIAAL RAGGAMTHGA LAMKLYDEN

> RXA02752 (1-495, translated) 165 residues  
MAVKIKLQRL GKIRTPHYRV VIADARTKR GKVIENIGIY EPKAEPVVIK INSERAQHVL  
SVGAQPTAV AALLKVTGDW QKFKGIEGAE GTLRVAEPKP SKLELFNQAL SEANNGPTAE  
AITEKKKKAR EDKEAKEAAE KAAAEKAAAA ESEEAPAEAA AAEAA

> RXA02755 (1-1995, translated) 665 residues  
MSAPESPTNT TPDPLNASTE ELLTAAVEAL GGARRAGQEA MAKAVTKAFD TERHLAVQAG  
TGTGKSLAYL VPSIRHAQKS DSTVIVSTAT IALQRQLVNR DLPRLVDALE PLMERRPTFA  
IMKGRSNYLC MNKVARQEEL NQEDALIEQE DISWLGHKIV RLNEWANETE TGDRLDLDPG  
VPDLAWKQVS VTARECIGAS RCPHGEDCFA EIARGKAKEA DVVVTNHALL AIDALSDVS  
LPEHDVVVID EAHELDGRIT AVASAEITVN SLNLAARRAS KLDSKREER VQEIAGDLET  
LLQTMQPGRW NDMDEGSKGT LVALKDALWA LRAQIAGAPE GEAANDPERF AERQNLNHL  
MEIHDANVRI LEVFAEEDPS KQYDVVWHNH DRRGDSLNV APLSVAGLLH EKLFAENTVV  
LASATLTIGG NFNAMAASWG LPKGSWDSMD AGTPFDPKAS GILYTARHLP DPGRDGLPEE  
TLDEIYELIT AAGGRTLGLF SSKRAAEQAT KAMRLRLPFD VLCQGDDNTA ALVKKFSDSE  
NTCLFGTLTL WQGVDPVGRS LSLVLIDRIP FPRPDDPLLQ ARKEAADAEG RNFMEVAAT  
HAALLMAQGA GRLLRHVGDR GVVAVLDHRL STKRYGGFLR FSMPRFWETT NPETVRAALK  
RLVTK

> RXA02764 (1-2784, translated) 928 residues  
MSEYKPPIPS DPQVRLIKPT SKLRPRSWEG EVSHLVKQGT GLWRVTGEAG SGVSSAVVDT  
VLERIRQWE PSSMLVVATS KEAASRLRQE ISESVAQMDY VSEGPLVRSV HSAFALIRD  
ASDDDVRLIT GAEQDAVIRE LLRGHADDGR GGWPQEQREG LRMVGFARQL RDFLLRAVER  
GVGPDELVEL GERFERANWV AAGEFLREYK QVMKLSGAHS FSASELVTEA LRGEPSVKY  
RGVFIDDAQH LDPKSAELVS RFFPEAELAV VAGDPQQSVF RFRGANPDFL TKLSVDHEVV  
LKGRRKASTS IVVAETESAH ADLLADTVRR AHLIDGRSWS EIAVIVRSAG MIAPIWRTLL  
AAGVPVHISP TDVVLAEQRI VAAMILGLRA LTESLNAIEL EDLLLGPIGG ADPVTLLRLL  
RGLRQAEMKM GGQRRAEVL RSLAESDAE MLGFLTDREL NLLERVRSVL EAGREALAEH

GSIEEVLWAL WSATDLSNSL SAISLRGGAS GSQADRLDA MMALFDAAGD YVERYPSAGV  
 RSFILHISEQ ELPTGMRERR GAIPEAVEVL TAHATTGREW KRVIVAEVQE GSWPSLGETG  
 TLLGQEEFVD LVDEGIDPDI IISRSAERLA EERRLFYLAT TRSTESLLVT AVNSPDSDEV  
 REPSRFLELL SQPIVVLEGE EASAI AEPEE IGHRLLSIPA MVAELRRVVN DPRDPRRKQA  
 ARQLSRLAEA GIPGANPAEW TNLRTPTSTDE ELIKGAVSLS PSRIEQLLNC PLRAVLDRLD  
 SEEETPIAML KGTLVHAF AE AVAGGVDAAL AEEKVTSAYM QLANVPSWSR ESTEIAFRRI  
 LSRTDTWLKT SRADTFEVTG EMDVSVTIDD SVSIRGRMDR LERNKSGELV VVDFKTGKTQ  
 IAAKDMGDHP QLFAYQLALS KGVHLHGDK

> RXA02785 (1-3855, translated) 1285 residues

PVSYPVEDI EVVLDTIATA QHEDDYAQLC FRVFCCKVWL CEADLHAAIS AYAHDLTAA  
 ILQHAADSTP LSRRDQDEV ALPELVLGAT ARILGEVKAA EFISHALAAM AFVRAEYGVK  
 AAWGAKRLPG VETHLWVREV SRIDRALGVG DEQSMFRWSD DGPAEDANTQ QWLPACYCRS  
 CGRSGWMVSL EQGTNIPVLE EQKIRLNSFE QPHKQRALLD ATSEQRAAIE QGRSVAGPRG  
 VDGTSAVLWF HSASNELSTR QPSPEEQSG SSI AVLTHFG PEADDLSAQ TPCSCGDVDS  
 IRYIGSGIST LLSVLSNLF GMADLDSA EK KTLVFADSVQ DAAHRAGYVQ ARSRAFALRT  
 YTRRAVG DNE VTLPSISRAL MDNATSGRTR YELLPPDLTD LDIYKPYWHP DASKAERREA  
 SRNVHKRLSF DLAEFGQRA DLPRSLALTG ALSAFVDLPK GVALSAAAEA LYAIEVPTLD  
 IEDENLRLRW VQGALELLRA RGGINHEWFG AYLRTDGNPY MLNRRQARAE GIPGFVRGGA  
 PEFPRVGSAL SGSLRSSTGT TPLGSPRGY ASWTSQVLGI STHDAATAIT KLFDALS NRS  
 ILSISTDSG GKIYCLEAER IRIFSEDHPE VLECSVCHAQ TGVTDHVRDF LDGAPCFSPS  
 CGGV LHIEEV EDNYRRLYS AIEPRTVIAR EHTSMLKKKD RLAEQSF RG GEGSAKQSPD  
 APNVLVATPT LEMGIDIGDL STVMLASLPT SVASYVQVRG RAGRLSGNSL VLAVVRGRGV  
 TLPRLNQPLS MIKGAITPPV AYLSASEILH RQFLAYVIDC LDTRAE LPKL ETAIDVFDNA  
 AGKTPLVALL KQIHAGLDP LLEEFVRTLN MQISIDNIFE LRTWASGNST DSSLALLET S  
 QKEWMEERRS LTARRGELEK IFDKLDARND AHDEELKEEK RKTAASLKAV KLQIRDLLGE  
 FWIAALERYG LLPNFTLVDD SVELNVA VTS FNPQEVFDT KNHAYSRGIS AALFELAPGA  
 TFYAQGIAAK VDSIEIGE HG SAIEQWRLCP VCSHSEILQP GVSTPGSCPT CGSPAFADKG  
 QILEVVQMRK VSSAVEKTRA AISDDREDRF STRFNQHV SF VVPPDGHGKS WYLDNGFGIE  
 HLPKVELRWL NLGIGNGQKR RLGGFEVTSF LFNVCRHCGH LDSEAGANSR WDHRPWC PHR  
 YEQKEDTVSF ALGRTLKTQG VLMLLPEYFG SEADSMV VTS LIAAIKLGFR EVLGGDPDHL  
 DVTSVQVPRT SGD GALLDALL LHDQV

> RXA02819 (1-612, translated) 204 residues

KLQIGDVIAM PGRKRPVLAV VMTPANQSRD PRPWVTESG WSGRVDAESF TNPPITIGHM  
 RLPRQAIEEP RRNARRVQEL FRREHFKRPN KMREFARVRP NEAVTKLRNA IRDHEAHHWP  
 DREHLARTAE RMIRKERDLA KLTGNVDKAR ETLGRTFERI LSLLEMDYV DYSNPDNPVI  
 TDEGERLAKI HSEADLLVAQ CLKR

> RXA02826 (1-399, translated) 133 residues

MAPKKKKKVT GLIKLQIQAG QANPAPPVGP ELGAHGVNIM EFCKAYNAAT ENQRGNVVVP  
 EITVYEDRSF DFKLKTTPAA KLLLKAAGLQ KGSGVPHTQK VGKVSMQVR EIPATKNEDL  
 TLAISTLLRR SSL

> RXA02833 (1-579, translated) 193 residues

TRVLSLRMGR SFSLAVSVEP EQEIPKPQLK QEFKYQPDAL VFSSNKAPKQ YEVGGRGEAS  
 TSDGWEGTHS APAPEPHPAP IADREPELAT PQRIPRETPA HNP NREVSLN PKYTFESFVI  
 GPFNRFANAA AVAVAESPAK AFNPLFISGG SGLGKTHLLH AVGNYAQELQ PGPRIKYVSS  
 EEYHQRLHQL RAR

> RXA02883 (1-912, translated) 304 residues

MSFHITSVNV NGIRAAVKQR SETNLGFLPW LEETRDPDVL LQEVRASEKD TATALQPALD  
 NGWHYIGAPA AAKGRAGVGI LSRHELEDVN IGFGSFLDSG RYIEATIKDT TLDVPVTVAS  
 LYLPSSG SAGT DKQDEKYRFL DEFEGFLDQR AKERSHMVIG GDWNICHRE DLKNWKTNQK  
 KSGFLPDERA FMDSVFGTFP DEATQVAGAG DFFGAVDYEG TRRREATTDP AWF DVARRLO  
 PEGDGPYTWW TYRGKAFDTG AGWRIDYQAA TAAMLERAER SWVDKAAAYD LRWSDHSPLN  
 VIYS

>RXN00061 TRANSLATE of: rxn00061.seq check: 8093 from: 1 to: 2667  
 VTEKTDQTLMLIDGHSMFAFFALPAENFSTSGGQATNAVYGFSLMLSTLLKDEQPTHV  
 AVAFDVGRKTFRTDMFPAYKAQREATPPEFKGQVEILKEVLSTLGITTIEKIDFEADDVI

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>RXN00066 TRANSLATE of: rxn00066.seq check: 6030 from: 1 to: 813
VTDPLSAALDSGRINHAYLFSGPRGCGKTSSARILARSLNCVEGPTSTPCGVCNSCVALA
PGGPGTLDVTELDAAASNNGVDDMRELRLERANYAPAESRYRVFIIDEAHMISTQGFNALLK
IVEEPTPAHLIFIFATTEPDKMIGTIRSRTHNYPFRLLTPGDMRKVLKNAVDGEGVHVDDSD
VYPLVIRAGGGSPRDSLSILDQLIAGSGPEGLTYERALPLLGVTSFTLIDDSIHALASKD
NASMFTTIDNVIEEGLEPRRFTIDFLSTRSG
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>RXN00103  TRANSLATE of: rxn00103  seq check: 3594  from: 1  to: 4560
MAKSNSLSRFRPQVAEWFDRDVFASPTPVQEGTWEAVSKGKNALVVAPTGSGKTLAAFLWLW
DSLTEQTGGQVLDLTGTPVPVRGGKVVLVYISPLKALGVDVNNLRAPLTGIARTASRMGL
DVPNITVAVRSGDTPSAERARQVRKPPDILITTPESAYLMLTSKAGATLSDDVDVVIIDEI
HAMAGTKRGVHLALTLEKLEKLVGRPVQVRVGLSATVRPLETVAGFLGGGRPVEIVAPPAE
KKWDLTVTVPVEDMSDLPVQEPGSTIGELVMDDPLGITGESALPTQGSIWPHIEQQVYNQ
VMSAKSTIVFVNSRRSAERLTSRLNEIWAMEHDPESLSPQLRRDPAQIMSSADVAGKAPQ
VIARAHHGSVSKDERATTETMLKEGRLRAVISTSSLELGIDMGAVDLVQVESPVFASVG
LQVRGRAGHTVGATSIGSFYPKHRSDLVQTAVTVQRMKEGLIEEIHVPKNALDVLAAQQT
AAVSIKDVQVDEWYETIRKAYPYRDLAREVFDSVIDLVSGVYPSTDFAEKPRVVYDRVS
GVLEGRPGSQRVAVTSGGTIPDRGMFGVFLVGDGPRRVGELDEEMVYESRVGDVFTLGAS
SWRIIEITRDQVLVTPAPGHTGRLPFWTGDAAGRPAELGKALGAFRRSTLTDPSSSGLEG
WAHDNLI AFLQEQEESTGVLPDEKTLVLERFKDELGDWRIVLHTPYGRGVNAAWALAVGA
KIAETGMDAQAVAGDDGIVLRLPEGDEDP SAALFMFEAEIETLVTEQVGN S ALFASR
RECAARALLLPRRNP GKRAPLWQQRQRAAQLLDVARKYPSFPIIETVRECLQDVYDLFA
LKNLIEDLQLRKVRIA EVTTQQPSFASALLFN YTGAFMYEGDSPLAEKRAAALDPAL
LAKLLGEVELRQLLDPDIIAEVHQQLRRQGDRAARNNEELADSLRILGPIPLDELGEHIT
FENPDLEDRAMTVRINDREIGHAQVLDDAPLLRDALGVPVPPGPVPAQVETITDALEQLVNRW
VRTRGPFTANDLAEAFGLGIATAITALQSAPVIEGRYRQGVVDVQEYCATEVLSIIRRS
AAARKQTRPVSQS AFARFLDWQQIAPVGATPELRGVDGTYTVIEQLAGVRLPASAWEDL
VLPRRVADYSPIHLDELTSNGEVLIVGAGQAGSRDPWISLLPVDYAAQLVGEASTSMSPL
QDAVL DQLRAGGAFLFSDILEENFGYT TAQLQEAMWGLVEAGLVSPDSFAP IARLASGT
TAHRAKR RPARSRLRTRTSFASDVPPDMRGRWTL SVQPADATSR SVAHGEGWLD RYGVLT
RGSVVAEDIVGGFALAYKVLSGFEESGKAMRGYFIEGLGAAQFSTPAIIDRLRGHDDSPD
VEGWPSGATDPDVYLIAAADPANPYGAALPWEQGPSRAAGAMVVLCDGLLLLAHLTRGGR
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FVSVCVLALPDQGFEVQEGRWGQLLRGPKENGFGYDPLFIPAEIEDGQGRSSAELSAE  
EKDALSHRGQALRGLVEKIAQWAAAS

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AEPISAGLLFERFLSPDRDGPDPDIDIDIESGRREEVIQYVYEKYGRDNAAQVANVITYRT  
 KGAMRDAARALGYPQGAADAWAKGTSEPPDDVLELAAQFKGQPRHLGIHSGGMVICDRPI  
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 SVHPYLRRRAGEEAITYDHPVLEKSLGKTLGIPLFQEQLMQVAVDAAGFSGGEADSLRRA  
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 IRLGLNLVKGLGHDAQRIEDNAPFDSIPDLSSRRADLNVAQVEALARAGAVDCLGVGRRQ  
 ALWQAGVAATEKPGMLPGLSVIEAPALPGMSAFELMATNISATGVTADYQPMALIRERME  
 ELGIVPADRLLEVEDGTRLRIAGIVTHRQRPQTASGLTFLGMEDETGLMNMVSVGLWQR  
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>RXN00542 TRANSLATE of: rxn00542.seq check: 3719 from: 1 to: 675  
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 WRQAAENVAESLSKGM RVIVTGR LKQRSYETREGEKRSVFEVEADEVGP SLTFAKADVQR  
 TPRGNSGGNYGGGNQGGGLGNNQGNQGGFSNQNSGGFGGNQGNQQQSNQGGFGGNQGNQ  
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>RXN00545 TRANSLATE of: rxn00545.seq check: 1627 from: 1 to: 267  
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>RXN00562 TRANSLATE of: rxn00562.seq check: 810 from: 1 to: 723  
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 TYTPLCLIVLEPGTAAWMLGIAWVG AIDSVIMNMVWINHPRWLSVLVYLALGWLIVPLVP  
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>RXN00625 TRANSLATE of: rxn00625.seq check: 6900 from: 1 to: 942  
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 FKSKG SVTRGDADTGDGQGNANVRVAQAQALIDHLENQDDWASKPIFILGDTNSYAKET  
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 FEYSRRLNNTSDVFENNVRSSDHDPIKVGFNLSSETTEPTIPVEPTDPAEPTDPTTPVKP  
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>RXN00673 TRANSLATE of: rxn00673.seq check: 3349 from: 1 to: 402  
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>RXN00706 TRANSLATE of: rxn00706.seq check: 3516 from: 1 to: 573  
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>RXN00714 TRANSLATE of: rxn00714.seq check: 3128 from: 1 to: 561  
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REYIPIYAGTATMTTWRIAAVQVRVLETMPVIKEPLSVVPEGMPSFDEAIRGIHDPGHES  
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QIHQLRGRVGRGQHDSLCLLHTTFDEDSPOGQRLAAISTTTDGFQLSLELDLQVRQEGDVL  
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IGHEPDTPVLNDNVADLRAATPTDAKRVVPDVAERMLINQLRSRSAALRGWVQREQQA  
LAAIRTRPVLADPMTPINRRRDEIAQAVGLIRRDVTHLVRTEQALVASLRAQVSALGPSA  
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>RXN00807 TRANSLATE of: rxn00807.seq check: 4862 from: 1 to: 1242  
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VIKAAAVSPVAGNWRVVFENADRLTMQAANALLKTVEEPTTESTVMILCAPTTDPRDIAI  
TLRSRCRHLIYIPTPSIAEVARILVAEGNVSQADAELAAAASGAHIGRARYLAHNNAQRR  
RASILNLAELIFHGDVAFRSVNTLVKVMVETEAKDSNKEKEEGDLEAVRISLGMGAKGKGV  
HKAVRGGAGDFKALEDQQLRRTFLRDSLDLALVDLAGIYRDAAIISSQAQVGLTHPDM  
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>RXN00817 TRANSLATE of: rxn00817.seq check: 6901 from: 1 to: 2394  
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LTPTKALGSDQLTSTSTLLRDI PDFHPINPAPYDGDTPSEARSGIRDLSRFVFTNPDMVH  
ASMLANHPRWARLLRHLKFIVIDECHAYRGVFGANVSMVLRLLRIAIFYGSHPTVILAS  
ATSSDPEIHASRLLGAPVKAVTEDGAPTGERTVLLWEPGFIEGAEGENGAPVRRRASTE  
ANIMATLISEGARTLTTFVRSRRQAEIVALRAQEELSTLGRPDFARRVASRAGYLAEDRR  
RLERLLDDGTLLGVASTNALELGIDVGGDLAVVTAGFPGTVASFWQQAGRAGRRGQGS  
VLVARDEPMDTYLVHHPAALLEKPVEAAVFDPTNPHVIRGHVYCAAVEKPLTEAEVAAFG  
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AVAYTIDPLALEAMGIPADIPGALHAAEHAAIGMLPLLATCDRWDIGGVSTALHADTGY  
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RSVAVLSGLAKILGPIARGLIWIGNIIAPGPGFRNGPYATEVELREMDIAQEHGIVEIE  
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IGIVYLKDLVQKTTYATDGGKSVLVDEVREATFVPDSKSLDALLQEMQEDHKHIAILVD  
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>RXN00994 TRANSLATE of: rxn00994.seq check: 7403 from: 1 to: 351  
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>RXN01030 TRANSLATE of: rxn01030.seq check: 392 from: 1 to: 1176  
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 YEETATTPPTLYYITINLLEDIVNYFGDRWPFWTVIDESQTISDISSKRTRALFSVRPY  
 IGRLLILLTGTPSANKFDSIYAQVAVLDYGASLGDNDVFRARWCAPDIITDKQVRRWKPA  
 NKQAEAEVYRTISHLVMSAVNTDIKLPPLHFVDHEVHMSDDEHRDYELFKKDAVLAALLD  
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>RXN01066 TRANSLATE of: rxn01066.seq check: 7389 from: 1 to: 726  
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 MAKIGRIARVLGPRGLMPNPKTGTVTNDVAKAIEEVKGGKISFRVDKASNLHAAIGKASF  
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 DVMVNADGKATLIDGRSGEPYPYPVSIGYMYMLKLHHLVDEKIHARSTGPYSMITQQPLG  
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>RXN01563 TRANSLATE of: rxn01563.seq check: 3710 from: 1 to: 1209  
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 AGFDHVNLAAMVEQIFDLHLLKGHRSEDWSKRPLPESWLNAAALDVEMLLELADVMAEIL  
 DQQGKLPWAEQEFVHIVDQFATMTEPSETSWQDLKGLSTLKRPDQLVVAREMWLERDSFA  
 ASRD LAPGKVL SNKVIVEVARVLPRTPAELAQVKGFGRSQGATKRWFRIITRALKSPRR  
 NWPKPQQRKDGIPDRRAWASYPPEEHEVLQEIIRALIDDLAADINVPGENILQPSTLRVAV  
 WMAKHTGEIHNAETLNAVLRDYGARQWQIDQTFPILSANLLKL

>RXN01575 TRANSLATE of: rxn01575.seq check: 4786 from: 1 to: 1020  
 MKSIDLEQLAGTQSRTYQSRKITDEMVARPVHVAIALWEVPWESAKSGKIEGWVIAVDSP  
 RGRFVRSGQTKNGDAVNRTVSMKLSALKGVGRKAWIVTGRRQAALRAALVRENLYVTGSF  
 AEQNRAGVKASASIRRAEQSALYKAKKIGEFATERAPRVKERQEAHWWPRLSRTQGTAGVL  
 RLATDASTDGVFRGAMCFVASNGDYLLTQDTTASSDELELESITHALIYKLTIGATQAI  
 IESDSKAALEAIDFILNNRPRRGRWRGITACARNRFRDAWEALIDDCVVELSRVLGHAGD  
 PLNQAADQIAYMGMRAVIFEQKSAHPTLLKGIDKALRKA

>RXN01594 TRANSLATE of: rxn01594.seq check: 4466 from: 1 to: 819  
 MVARRRLDAELVRRKIARSREHAVEMIRGRRVVFAGMLALKPATVVEPEVSIRVEEDASE  
 DWASRGAKLLGALESFEPLGLKVKGRVLDAGASTGGFTDVLRRREASEVVAVDVGYGQ  
 LIWRLQNDNRVRVDRVTNIRYMTLEDTGGECDMMVGDLSFISLKLTLPAIAKVLSDGADL  
 LPMVKPQFEVGKDRLGSGGVVRSPELRAEVTADVAKFAATLGLSLKHVVASPLPGPSGNV  
 EYFLWLKDGASMPDDQQLSAMIDTAVKEGPQ

>RXN01606 TRANSLATE of: rxn01606.seq check: 3298 from: 1 to: 2676  
 MAESNAMDRAQISALLDRAQHTINLAEQANNVRLRLKTPGTATVGDNGLTGTDTYLIPSR  
 NITWPDNLYVNVFLDGMNAEATLTDYVASVASIPRLCQIINEGQGMFRRLFNPTKVQAG  
 DQAVFDLMVKLDEISSTHEVSRMLEGVHAARTRQQQGVLFPGIHVGGERYIERAQQVL  
 ASALGIAGFGAEPWDGHTLAQARRVQRYAQDPNSEYRLKSEAELKHTSINELRVQILLE  
 QLPVDALRMDTHRLRFGSLDSIHVATVADVLKHTSILTTVQGIGAQTAGRMKAAEATL  
 KQEALRRQNTSIGDEPTQPAMRLINVLARFDQTETITPEERARRTRVIDYVEHIPPSLDP  
 YIVINPATPEFNNFTDDLRLWIDANPNLFHPQTITTPADIWDDYISRPAHYQGLLATLLG  
 RDIEGADELLDATTQLKIRDLTLDKTHLTDLHLRGYQSFGARFAIIQKKTLGLDDMGLGK



TVQALSAAHAAATEKDFRTLTVVVPASVIVNWTRECKRFLNLPVFIAHGDNDKQDAINAW  
 NTNGIAICTYDGVRTMDIPAPGLVIADEAHLIKNPSTKRTQALRKLIDAAPYTLTMTGTP  
 LENKVEEFVNLVRYIQPELITRGMKMQAENFRERIAPAYLRRNQADVDELPERTDSID  
 WIDLTPEDRSAYDDQVRQGSWMGMRRSAMLSTPRLTSAKMQRIELFEEAEHGRKALI  
 FTYFLDVLDELEKHLGERVIGRISGDVPATKRQLLVDALSHSKPGSALIAQITAGGVGLN  
 IQSASLCIICEPQVKPTIEQQAVARVHRMGQTATVQVHRLIGDETADERMLEILAGKTHV  
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>RXN01637 TRANSLATE of: rxn01637.seq check: 3317 from: 1 to: 663  
 MVNSGLDDMRGATSPRLLLEILCARLLASNTVAGPAVSSSTDAAPAATPGGLTGIAAAR  
 AKAREYGQKKAAPAPAPTPAPEPVREQSLAPTPEPTAAEPTSQPAPEPEPAREPVVEVR  
 EASVEKQPASSDPLETIRSRWSELNIVEKQSVRTSIMLTEARVLGLRGDTLVLGHSTGA  
 LAARLNAADHNGILVKVLAEEETGLQLKVECI VGTNPAAEAGF

>RXN01683 TRANSLATE of: rxn01683.seq check: 9344 from: 1 to: 2568  
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 YRPDRSYVKSAPVADTMGNFHPHGDTAIYDTLVRMAQPMRYPLVDGQGNFGSRGNDG  
 PAAMRYTECRMTPLAMEMVRDIRENTVNFSPNYDGKLEPDVLPSPVPNLLMNGSGGIAV  
 GMATNIPPHNLNELADAI FWLLENPDAAESEALEACMKFVKGPDFPTAGLIIGDKGIHDA  
 YTTGRGSIRMRGVTSEIEEGNRTVIVITELPYQVNPNDNLISNIAEQVRDGKLVGISKIED  
 ESSDRVGMRIVVTLKRDAVARVVLNNLFKHSQIQANFGANMLSI VDGVPRTLRLDQMLRY  
 YVAHQIEVIVRRTQYRLDKAEERAHLLRGLVKALDMLDEVIALIRRSPTPDEARTGLMSL  
 LDVDEAQADAILAMQLRRLAALERQKI IDELAEIELEIADLKAILASPERQRTIVRDELT  
 EIVEKYGDERRSQIIAATGDVSEEDLIARENVVITITSTGYAKRTKVDAKYSQKRGKGKV  
 RGAELKQDDIVRHFFVSSTHDWILFFTNYGRVYRLKAFELPEASRTARGQHVANLLEFQP  
 GEQIAQVIQLESYNDFPYLVLATAHGRVKSRLLDYESARSGGLIAINLNEDDRLIGAAL  
 CGEEDDLLLVSEFGQSIRFTADDEQLRPMGRATAGVKMRFRDNDQLLSMSVVRDGEFLL  
 VATSGGYGKRTPLEDYSTQGRGGLGVVTFKYTPKRGRLVSAIAVEEDEIFAITSAGGVV  
 RTEVKQIRPSSRATMGVRLVNLEEGVELLAIDKNVEDQGEASAEAVAKGAVEGPASKTAA  
 EETDSVDNGSDENGEE

>RXN01688 TRANSLATE of: rxn01688.seq check: 5568 from: 1 to: 930  
 QFEGQTKTKLGNTIEIKSFVQRMANEHIGHWLEANPAEAKVI INKAVGSAQARLAARKARD  
 LVRRKSATDLGGLPGKLADCRSKDPEKSELYIVEGDSAGGSAGSRDSMFQAILPLRGKI  
 LNVEKARLDKVLKNAEVQAIITALGTGIHDEFDINKLRYHKIVLMADADVDGQHIATLL  
 TLLFRFMPDLVAEGHVYLAQPPLYKLKWQRGEPGFAYSDEERDEQLNEGLAAGRKINKDD  
 GIQRYKGLGEMNASSELWETMDPTVRILRRVDITDAQRADELFSILMGDDVVARRSFITR  
 NAKDVRFLDI

>RXN01689 TRANSLATE of: rxn01689.seq check: 4148 from: 1 to: 1116  
 VANTEHNYDASSITILEGLEAVRKRPGMYIGSTGPRGLHHLIWEVVDNSVDEAMAGHATK  
 VEVTLLEDGGVQVVDGGRGIPVDMHPSGAPTQVVMVMTQLHAGGKFDSDSYAVSGGLHGVG  
 ISVVNALSTRVEADIKLHGKHWYQNFEXSPDELIIEGNGARGTGTTIRFWPDAEIFETTE  
 FDFETISRRLQEMAFNLKGLTITLTDNRATDEELELEALAEQGETATELSLDEIDNETEL  
 VEETTDAPKKPKKREKKKIFHYPNGLEDYVHYLNRSKTNIHPSIVSFEAKGDDHEVEVAM  
 QWNSSYKESVHTFANTINTREGGTHEEGFRSALTSMLNRYAREHKLLKEKEANLTGDDCR  
 EGLSAVIFRARW

>RXN01770 TRANSLATE of: rxn01770.seq check: 9268 from: 1 to: 3765  
 MPIIIDNLNSDDDDSTIGTATEYNPDTDADLLDAINADADLDGDATISTNATEEGVDAAAE  
 KPKKKRRKAPALKPKGLTAKFFHRDLTGVGGRTRGLNKNVHPTNPDLISYQPVSDVYTPQSA  
 DHKGIKTRYILTHPTPAVVLSESI SNAFHVSTLRRNNNVNNSDSELAAWPYLYQLDIPQL  
 DQMINVADICDYHFHGYNLWVDFTPQTIALRSGKTVLDDGTTASDNTTHVYRVTVHVA  
 GQDHGSTLLDDQGNQVLD RDDNP ISTPSIKRIGAVTDLFDHNPFGFASVNSFAFVDFSWD  
 PATTLVDMLNLD SYLSNHINIASSPTPIALDMVVLNEWSEKSYQLCERVVAQAKLINSN  
 KITAHVSDVIKQNAHNILWFTEQMNPGTTNLSEVPISKKSMLPMSRQLRILEHYDVPLTA  
 YSALFWTVSAIKNESMVQYLVRQNMQLTLSSNLDALNSIVS QLPVPDKDVVAASGYQIQP  
 HFSTQQREAITTDNPLAI IQAGAGTGKSTVILERIEYLCAAGTNPEEIAVLSFTNAAADN  
 ITAKNDKVTSMTISKMVHEIYAHNFPDHEISTIDTIINTLDIEYGDQMVTS DYMQLRDL  
 LYKVMTOGGNANLTALSIFMESHIEAFISVLDQIKQTSLELEIICYLLLDKLIEPHASP  
 KYLIIDEVQDNSVFVFFALRFAAKHNTSLYLVGDSSQTLYEFRSANPKALNSLEASGVF

GTYRLTTNYSRNOEILDFANIHLSDIEANQFAGIQLYANSFDAPTADSFEKVELDMHHV  
 SKQSEFTDSIPYFMESNKARFDAAILNNEQTIVLAHSGREIRAAQQAALAEYPSITVRNL  
 QSDKGFNNTVFSTFIKDFWFEVTAVDPAHAAFTFTSQVTAHLDKLVRGKREQMEDRVIRS  
 MAAWWRENERDIQGWVQQTQSGAITNEEFFYRLRQCILDYEIRNNRARSMLNARNNANK  
 EAVAQEKPLLMVSTIHSAGLEFDNVIVLQKPSSDAEMTEEGKRATYVALTRAKKRELI I  
 AGSTRAYPRIVTDYEQIVDLLEKRDEERKIKEEEAAALATLEAEQETRALAAEAQAQAL  
 LLEHNPWLRLDLSDEEVTALTEQEIINNVEPALQIEEEEEEARALAAEPAIQOYLSQFAF  
 DEFDDDNVANTVVHVAPQPIHLQAVPADVTVQSSTAPVTPVVADLEVTTVAADPVEPTI  
 VAAQPEVDDNLVYSTSTPNSHSDVIAVNSDTSENA AVNPVLSDIEALRAIFNNQD

>RXN01772 TRANSLATE of: rxn01772.seq check: 5291 from: 1 to: 4938  
 MECMSTITDAVSALRTLPSQSAQGLAFEKLMVNFIKSDPTLSTEFDEVHRVWDWPYNGGT  
 MDTGIDLVAYNKDDDAYTAIQCKFYLPSTSLAKGQLDSFFEASGRFTETPEGTRSFNRL  
 VISTTDKWSSNAEKMLNQTIPTRIGLSAIAESPIDWDIAYPGSELTINLQLKEPYSR  
 PHQQTALIEKAIEGFQTHDRGKLIMACGTGKFTALRLSEEVARLNGNKARILFLVPSISL  
 LSQTLKEWTAQKTMDLRPVAVCSKSKVSKAAEDIAAYDLEVPVSTDGALIAEKLHRKRA  
 AGLTVVFSTYQSLPAVHAAQEAGAEPFDLVICDEAHRRTGITLAGEDPSNFTRIHDASYI  
 KAAKRLYMTATPRLFDDSVKGAADHSAEVSSMDDEAIYGPEFHRLGFGEAVEKGLLTDY  
 KVVVMTVDEQVAASALTVLGSTPGEELTDMTSAIIGAWNGLAKRSGKEQDTKTGFSDD  
 AAMERAVAFARDIKTSQQAIESFPVRVNAVYTTLEVKNDVDDEHNLNLSVACQHVGDGSMN  
 ALERNRLTWLKAPTQSMETKILTNRCLSEGVDPALDSVIFNPRNSMVDVVQSVGRV  
 MRKSPGKNYGYIILPVAVPPGVAPSAALNDSRRFKVWQVLNLAHDDRFRNAMVNSIAL  
 NEGNIKDLPVETEHTGPTSKDRDNAPYDSAESATQYVLFSLQWQEAITYKLVDKVGTRT  
 YWEDWADDVADIAQAQITRIKALLDNASPTIKEEFERFVEGLRGNLNESISDDEAISMLS  
 QHLITAPVFDALFAESSFAKQNPVSQVMQRMADALNSAELNSETEKLEKFYDSVRIRAAE  
 VSSAAGKQAVIKDLYERFFKAFKKQSEALGIVYTPVEIVDFILRAADDVSKKHFGRLS  
 DKDVHVLDPFTGTGTFMVRLQSGLIKPEDLARKYANELHATEIMLLAYYVAAVNIETTY  
 FGLEGERALRNGEDAPVYEPFDGIVLGDTFQMYEDDDKLDLDVFTANNDRMERQRLTPVQ  
 VIVGNPPYSVQGSSANDNNANLKYPTLDRRIEDSYAKYSTATNKNLSYLSYLAFRWATD  
 RIHTQGVVAFVSNNGWVDGNTADGVRLSLAQDFSEIYVFNLRGNSRTGGDLAKREGGNVF  
 NVRVGTQIIVAVKNPQLSGCRILYKDIGDNLADAKLNEIAVATIEGAEWQTISPNEYGD  
 WISQRSVDFDTPVVLGDKKNKSALKVFQTFSAGLKTGRDAWCYGPSTSAQVKTNITRLLET  
 YEQAQQRFNSWVVDNGVTSPKEADVNFQFLKQNPDLADSKKISWDSNLKMSLSRGDTFSFD  
 PSSIQMSLYRPFPPQQTIFYHVS LNQRRYQLPSMFPTPEHDNQGFYIVNPGSAKPFSTLAT  
 NLLPDLAMWGSNAGQFFTRWTWEPIETREGELDFGNGLFSTTPKKGVEGEILDGYRRVDN  
 ITDEILKLYQSSLGEDVTKDDIFYFVYAQLHDPAYREAYAADLKKMLPHIETPTDRARFD  
 HFVTAGKELMDLHINYEDVEPVDVEVKVEKADPTDRETWRVTMKMKWAKVRDPETKKLVE  
 DHTTLIYNSSITISGIPAEAENYQLGSRSAIAWLIDRYQVKKDKASGIVNDPNDWADEVG  
 NPRYIVELIAKVTRVAVETMRIVEEL

>RXN01786 TRANSLATE of: rxn01786.seq check: 2034 from: 1 to: 684  
 MRAAKITRGFTSNPAGSVLVEFGNTRVMCTASVELGVPRFKRDSGEGWLTAEYAMLPAAT  
 AERNRRESMAGKVGRTHEISRLIGRSLRAAVDLSQLGENTIAIDCDVLQADGGTRTASI  
 TGAYVALADAIKVLQERGVVPGSPLLAPVAAVSVGLVDGNVCLDLPYEEDSRADVDLNV  
 MTEHGEFVEIQGTGEETTFTRAQLNDMLDHAKEGCRELVAAQKAALGI

>RXN01876 TRANSLATE of: rxn01876.seq check: 6935 from: 1 to: 1851  
 MARPFYLATTVSPEGVHIRRHIRTGRVVTGVDDDEVLTGEMADVIEQGGVGSSESVLHQAL  
 EQARSGHMRNIVETIQREQDEIIRDTRGVMVVGPGTGKTAVALHRVAYLLYTWRDQL  
 AKSGVLIIGPNKTFLEYISHVLPELGETGVVLSTVGELFPGIVPTGSEDTLTREIKGSEE  
 MASILAEAVKAYQVLPEKTIIVSVSDGIEISIDEKTVAKSRTRARRARQSHNSARPIFREH  
 LVEQLAHQMAQTIGADPLGKNLLSAAIDQLHDDLLDDAALQSVIDDFWPELRLPQDVLH  
 DLLISEERINVAAAGYDEETKSALLRGELDPWAPSDAALLDELALLIGLPDPEEAREKAE  
 AKWREQIDDAQEVLVSSSQSSDIDDVTEAEVLSAFDVIDAETLAQRQTVTDNRRTAER  
 AQADHKWAYGHVIVDEAQELSMEWRMVFRSPSRWMTLVGDIAQTGWPAVDDWAESLW  
 PFVEKFRFRHHELTVNRYTPAEIMSVANELLTQINPDIAPAMAIRESGREVVNLPLDADLS  
 AVMDSLREEDSQRTIAVISSRRHHESDFYLVDDIKGLEFDHVIIVDPAGIVEESFQGLQD  
 LYVAVTRATQSLTILGE

>RXN01912 TRANSLATE of: rxn01912.seq check: 1693 from: 1 to: 738  
 MRRFIFTERNGIYIIDLQQTLYIDQAFEFVKETVAHGTVLVFGTKKQAEAVQVEADR

VGMPYVNHRLWLGMLTNFQTVSKRLNRMKELQAMDAENGEGRTKREVLMLTRERTKLE  
 RVLGGIAEMTRVPSALWIIDTNKEHIAVAEAHKLNIPIVVAILDNTCDPDVDFPVPGNDD  
 AIRSTALLSRVISTAVEEGKKAREERQLAAAKDAAGDAKPEAEAEAPAAAEAEAEAE  
 EAPAAE

> RXN01951 (1-561, translated) 187 residues  
 LLHYFDGEKR YILAPKGLTQ GTVIESGAAA DIKVGNNLPL RNIPGTGTTIH NVELKPGAGA  
 KLARSAGASI QLLGKEGSYA VLRMPSSSEIR RVNIRCRATV GEVGNAEQIN IRWGKAGRMR  
 WKGWRPTVRG VVMNPVDHPH GGEGKTSYG RHPVSPWGQK EGRTRKPKRY SDDMIVRRRR  
 ANKNKKR

>RXN01966 TRANSLATE of: rxn01966.seq check: 3341 from: 1 to: 657  
 VSESENNTTPAARDDRLVWVLEMTGLDLKRHVIVEVAALVTDANLNVLGEGVDLVVH  
 ATEEELAQMDDFVTNMHESGLTEQIRESAVTLKEAEDAVLALIEKHCDPAHPAPLAGNS  
 IATDRAFIREHMPRLDEALHYRMVDVSSVKELARRWYPRVYKQPEKGLAHRALADIVES  
 IRELDYYRRSFFVAEPGPTSEQCADDAAQAVDRFAPYFD

>RXN01979 TRANSLATE of: rxn01979.seq check: 2139 from: 1 to: 1581  
 LGHDFRPDYRRIRDLLAGLAPNIPVLATTATANDRVVEDVRAQLEDGTGLFRGGIDRESL  
 YLSVNNLLNPTERPAWLATHLKELTGSGIIYCLTVSAAHDLADALNSVGWNVAAYTGRTE  
 AGERERLEHALINNEIKALVATSALGMGFDKPD LGFVVMGSPSSPVSYQQIGRAGRGT  
 ARADVILLPGTEDKEIWEYFASVSFPREEVVRQLLAVLTDEAQSTVKLESQVDLSRSRLE  
 QVLKVLVDVDAVKVRVGGWVSTGQEWIYDAERYAGLEQARKIEQQSMVNYQNTTECRMLY  
 LRKELDDVEATTPCGRCDNCTGKTWGLD TDASITLKVDQQLQTPGVKIAPRKMWPTGISV  
 RGKIAGLEEGRALGRINDIARGPALKALLDSGAYSDDPMMARIIEVLKNWDWTNR PANVV  
 ALGNTNFGSTEMIIQVAQSIAAVGRMNFAGVLPAPGAEEVMAQNSAYRVEALLKQWDWS  
 QGLQLVPGPILLVTDLIDTGSVTVAGNGIAQRTSEKVL PFALASRG

>RXN02038 TRANSLATE of: rxn02038.seq check: 6905 from: 1 to: 369  
 MSEPIQENVENSVADAADIAATAATEEFTNTIGDAIATASEEETIEAAPVVDGPIQT  
 VGRRKRAIVRVLVAGSGEFKCNRTLEEFYFNKLHQQLIKAPLVLLDRLNQCNIASIK  
 GPK

>RXN02070 TRANSLATE of: rxn02070.seq check: 1536 from: 1 to: 1122  
 MTQVTESAVRSALSRVEDPEIGKPITELGMVKSVSIDGSDVQVEVYLTIAACPMKTTIIVT  
 NTEAALKDIDGVGQVHVTTDVMSDEQRRALRVSLRGETSEPVIPFAQPGSTTRVYAVASG  
 KGGVKGSSMTVNLAALAKRGLSVGILDADIYGHVSGMLGSDQRP HQVDDMIMPPQAHG  
 VKMISIAHFTEGNAPVWVRGPM LHRAIQQFLTDFWGLDILLDLPPGTGDI AITVAQL  
 IPNAELLIVTTPQAAAAEVAERAGTISVQTNQKVAGVIENMSAMVLPDGT TMDVFGTGGG  
 QKIADRLTAVTGEEVKVIGSVPLDPNLRI GGDVGNPIAISEPHSPTAA AINEIAEHLAHR  
 KVSIVGKTLGLGVK

>RXN02082 TRANSLATE of: rxn02082.seq check: 737 from: 1 to: 2910  
 MYLKSLTLKGKFSFASATTLKFEPGICAVVGPNGSGKSNVVDALAWVMGECSAKTLRGGK  
 MEDVIFAGAGDRKPLGRAEVTLTIDNSDGALPIEYTESVTRRMFRDGASEYEINGAKAR  
 LMDIQELLSDTGIGREMHIMVQGKLAIELESRPEERRAYIEEAAGVLKHRRRKEKAQRK  
 LQGMQVNLDRQLDLTHELAKQLKPLARQAEAAQRAATVQADLRDARFQIAGFEIVKLSEK  
 LETSTEREKMIREQAEAAQEQL EEAATTTQMEVEMELAEITPQAEAAQQLWFDLSSLAERV  
 SATMRIAADRASSGAADVVPYAGQDPDELLGRAETADKELEELMAVEMTTERLTSIQEEA  
 EDKAAQAREAREHLAQVRAISDRREGVVRLLASEESLRTQHTSAEEEEAEERLSEQLEEF  
 GRILDVERERRLTDERKQGVDTDRAPLEELKQAKHEAEAAETRLEELRTRKSDLEKEVS  
 RLQSRIETLNQNRPRSDAADVVDYPQLATLIRPQRNVKALAAALGAHAALAGEAAEGL  
 VEKLIDAGVARTIIVDGTQAGGAWRLDANIPAGASWLLDHVDLDPAIAGPVNRLADVVL  
 VDDPSLGRQAIEDDPRLRAVDRNGVLIGAWIQVGTETSTVEITAHIEEAEALAAASAA  
 LDDIAGTFDGLHAADNTRVEVAARTAAALRELDMTDSITRDLARLDKQHEAAESERVRH  
 VGRLLHAAETRREELREQLEDIVRLSRVEDEEDADEPSTTARDQANAELQQIRAMEMEAR  
 LAQRTAEERAGQQRGKGD SLRRQAEHERQAKIRHEQAMEARRRRTQLAAAVHNGARDVAE  
 RVSSVLAQAAIERDQHNDRKALLTSHLARAKDAVSAARQHLNRLSDNAHSMELARSQAQV  
 RMEEAVAKITEQLGIPVAELLRDYTPDENFDEKFQARLQAEKDLAALGKVNPLALEEF  
 KALGRALRP

>RXN02131 TRANSLATE of: rxn02131.seq check: 894 from: 1 to: 1671  
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 AGHDAEQVVDMLERFSRFPVPQALLIDIAETMSRYGRVRLHRRHPAHLILESSEPAIIVE  
 ISRHKKIKPMLGAQVDPETIVVHPSEGRRLKQELLKVGWPAEDLAGYVDGESHPIGLSTE  
 FEDWSLRDYQQMAADSFWEAGSGVVVLPCGAGKTMVGAASMARAAQATTLILVTNTVAGRQ  
 WKDELLRRRTTLEDEIGEYSGERKEIRPVTIATYQVVTRRTKGEYKALELFDSDRWGLII  
 YDEVHLLPAPVFRMTSDLQSRRLGLTATLVREDGREGDVFSLIGPKRYDAPWKDLESQG  
 FIATADCEIRSTMTDAERMVYATAESADRYRLAATAHTKVAVVRKLLLEEHAGKPTLIIG  
 AYLDQLEELGAEFNAPVIDGKTPNKKREALFDQFRSGSLSVLVVSKVANFSIDLPEASVA  
 IQVSGTFGSRQEEAQLGRLLRPKHGSEAHFYSIVSRDTLDTEYAAHRQRFLAEQGYAY  
 RILDADDILFPLPKKEL

>RXN02293 TRANSLATE of: rxn02293.seq check: 2677 from: 1 to: 2388  
 MSSRIGNFLINRISTGLPVENIIPHLQEAFSAGPKNLVIQAPPGTGKTTLPLPLVANILC  
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 GVLIRQLLNNPELPGIGAVIIDEVHERQLDSDLMLLAELSQRDDFSLIAMSATLDS  
 KFANLLDAQVLSVEAPIFPLDISYAPARAPRLNAKGVWDWFLDHMAQKTHDAVTHSEHSA  
 LIFVPGVREIDRMSTLKSGLHNNVFLHGQLSPTEQDRALAPSQQQRIIVSTPVAESSL  
 TVPGVRIGVDSGLSRSPKRDSARGMTGLITSSCAQASAGQAGRAGREGPGQIIRCYSSE  
 DFSHFPRFVTPEISSADLTQAALWLAQWGTSPADLPLDQPPHAAWTAAQQLRLIGALE  
 GDAITSLGHLRLSTLPLCPQLSASLLRFGEQSakilAVVSENPPQGDVEKQPKREVERLR  
 RLAPASVGKASAGQIVGAAPQLIGRKIDNGEYLLASGTRARLMSDLKDAEWISVAAIN  
 RSQNSAIRAAARISEDDAIDIIGVVEETRAIFVNGKVQARKVKAAGAIELSSTPTKPTP  
 AEASETIATALAKGGIDLHFHSDKAASLRDLKFIHEHRGEPWPDIEADPHLWLSPEIE  
 ALSHGTRLNNIDMYPALQRLLPWPEATNFEEFAPSHLSVPSGNQHRLDYSSGRPVIRVKL  
 QECFGLSESPQLCGIPVQFHLLSPAGRPLAVTDDLRSFWSGPYSQVRAEMRGYPKHPWP  
 EDPWTAPATARTKNRM

>RXN02357 TRANSLATE of: rxn02357.seq check: 4829 from: 1 to: 6300  
 MSSLIPVHAAGSIQEGITEYLTSFSLADKQVATELKRFLGHGDSGMFHGPYVRARLPYA  
 QAQEWENVLSWLPENFVPHYHQAQAFQRLSSLDNRGKDRRPDPTLVVTGTGSGKTESFLY  
 PILDHALRLRKRQGGIKALLYPMNALANDQADRLARLIHNNPALKGVTAGIYTGEAKG  
 NRTQMGERELINDPQAMRVSPDILLTNYKMLDQLLLRSVDREMWQKSATSLQYLVLDEF  
 HTYDGAQGTDVALLRLRLGLMLKSQQPANFLDDSAMHRPLGIITPVATSATLGSGDSGSP  
 MLDFAYTIFGERFPADAIVGETRLELDQWRAEIAQNFAPAVSEPRELPTVEDIEVLDT  
 IATAQHEDDYAQLCFRVFCEKVWLCEADLHAAISAYAADLTAAILQHAADSTPLSRRDQ  
 DEVTALPELVLGATARILGEVKAAEFISHALAAMAFVRAEYGVKVAWGAARLPVETHLW  
 VREVSRIIDRALGVGDEQSMFRWSDDGPAEDANTQOWLACVCRSCGRSGWMVSLEQGTNI  
 PVLEEQKIRLNSFEQPHKQORALLDATSEQRAAIEQGRSVAGPRGVDGTSAVLWFHSASNE  
 LSTRQPSPEEEQSGSSIIVLTHFGPEADDLASAKQTCPCSGDVDSIRYIGSGISTLLSVSL  
 SNLFGMADLDSAEKKTLLVFADSVQDAAHRAAGYVQARSRAAFALRTYTRRAVGDNVTLPSI  
 SRALMDNATSGRTRYELLPPDLTDLDIYKPYWHPDASKAERREASRNVHKRLSFDLALF  
 GQRADLPRSLALTGALSFAVDLPKGVALSAAAEALYAIEVPTLDIEDENLRLRWVQGALE  
 LLRARGGINHEWFAYLRTDGNPYMLNRRQARAEGIPGFVRGGAPEFPRVGSALSGSLRS  
 STGTTPLGSPRGYASWTSQVLGISTHDAATAITKLFDAISNRSILSSISTDSGGKIYCL  
 EAERIRIFSEDHPEVLECSVCHAQGTVDHVRDFLDGAPCFSPSCGGVLHIEEVEDNYR  
 RLYSAIEPRTVIAREHTSMLKKKDRLEQSFRRGEGSAKQSPDAPNVLVATPTLEMGID  
 IGDLSVMLASLPTSASVYQVRVGRAGRLSGNSLVAVVRGRGVTLPRLNQPLSMIKGAI  
 TPPVAYLSASEILHRQFLAYVIDCLDTRAELPKLETAIDVFDNAAGKTPLVALLKAQIHA  
 GLDPLLEEFVRTLNMQISIDNIFELRTWASGNSTDSLLALLETSQKEWMEERRSLTARRG  
 ELEKIFDKLDARNDADDEELKEEKRTAASLKAVKLQIRDLLGEFWIAALERYGLLPNFT  
 LVDDSVELNVAVTSFNPQVEFDTKNHAYSRGISAAALFELAPGATFYAQGIAAKVDSIEI  
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 DALLLHDQVPGGTGYLNQFADPTKVPELISRAWERSRCQCQYDETLACPECLLPYTRTD  
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 RALKNRHAKLVDRVNGSNSYVDIEMSSGVRWRMSEQVDRGYTRPDFWFEPLNGNYPTVAV  
 FTDGAAFHISSANYRLDGDQKRMKLALDPDNLIPWNITSLDLDRFSNPAAQGEPAWFS  
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GDGIVGTRFNKISLRATMVNRELRLARQLWLAPTTPPEELEVDTWTAFLNLNLMWLAPESV  
YVSTNGSPHKIDIVPAPAAPLVVEVPELWAPILDGFTADEDEEAEGALQILAKEHALVPE  
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>RXN02370 TRANSLATE of: rxn02370.seq check: 1226 from: 1 to: 792  
MTPIYDDVDNDKLDEPERILAESTVEPEEGPRMRARRQRQESAADDIAAIAAAVADIASE  
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SDHAPKPEDFAPVVEEVAETPVKTPARKAPRRNRPSSELSSGAPSSAPSTRNRRRAVRRQL  
VEAPETVVEIAPEAAPEQVAEPQVEFDQPDNRKRRAVRVTAAPVEKKVASTSNARAPK  
KEPQAASTTNPGRRRRATRGRPRS

>RXN02371 TRANSLATE of: rxn02371.seq check: 7071 from: 1 to: 315  
MYAIVKTGGKQYKVAEGDLVKEKIEGEPGASVALTPVLLVDGADVTTAADKLASVSVNT  
EIVEHTKGPKIKILKYKNKTGYKKRQGHRLPLTVLKVTVGNQVSPR

>RXN02468 TRANSLATE of: rxn02468.seq check: 4275 from: 1 to: 1224  
VEITDALEALGINRTFAIQEYTLPIALDGHDFIGQARTGMGKTYGFGVPLLDVDFDSADV  
AETDGTPRALVIVPTRELAVQVGGDLQRAATNLPLKIFTFYGGTPYEEQIDALKVGVDDV  
VGTPGRLDLHKGRLSLDKVAILVLDDEADEMLDLGLPDIEKILRALTHQHQTMLFSAT  
MPGAILTLARSFLNKPVHIRAETSDASATHKTTQVVFQAHKMDKEAITAKILQSKDRGK  
TIIIFARTKRTAAQVAEDLASRGFSVGSVHGDMPAREKSLNAFRTGKIDILVATDVAAR  
GIDVDDVTHVINYQTPDDPMYVHRIGRTGRAGHNGTAVTLVGYDETLKWTVIDNELELG  
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>RXN02727 TRANSLATE of: rxn02727.seq check: 1998 from: 1 to: 912  
VVLLPLLVPQLQVQPLQLPSLLTRQRCARKSKRSCAPNTASKLDDASKAAQKAQNDAKS  
AQDQLQRAQADAKAARDEAEKAKAEAKSAASSSTTKAAAVGAVGAGTGAAVATGAANVDT  
HMQAQKVLGLAQEMADRLTSEARSESKSMLDEAREAAEKQIEEANSTSNRTLEDARANAE  
KQIAEAQNRAADTLVNEADAKAKNLVSEAEKKSAAATLAASTSRAEAQIRQAEDKANALQAD  
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PSGE

>RXN02764 TRANSLATE of: rxn02764.seq check: 4873 from: 1 to: 2784  
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VLERIRQGWEPSSMLVAVTSKEAASRLRQEISESVAQMDYVSEGPLVRSVHSAFALIRD  
ASDDDVRLITGAEQDAVIRELLRGHADDGRGGWPQEQREGLRMVGFARQLRDFLLRAVER  
GVGPDELVELGERFERANWVAAGEFLREYKQVMKLSGAHSFSASELVTEALRGPEPSVKY  
RGVFIDDAQHLDPKSAELVSRFFPEAELAVVAGDPQQSVFRFRGANPDFLTKLSVDHEVV  
LKGRRKASTSIVVAETESAHADLLADTVRRRAHLIDGRSWSEIAVIVRSAGMIAPIWRTLL  
AAGVPVHISPTDVVLAEQRIVAAMILGLRALTESLNAIELEDLLLGPIGGADPVTLRRL  
RGLRQAEMKMGQORRAIEVLRSLAESDAEMLGFLTDRENLNLERVRSVLEAGREALAEH  
GSIEEVLWALWSATDLSNSLSAISLRGGASGSQADRDLAMDALFDAAGDYVERYPSAGV  
RSFILHISEQELPTGMRRERRGAIPEAVEVLTAAHTTGREWKRIVAEVQEGSWPSLGETG  
TLLGQEEFVDLVDEGIDPDIIISRSAERLAEERRLFYLATTRSTESLLVTAVNSPDSDEV  
REPSRFLELLSQPIVVLEGEESAIAEPEEIGHRLLSIPAMVAELRRVNDPRDPRRKQA  
ARQLSRLAEAGIPGANPAEWTNLRTPSTDEELIKGAVSLSPSRIEQLLNCPLRAVLDRDL  
SEEETPIAMLKGTLVHAFAEAVAGGVDAALAEKVTSAYMLANVPSWSRESTEIAFRRI  
LSRTDTWLKTSRADFTVEGTEMDVSVTIDDSVSIRGRMDRLERNKSGELVVVDFKTGKTQ  
IAAKMDGHPQLFAYQLALSKGVLHGDK

>RXN02819 TRANSLATE of: rxn02819.seq check: 6309 from: 1 to: 1047  
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DREHLARTAEIRKERDLAKLTGNVDKARETLGRTFERILSLLSEMDYVDYSNPDNPVI  
TDEGERLAKIHSEADLLVAQCLKRGIVDNDLPAELAGVSMCTFENRRETGGEAQAVTEA  
MADSMNSVERIWGELVEDERRHRLPITRQPEAGFATAIHQWASGAPLGYCMAAAAENGAE  
LTPGDFVRWCRQVIDLLEQVAKTAYFDETRNARQAIDAIRRGVVAIGS

>RXN02826 TRANSLATE of: rxn02826.seq check: 160 from: 1 to: 435  
MAPKKKKVTGLIKLQIQAGQANPAPPVGPALGAHGVNIMEFCKAYNAATENQRGNVVPV  
EITVYEDRSFDFKLKTPPAKLLLKAAGLQKSGSVPHTQKVGKVSMAQVREIAETKKEDL

NARDIDAAAKIIAGTARSMGITVEG

>RXN02833 TRANSLATE of: rxn02833.seq check: 6083 from: 1 to: 783  
 LLETWRQVVADLTTLQQADSGFDPLTPTQRAYLNLTKPIAIVDGYAVLSTPNAMAKNVI  
 ENLDGDLALTRVLSLRMGSRFSLAVSVEPEQEIPETPAQQEFKYQPDAPVISSNKAPKQYE  
 VGGERGEASTSDGWERTHSAPAPEPHPAPIADREPELATPQRIPRETPAHNPNREVSLNPK  
 YTFESFVIGPFNRFANAAVAVAEPAKAFNPLFISGGSGLGKTHLLHAVGNYAQELQPG  
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>RXN02943 TRANSLATE of: rxn02943.seq check: 6621 from: 1 to: 1668  
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 NLAMGASQGSVALTDNSGLTADLVGFGGTSMEFGTAAAPETSNKLSVQRKEVGADSDNNS  
 VDFETGAPTPTSSGGSAPVDPGEPETPVNPGETVSIAQIQGTGLATPLEGQTVTTEGIVT  
 AVYAEGGFNGYYIQTGSGTAPKVAGDASDGIFVYVGSNGSYPELGASVTVTGKATEHYE  
 MTQLGNSSFTVSDTAFEPTVPLELDTVPTGDDIREAYEGMLLKPTGAHTVTNNYATNTFG  
 EIALAPGNEPLYQATQMVPAGAEAIAYEAENVAKQITLDDGRSGNYTRGDSSTPMAWLVQ  
 DGGETIKSIRTGDQVEFQAPVIFDYRYDLWKFFQPTTPTGNTASSDLPTWDDTRAELA  
 SINDVAGEFHIAFNVLYFTSLGEDEPGCSAYRDINNTPTANNCNVRGAYTEEALEDQ  
 QSKIVEAINRLDQDVL

>RXN02981 TRANSLATE of: rxn02981.seq check: 3652 from: 1 to: 366  
 MARLAGVDLPRNKRMEVALTYIYGIPARSKQLEETGISPDRLTDNLTDEQIAALRDVI  
 EGTWKVEGDLRRQVQADIRRKIEIGCYQGIRHRRGLPVRGQRTKTNARTRKGPKKTIAGK  
 KK

>RXN03093 TRANSLATE of: rxn03093.seq check: 5261 from: 1 to: 1839  
 VADTAGTTGSKKKYLIVIVESATKAKKIQPYLGNDYIVEASVGHIRDLPARGAADIIPAKYKK  
 EPWARLGVDTRGFAPLYVVPSPDKKKKVADLKAKLKLVDLLELLATDPDREGEAIAWHLE  
 VLKPTVPVRRMVFNEITKPAILAAAENTRELDENLVDAQETRILDRLYGYEVSFVLWKK  
 VMPRLSAGRVQSVATRVIVERERERMAFVSADYWDLSAEFNARENGKADSDNPSSFTARL  
 STIDGNRVAQGRDFNDRGELTSEAVVVDKQRAEALAELEGQEMAVVGVEEKPYTRRPPYA  
 PFMTSTLQQESGRKLHYTSERTMRIAQRLYENGHITYMRTDSTSLSEQGMKAARDQALEL  
 YGAEYVSPSPRTYDRKVKNQEAHEAIRPAGETFATPGQLHGQLDAEEFKLYELIWQRTV  
 ASQMADAKGTSMKVTIGGTAKTGEKTEFNATGRTLTFFGFLRAYVETTRTADGRDVADNA  
 EKRLPLLSEGDLLKVLSEADGHSTNPPARYTEASLVKKMEDLGIGRPSTYASIIKTIQD  
 RGYVYSRGNALVPSWVAFVAVVGLLEANFTSLVDYDFTSSMEDELNDIAAGREGRTEWLNG  
 FFYFGRCRSGSVHG

>RXN03139 TRANSLATE of: rxn03139.seq check: 8976 from: 1 to: 249  
 MKQRNNAKVRLEQTRRPKKNPKAAGIEKVVDYKDINTLRQFISDRHKIRSRRVTGLTPQ  
 QQREVATAVKNAREMALLPFTSR

>RXN03148 TRANSLATE of: rxn03148.seq check: 7950 from: 1 to: 366  
 MVINFIIILFLMIAITSFFVASEFALVKIRRSRLEQLEKENVKNAKLALHVTHHLDNYLSA  
 SQLGITLTGLIIGWVGEGSVAALLEPVIGKLPFSSAISSTISVALGFILVTYRCGYWRT  
 AS

>RXN03163 TRANSLATE of: rxn03163.seq check: 610 from: 1 to: 1497  
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 MSRTAQTSHEGKLMWLDRIPIVVYPPQTAKLIEQLSDRYGGVRSDLIRSALPARHAGA  
 EEADTSTSWESLGEVKEPDLSSWSAYQHGSFVDAVLGTTARASWQIAPGDDWALALAS  
 LAVKVVKGDDGALLVVPDQRLDLRLEAALRGLVAAKQITVLNSGLGPQARYRRFLSVLSG  
 QGRLIIGTRSAAFAPVKDLKLAVILNDGDDNLVDPRAPYAHAREVLTTRSSLEASSLIIA  
 GHARTAETQLLVESGWMHNLIAPRDTIRTRMPRIQAVGDSDFQMERDPMARSARLPGIAF  
 HAVRSALERDQPALIQVPRKGYVPTLACGNCRTPARCRHCNGPVGLPQGSSDLAGVPTCR  
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>RXN03166 TRANSLATE of: rxn03166.seq check: 5429 from: 1 to: 2235

MTTSETAPSKASLYELLEGVSLSDERTFRRRLSKARAPKALGAIKADIDKARLLIDEKSQ  
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HTQPRRLAARTVAERIADELGQDIGESVGYAIRFDDRVSSTSVKLMTDGILLAEMQDRD  
FLNAYDTIIIDEAHERSLNIDFILGYLRQLLPKRPDLKVIITSATIDPERFAEHFADASG  
KPAPIIEVSGRTFFVEIRYRPLEVLDGDKIIDTDPLDGLCSALEELMAEGDGDILCFFAG  
ERDIRDAMEAIEARRWKGVEVTPLFGRLSNQEQHRVFSPHSGRRIVLSTNIAETSLTPVG  
IHYVVDGTARISRYSVRTKVQRLPIENISQASANQSRGRCGRVADGIAIRLYSEDDFNS  
RPEFTDPEILRTNLASVILRMASRLRGDINDFPFVQAPEQRSIRDGILLHHELGALDDT  
QADGSPQLTQIGKDLANIPVDPRMARMLEANTLGCLHSMVIVSALTIQDVRERPLEFQ  
AQADQAHARFKDTSDFLGFLKLWEYIADQRNQSSGNSFRKQMKKEFLHYMRIREWDLV  
RQLEQIGQQLGWAKKEQVAGTASPDIIHQSLLTGLFSQIGSRDGESKEFTGARGTKFLVF  
PGSALTKKPPQFIMAGQLVETSRLWARDVAKIEPEWVEKAAGPLLKHQYSEPYWSSKRGG  
CHGAPQINALRCDNCCRQGSSSLPHG

>RXN03175 TRANSLATE of: rxn03175.seq check: 2273 from: 1 to: 783  
VRASEKDTATALQPALDNGWHYIGAPAAAKGRAGVGILSRHELEDVNIGFGSFLDSGRYI  
EATIKDITLDVPTVASLYLPSGSAGTDKQDEKYRFLDEFEGFLDQRAKERSHVMIGGDW  
NICHRRREDLKNWKTNQKSGFLPDERAFMDSVFGTFPDEATQVAGAGDFFGAVDYEGR  
REATTDPAWFDVARRLQPEGDGPYTWWTYRGKAFDTGAGWRIDYQAATAAMLERASWV  
DKAAAYDLRWSHSPNLNVIYS

>RXN01389tr TRANSLATE of: rxn01389.seq check: 5202 from: 1 to: 684  
QDGDKLAGRHGNGKGVVGKILPQKDMFPLPDGTPVDIILNTHGVPRRMNIGQVLETHLWL  
ASAGWSVDPEDPENAEVLKTLPADLLEVPAGSLTATPVFDGASNEELAGLLANSRPNRDG  
DVMVNADGKATLIDGRSGEPYPYPVSIGYMYMLKLHHLVDEKIHARSTGPYSMITQQPLG  
GKAQFGGQRFGEVWAMQAYGAAYTLQELL